GenCore version 4.5 Copyright (c) 1993 - 2000 Comp

Compugen Ltd

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Result
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Maximum Match 100%
Listing first 45 summaries
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13.589 Million cell updates/sec
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Bcl2 polypeptide B
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Mutant Bcl-XL/Bcl-
Mutant BCL-XL/Bcl-
Mutant BCL-XL/Bcl-
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ABB52836	AAG25576	AAG54028	AAG54679	AAG54029	AAG25577	AAG54030	AAG25578	AAG25217	AAG25218	AAG25219	AAB70380	AAB70379	AAB37029	AAY05421	AAB37028	AAY05422	AAR95163	AAB70371	AAY96321	AAW61322	AAW61321	AAW61320	AAW61319	AAR95166	AAG67688	AAB48287	AAB70368	AAB13512	AAW55779	AAW32476	022	AAB70369	AAW58832
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## ALIGNMENTS

PT	UR.	P X	PA	PR	ХХ	X PD	XX	X	20	××	X	K K	KW	ΚW	XE	X	7 3	¥ č	×	Ħ	RESULT AAB37055
New peptide conjugates for modulating apoptosis or for inhibiting B	WPI; 2000-679325/66.	Huang Z, Wang J, Zhang Z, Shan S, Lu Z;	(UYJE-) UNIV JEFFERSON THOMAS.	07-APR-1999; 99US-0128202.	06-APR-2000; 2000WO-US09352.	12-OCT-2000.	WO200059526-A1.		Homo sapiens,	stroke; myocardial infarction.	melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;	apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;	cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;	Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;	Bcl2 polypeptide BH3 domain peptide #55.		28-FER-2001 (first entry)	AAB3/055;		AAB37055 standard; peptide; 28 AA.	LT 1 7055

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RESULT
AAB37056
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treating neurodegenerative disorders, stroke, or cancer -
                                                                                                                                                                                                                                                                                                       Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB37056 standard; peptide; 27
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                                                                                  07-APR-1999;
                                                                                                                         06-APR-2000; 2000WO-US09352
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                                         (UYJE-) UNIV JEFFERSON THOMAS
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  Wang J,
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  Zhang Z,
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WPI;
2000-679325/66
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treating neurodegenerative disorders, stroke, or cancer ptide conjugates for modulating apoptosis or for inhibiting B ymphoma/leukemia 2 (Bol-2) function, especially useful for

Claim 18; Page 19; 74pp; English.

CC (RX)n-peptide where n = 1:10; X = C=0, when the R-X group is attached cc to the Nterminus of the peptide, or a side chain of the peptide where cc the functional group of the side chain is NH2 or OH, or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, or a cc side chain of the peptide, where the side chain functional group is COOH cor COOH2; and R = 2:18C alkyl or alkoxy, 2:14C alkylsely containing one cc when the R-X group is COOH cc rtwo double bonds, cyclobutyl, cyclopentyl, cyclobexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group or benzyl. The peptides ABAS7001-B37058 represent examples cc fit peptide portion of the conjugate. The peptides represent analogues cc of a Bc1-2 superfamily polypeptide corresponding to amino acids 72-97 of ct the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for creversing B cell lymphoma/leukemia 2 (Bc1-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bc1-2 con-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or conjugate is also useful for treating a cute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

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                 1 KNIWAAQRYGRELRRMSDEFEGSFKGL 27
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27; Conserv
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RESULT AAB37001 W

AAB37001 standard; peptide; 26 ۶

Bcl2 polypeptide BH3 domain peptide #1. 28-FEB-2001 (first entry)

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bc1-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; stroke; myocardial melanoma; lymphocytic leukemia; neurodegenerative colorectal; odulation; B cell lymphoma/Leukemia 2; cancer; prostate; gastric; non-small lung; renal; thyroid; neuroblastoma; ymphocytic leukemia; neurodegenerative disorder; AIDS; infarction.

Homo sapiens.

WO200059526-A1

06-APR-2000; 2000WO-US09352

07-APR-1999; 99US-0128202

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AAB37002
ID AAB
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(R X)n-peptide where n = 1-10; X = Ce-0, when the RX group is attached to the N-terminus of the peptide, or a side chain of the peptide where ct the functional group of the side chain of the peptide, or a side chain of the peptide of the cannothed chain alkyl group, or benzyl. The peptides AB37001 Paptides represent analogues of the peptide of the conjugate is set of the peptide on the conjugate. The peptide conjugate is confused that a some that a subject, or for the side of the peptide of the conjugate is confused that a some that a subject, or for constitution of the conjugate is useful for modulating apoptosis in the cells of a subject, or for confused afflicted with a cancer conjugate is useful for treating a conjugate afflicted with a cancer characterized by cancer cells that cancer characterized by cancer cells t
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                                                                                                                                                                                             Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphome/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphomytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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RESULT
AAB37003
ID AAB3
XX
XX
AC AAB3
AC AAB3
AC BC12
XX
XX
BC12
XX
XX
BC18
KW CS1C
KW CS1C
KW CS1C
KW GS1C
KW GS1C
XX
XX
AC AB3
AC AAB3
AC AC AAB3
AC
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                                                                                              Cytostatic: neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bci-2 superiamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/Leukemia 2; cancer: prostate; colorectal: gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
    Homo sapiens
                                                                                                                                                                                                                                                                                                             Bcl2 polypeptide BH3 domain peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                         stroke; myocardial
                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2001
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The invention relates to a peptide conjugate having the formula:

(C (RX)n peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the spetide, or a side chain of the peptide, or a side chain functional group is attached to the C-terminus of the peptide, or a side chain functional group is containing one conformation of the peptide, where the side chain functional group is COOH COOHEZ; and R = 2-BC alkyl or alkoxy, 2-14C alkylenyl containing one correctly and R = 2-BC alkyl or alkoxy, 2-14C alkylenyl containing one correctly and the peptide, or a consubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides anabyroll-B37058 represent examples of the peptide portion of the conjugate. The peptides represent examples cof a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist BHd. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 subject afflicted with a cancer characterized by cancer cells that carner should be conjugate is subject to the cancer includes prostate, colorectal gastric conjugate is also useful for treating a cute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by concered apoptosis, e.g. neurodegenerative disorders, acquired conjugate is also useful for treating a subject afflicted with a cancer characterized by concered apoptosis, e.g. neurodegenerative disorders characterized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bel-2) function, especially useful for treating neurodesenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYJE-) UNIV JEFFERSON THOMAS
immunodeficiency syndrome (AIDS), stroke or myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US09352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; 74pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shan
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AAB37003 standard; peptide;
                                              1 nlwaagrygrelrrmsdefegsfkgl 26
                                                         2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                              Similarity
                                                                                     Conservative
                                                                                            93.2%;
                                                                                     0;
  27
                                                                                             Score 138;
Pred. No.
                                                                                     Mismatches
                                                                                              3.2e-14;
                                                                                                        DB
                                                                                                        21;
                                                                                                        Length 26;
                                                                                      0,
                                                                                      Gaps
                                                                                       0;
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(first entry)

26 AA;

В 8

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RESULT
AAB703
ID AAB7
XX
AC AAB7
XX
DT 02-W
DT 02-W
XX
EN Shor
XX
EN Shor
XX
Under Sho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a peptide conjugate having the formula:

(C (R/N) repetide where n = 1-10; X = C-0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where c the functional group is peptide, or a side chain of the peptide where side chain of the peptide, or a conversal peptide.

CC side (hain of the peptide, where the side chain functional group is COOH or county; and R ~ 2-18C sixyl group.

CC or county; and R ~ 2-18C sixyl or alkoxy, 2-14C sixylenyl extraining one consubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptide with a 1-5C straight or branched chain sixyl group, or benzyl. The peptide with a 1-5C straight or branched chain alkyl group, or benzyl. The peptide corresponding to amino acide 72-97 of the peptide portion of the conjugate. The peptides represent analogues of the peptide sortion of the coll death agonist Bad. The peptide conjugate is confused the side of the peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell importal televanta? (Bel-2) mediated blockage of subject afflicted with a cancer characterized by cancer cells that corresponding to the conjugate is useful for treating a collect afflicted with a cancer characterized by cancer cells that conjugate is a server afflicted with a cancer characterized by cancer cells that conjugate is a server afflicted with a cancer characterized by cancer cells that conjugate is a server afflicted with a cancer characterized by cancer cells that conjugate is a server afflicted with a cancer characterized by cancer cells that conjugate is a server afflicted with a cancer characterized by cancer cells that conjugate is a server and conjugate is a server and conjugate i
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Best Local S
Matches 26
immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiivital; antiaritritic; antiivitalmamatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
                                                                                                          Bcl-XL/Bcl-2 associated cell death regulator; BAD;
                                                                                                                                                                                  Shorter
                                                                                                                                                                                                                                                       02-MAY-2001
                                                                                                                                                                                                                                                                                                                           AAB70370
                                                                                                                                                                                                                                                                                                                                                                                               AAB70370 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (pdl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                  murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-US09352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,
                                                                                                                                                                          BAD mutant amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0128202
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                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 138;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 3.4e-14;
ches 0;
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                                                                                                                                                                              SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 27;
                                                                                                          mutant; apoptosis;
                                                                                                                                                                              NO: 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT AAR95168

AAR95168 standard; Protein;

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DЬ Ş

86

2 NLWAAQRYGRELRRMSDEFEGSFKGL nlwaaqrygrelrrmsdefegsfkgl 123

27

0;

06-JAN-1997 AAR95168

(first entry)

Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke, polypeptide; bcl-x; cell death; regulate; BH2; apoptotic cell death cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

bcl-x(L)/bcl-2 associated death promoter protein.

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The present invention describes an isolated or synthetic polypeptide (I) comprising a less than full length andino acid sequence of a mutant CC Enlance: a secolated cell death regulator polypeptide (BAD) or list fragment, which contains amino acid substitutions at Serill 0 of a human CC BAD (Serils of a murine BAD). (I) has immunostimulant, neuroprotective, nootropic, antisischaemic, vulnerary, cytostatic, antiviral, can be used as an apoptosis inducer or inhibitor. BAD plypeptides and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and compounds and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and compounds and drugs of continuous can be used for screening candidate compounds and drugs of continuous can be used for screening candidate compounds and drugs of conducting or inhibiting apoptosis in a cell. Candidate compounds cell survival or apoptosis. Other uses inducting or inhibiting apoptosis in a cell. Candidate compounds conducting or inhibiting apoptosis in a cell candidate compounds conducting or inhibiting apoptosis in a cell candidate compounds conducting or inhibiting apoptosis in a cell candidate compounds conducting or inhibiting apoptosis in a cell candidate compounds conducting or inhibiting apoptosis in a cell candidate compounds conduction or cell death, reperfusion cell death, wound healing, cancer, viral infections, inflammation and cutolimune diseases. The present sequence represents a specifically conduction of conduction and present appears of the present sequence represents a specifically conduction.
                                                   Best Local
          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Seril8, Seri35 or Seri13 -
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (APOP-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autolmmune disease.
similarity 100.
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APOPTOSIS TECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 148-149; 157pp; English
                                                                                                                                                                                                                         162
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                                              93.2%; Score 138; 100.0%; Pred. No.
     0;
          Mismatches
                                         DB 22;
2.4e-13;
          0
                                                                                  Length 162;
     0;
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RESULT
AAW61315
ID AAW6
XX
AC AAW6
AC AAW6
XX
DT 07-0
XX
DE Muri
                                                                                                                                                                 В
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                           This sequence represents the murine bcl-x(l)/bcl-2 associated death promoter (Bad) gene. Bad is a 22.1 kb protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2 related family clustered in the BH1 and BH2 domain. Bad has been found to hybridise to bcl-x(l) and bcl-2 in yeast two-hybrid eastsys and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of bcl-2. Bad expression can accelerate apoptotic cell death induced by cytokine deprivation in an II-3 dependent cell line expressing bcl-x(L). Bad expression counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad and be used to identify agents which inhibit its binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-2 or bcl-x(L) to form heterodiners. Such agents may be used to treat neurodegenerative diseases, immunodeficiency diseases,
                                                                                                                                                                                                                                                                                                                  e.g. AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Fig 1; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide encoding bcl \cdot x(L)/bcl \cdot 2 associated death promoter necting to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl \cdot 2 or bcl \cdot x(L) to form heteromultimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Korsmeyer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurodegenerative disease; senescence; ischaemia; neoplasia
             Murine BCL-XL/BCL-2 associated cell death regulator
                                                                                                                                                                                                                                                                                        Sequence
                                       07-OCT-1998 (first entry)
                                                                                              AAW61315 standard; Protein; 204
                                                                    AAW61315;
                                                                                                                                                                 140
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                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                          204
                                                                                                                                                                                                                                                                                                                    senescence
                                                                                                                                                                                                                       Conservative
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38..61
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191..192
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                                                                                                                                                                                                                                   93.2%;
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                                                                                                                                                                                                                                                                                                                    ischaemia.
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                     Score 138; DB 17; 
; Pred. No. 3.2e-13;
                                                                                                                                                                                                                       Mismatches
                                                                                               2
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                               Length 204;
                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                       Gaps
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell clearly regulator) proteins, having an amino acid other than Ser at C death regulator) proteins, having an amino acid other than Ser at C position 112 and/or 136, relative to the murine BAD 204 as sequence. The position in 112 and/or 136, relative to the murine BAD 204 as sequence. The Cream of mutant BAD protein able to decrease cell viability (2) tusion proteins of mutant BAD protein able to decrease cell viability. (2) CC fusion proteins of mutant BAD with a heterologous polypeptide that corprevent diseases associated with reduced apoptosis, e.g. cancer. Inflammation and autoimmune disease. Polypucleotide sequences encoding utant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD creatines phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is caping or ischaemic cell death. The apoptotic status of cells is companied by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have phosphorylated on the specified Ser, forming a product that does not become companied to the promoting activity than willd-type BAD which can become companied to the proteins in the cytosol, thus promoting cell survival. The mutants with cc ser substituted cannot bind 14-3-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 10; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viral infection
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DB; AAV27833.
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Sequence
                                          204
       93.2%;
       Score 138; DB 19
Pred. No. 3.2e-1
DB 19;
3.2e-13;
hes 0;
                 Length 204;
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AAW61316
ID AAW
                                                    밁
AAW61316 standard; Protein;
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                                                               2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                  9
                                                   nlwaagrygrelrrmsdefegsfkgl 165
204
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Matches Query Match Best Local

l Similarity 26; Conser

Conservative

0

Mismatches

Indels

0; Gaps

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07-OCT-1998 (first entry)

Mutant BCL-XL/BCL-2 associated cell death regulator #1.

Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

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ARMSIJIT 10
AAMSIJ
ID AAWSIJ
XX
AC AAWSIJ
XX
DT 07-OCT
XX
DE Mutant
XX
KW Murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell C death regulator) proteins, having an amino acid other than Ser at C position 112 and/or 136. relative to the murine BAD 204 as sequence. The position 112 and/or 136. relative to the murine BAD 204 as sequence. The CC present sequence represents a mutant BAD protein. Also described are: (1) CC fusion proteins of mutant BAD protein BAD protein. Also described are: (2) further of the second of the secon
                                                                                                                                                                                                                                                                                                                                                                                   Matches
Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein
                                               Mutant BCL-XL/BCL-2 associated cell death regulator #2.
                                                                                              07-OCT-1998
                                                                                                                                          AAW61317;
                                                                                                                                                                                    AAW61317 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
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N-PSDB; AAV27834.
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                                                                                                                                                                                                                                                                                             2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                 Similarity 100.
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA;
                                                                                        (first entry)
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                                                                                                                                                                                    Protein;
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                                                                                                                                                                                    204
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                                                                                                                                                                                                                                                                                                                                                                                 Score 138; DB 19;
Pred. No. 3.2e-13;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 204;
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell clearly regulator) proteins, having an maino acid other than Ser at costino 112 and/or 136, relative to the murine BAD 204 as sequence. The position 112 and/or 136, relative to the murine BAD 204 as sequence. The cost increases intracellular delivery. Mutant BAD protein. Also described are: (1) fusion proteins of mutant BAD protein able to decrease cell visbility; (2) fusion proteins of mutant BAD protein BAD by the heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, cillamation and autoimmune disease. Polymucleotide sequences encoding inflammation and autoimmune disease. Polymucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD can dinhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, can dinhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, cased in treatment of excessive apoptosis such as AIDS, neurodegeneration, cased to excessive apoptosis such as AIDS, neurodegenerati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 60; 95pp; English
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Sequence
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N-PSDB; AAV27835.
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204 AA
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DB 19;

Length 204;

0;

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AAW61318
                  RESULT 11
                                                                              Query Match
Best Local Similarity
Matches 26; Conserv
AAW61318 standard;
                                           93.2%;
ilarity 100.0%;
Conservative
Protein;
                                                                               0;
                                                                                      Score 138;
Pred. No.
                                                                               Mismatches
                                                                              . 2e-13;
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07-OCT-1998 (first entry)

XXEXEXXXX Mutant BCL-XL/BCL-2 associated cell death regulator #3

Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

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RESULT
AAW58832
ID AAW
XX
XX
AC AAW
AC AAW
AC AAW
XX
XX
DT 23--
XX
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XX
XX
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Best Local s
Matches 26
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N-PSDB; AAV27836.
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    BAD protein; Bcl-XL/Bcl-2 associated
                                       Murine BAD
                                                                               23-JUL-1998
                                                                                                                       AAW58832;
                                                                                                                                                             AAW58832 standard; protein;
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                                                                                                                                                                                                                                                              140
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                                                                                                                                                                                                                                                         nlwaaqrygrelrrmsdefegsfkgl 165
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                                                                                                                                                                                                                                                                                                                                       oh 93.2%;
l similarity 100.0%;
26; Conservative
                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                           204
                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                       9; Pred. No. 3.2
0; Mismatches
                                                                                                                                                             204
    cell death regulator; 14-3-3;
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                                                                                                                                                                                                                                                                                                                                                                               DB 19;
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Best Local 9
                   immunostimulant; neuroprotective; nootropic; antiischeemic; vulnerary cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; repertusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                      02-MAY-2001
                                                                                                                                                                                                                                                              AAB70369;
                                                                                                                                                                                                                                                                                                 AAB70369 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                      Bcl-XL/Bcl-2 associated cell death regulator; BAD;
                                                                                                                                                                              Longer murine BAD mutant amino acid sequence SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                   140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer and
                                                                                                                                                                                                                                                                                                                                                                                                niwaagrygreirrmsdefegsfkgl 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 8; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0707868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US15871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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В Q

mutant; apoptosis;

vulnerary; ind healing;

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serine phosphorylation; post-translational modification; apoptosis; signal transduction regulator; phosphoserine phosphatase; senescence immunodeficiency disease, neurodegenerative disease; infertility; cancer, vital infection; lymphoproliferative condition; arthritis; inflammation; autolimnue diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Bcl-X1/Bcl-2 associated cell death regulator). The serine residue is phospory lated in a post-translational modification and allows binding to the 14-3-3 protein which is a signal transduction regulator. Modulators of phosphory lated BAD, which act through inhibition activation of a phosphoserine phosphatase, are useful for preventing/treating increased/decreased apoptosis in a cell. The increased apoptosis may result from immunodeficiency diseases, senesscence, neurodegenerative disease, senesscence, and least transfer in the increased apoptosis may result from immunodeficiency diseases, senesscence, neurodegenerative disease, senesscence, neurodegenerative
                                                                                                                                                                                                                                                                                                                 disease, ischaemic cell death, reperfusion cell death, infertility and wound-healing. Decreased apportosis may result from cancer, viral infection, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. Measuring the amount of phosphorylated and polypeptide and/or total BAD in a cell is useful for determining the apoptotic state of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine-phosphorylated Bcl-X-1/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents a novel serine-phosphorylated protein, BAD associated cell death regulator). The serine residue is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunodeficiency diseases
                                   Score 138;
Pred. No.
Mismatches
                                         DB 19;
3.2e-13;
     0
                                                                                         Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             senescence;
0
Gaps
0;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an isolated or synthetic polypeptide (1) comprising a less than full length makno acid sequence of a mutant CC Sci. XL/Bci. 2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Seril3 of a human EC BAD (Shorter murine BAD). (1) has immunostimulant, neuroprotective, notropic, antiischaemic, vulnerary, cytostatic, antiviral, endough and poptosis inducer or inhibitor. BAD plypeptides and can be used as an apoptosis inducer or inhibitor. BAD plypeptides and polynucleotides can be used for screening candidate compounds and drugs for activity that promote cell survival or apoptosis. Other uses include continuous gor inhibitor, apoptosis in a cell. Candidate compounds continuous gor inhibitor, and poptosis in a cell. Candidate compounds continuous gor inhibitor, and poptosis in a cell. Candidate compounds continuous gor inhibitor, and poptosis in a cell. Candidate compounds continuous gor inhibitor, and poptosis in a cell. Candidate compounds continuous gor inhibitor, and poptosis in a cell. Candidate compounds continuous gor inhibitor, and continuous cell death, reperfusion cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and subclammate diseases. The present sequence represents a specifically content of the present content 
                                                                                                                                                                                                                                                                                                                                                                                 Best Local
                                                                                                                                                                                                                                                                                                                                                                   Matches
   Chimeric
                                     diphtheria toxin, apoptosis; cancer; spinal muscular atrophy; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; sninal mandian disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Seril8, Seril5 or Seril3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI:
                                 Huntington's disease
                                                                                                                              Bad-DTTR apoptosis-modifying
                                                                                                                                                             31-MAY-2001
                                                                                                                                                                                             AAU00220:
                                                                                                                                                                                                                           AAU00220
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 148; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (APOP-) APOPTOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-2001
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Synthetic.
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                                                                                                                                                                                                                           standard;
 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                204 AA;
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US11864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9908-0136783
                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                 93.2%;
                                                                                                                                                                                                                                                                                                                                                                 Score 138; DB; Pred. No. 3.2
                                                                                                                                                                                                                           567
                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                            fusion
                                                                                                                              protein.
                                                                                                                                                                                                                                                                                                                                                                           3.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                              Length 204;
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                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                               Gaps
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AAW32476
ID AAW3
XX
AC AAW3
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DT 15-J
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BBC6
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                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                              RESULT
BBC6 protein for regulating cell death
                                 15-JAN-1998
                                                               AAW32476;
                                                                                              AAW32476
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15

standard;

Protein;

166 A

Gaps

0

(first entry)

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cc linker to diphtheria toxin translocation domain (DTTR). The functional apoptosis-modifying fusion protein is capable of binding a ct target cell and integrating into or crossing a cellular membrane of the ct target cell. The apoptosis-modifying fusion protein comprises at least two domains: the DTR domain, which targets the fusion protein to the two domains: the DTR domain, which targets the fusion protein to the ctarget cell and the Bcl-XL domain, which modifies an apoptocic response of the target cell. The fusion protein is useful for modifying confidence, neoplasm, macrophage, epitherial, stem, tumour or lymphocyte, cancer, neoplasm, macrophage, epitherial, stem, tumour or hyper-proliferative cell or an adipocyte. It is also useful for reducing apoptosis in a subject after translent ischaenic neuronal injury. The fusion protein may be used to treat various diseases and injury conditions through inhibition or enhancement of apoptotic cellular response, including neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, spinal muscular autophy, stroke episodes and unregulated cell growth as in tumours and effectively throughout the body and targeted to selective tissue and
                                                                                                              Matches
                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents the amino acid sequence of Bad-DYTR modifying fusion protein comprising Bad gene sequence fused linker to diphtheria toxin translocation domain (DTTR). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 59-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel fusion protein for modifying apoposis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      кеу
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Chimeric -
                                                                                                                                                                                                                                                                                                cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Youle RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-218343/22
DB; AAS00248.
                                                                                                           26;
                                                                                                           Similarity 100
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium diptheriae 
Synthetic.
                                                                                                                                                                                                                                             567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
3.,12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collier
                                                                                             93.2%; ---
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "10x histidine
                                                                                                    ; Score 138; DB
b; Pred. No. 9.8
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tag"
                                                                                                       . 9.8e-13;
ches 0;
                                                                                                                                                                DB 22;
                                                                                                                                                          Length 567;
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis-
via a short
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Search completed: September 20, 2002, 10:35:59 Job time: 427 sec
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                                                                                             οy
                                                                                                                          Query Match 77.0%;
Best Local Similarity 91.7%;
Matches 22; Conservative
                                                                                                                                                                                                                   The present sequence represents a protein of 166 amino acids. The sequence is disclosed as being a protein called BB06 which regulates cell death through interaction with BC1-2. The DNA may be used for the production of the recombinant protein, which can be used in unspecified therapeutic or diagnostic procedures, as a molecular weight marker, and to raise antibodies that can be used in unspecified diagnostic or therapeutic applications and to reduce or eliminate the biological activity of the BBC6 protein in vivo.
                                                                                                                                                                                                                                                                                                                                                Claim 1; Column 11-12; 7pp; English.
                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-447980/41.
N-PSDB; AAT91561.
                                                                                                                                                                                                                                                                                                                                                                               Isolated BBC6 gene - encodes a protein that regulates cell death through interaction with Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-SEP-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5663316-A.
                                                                   (CLON-) CLONTECH LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BBC6 gene; cell death; cell cycle; Bcl2; human.
                                                                                  2 NLWAAQRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                166 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0665617.
                                                                                                                     Score 114; DB 18; Length 166; Pred. No. 1.2e-09; 0; Mismatches 2; Indels
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GenCore version 4.5 Copyright (c) 1993 - 2000 Com

Compugen

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27, Appl
18, Appl
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40, Appl
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40, Appl
40, Appl
170, Appl
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Sequence

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Minimum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/2.

2: /cgn2_6/ptodata/2.

3: /cgn2_6/ptodata/2.

4: /cgn2_6/ptodata/2.

5: /cgn2_6/ptodata/2.

6: /cgn2_6/ptodata/2.
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Match
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148
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/cgn2_6/ptodata/2/iaa/5a_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5a_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6a_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6a_COMB.pep:*
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US-08-61-1479-2
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US-08-73-505A-5
US-08-73-705A-7
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sequence 2, Appli
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sequence 37, Appli
sequence 38, Appli
sequence 39, Appli
sequence 30, Appli
sequence 31, Appli
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US-08-333-565-2
; Sequence 2, Ap
; Patent No. 562
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE:
COMPUTER: Eloppy disk
COMPUTER: FLAM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTMARE: PSTEMIC FOR PLANCE
SOFTMARE: PSTEMIC FOR PLANCE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,565
FILING DATE: 31-027-194
CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: SMILH. WILLIAM M
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 30,23
REFERENCE/DOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVPLICANT: KORSHEYER, Stanley J.
TITLE OF INVENTION: Bc1-x/Bc1-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourle and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
COUNTRY: Calliornia
COUNTRY: US
                                                                                                                             us-08-333-565-2
         Query Match
Best Local S
Matches 26
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                                                                                                                                               FEATURE:

NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
         y Match 93.2%; Score 138; DB 1;
Local Similarity 100.0%; Pred. No. 1e-13;
hes 26; Conservative 0; Mismatches 0
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of mouse BAD."
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US-08-497-312-19
US-08-718-738-18
US-09-718-738-18
US-09-718-738-18
US-09-718-738-18
US-09-718-738-18
US-09-718-738-18
US-09-718-738-18
US-08-997-180-79
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         Indels
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Gaps

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RESULT 3
US-08-733-505A-
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                                                                                                                                                                                                                                                                                                                                                                                                                           : NAME/KEY: Protein
LOCATION: 1.204
OTHEN INFORMATION: /note= *Deduced amino acid sequence
OTHER INFORMATION: of mouse BAD.*
US-08-661-479-2
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Sequence 1. Application US/08733505A

PATENT NO. 5856445

GENERAL INFORMATION:
APPLICANT: KORSHEYER, STANLEY J.

TITLE OF INVENTION: SERVINE SUBSTITUTED MUTANTS OF

TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                             Ouery March 93.2%; Score 138; DB 2; Length 204; Best Local Similarity 100.0%; Pred. No. 1e-13; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEGAX: (415) 36-342 INFORMATION FOR SED ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 204 amino acids TYPE: amino acids STRANDENESS: single Single TOPOLOGY: linear MOLECULE: TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08661479 Patent No. 5834209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Pateolin Release #1.0, Ver
GURRENT APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-195
CLASSIFICATION HUMBER: US/08/33,565
PRIOR APPLICATION NUMBER: US/08/33,565
PRIOR APPLICATION NUMBER: US/08/33,565
PRIOR APPLICATION NUMBER: 30,723
REGISTRATION NUMBER: 30,723
REGISTRATION NUMBER: 30,723
REGISTRATION NUMBER: 15726A-0007
TELECOMMUNICATION IMPORMATION:
REFERENCE/DOCKET NUMBER: 15726A-0007
TELECOMMUNICATION IMPORMATION:
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                                                                                                                                                                                                                     APPLICANT: KORSHEYER, Stanley J.
TITLE OF INVENTION: BC1-X/BC1-Z ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESSPONDENCE ADDRESS;
ADDRESSPONDENCE ADDRESS;
ADDRESSPONDENCE ADDRESS;
ADDRESSPON TOWNSEND and Townsend Khourie and Crew
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Best Local S
Matches 26
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-733-505A-1
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ATTORNEY/ACENT INFORMATION:
NAME: NOLLAND DONALD R.
REGISTRATION NUMBER: 35.197
REFERENCE/DOCKET NUMBER: 9554
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314) 727-5188
TELEPHONE: 314) 727-692
INFORMATION FOR SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
FEVERIA: 704 ANNION 20148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08733505A
Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patcntin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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MEDIUM TIPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
                                 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESSE: HOWELL & HAFERKAMP, L.C.
ADDRESSEE: 17733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL 6 HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KORSMEYE TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 NIWAAQRYGRELRRMSDEFEGSFKGL 165
REFERENCE/DOCKET NUMBER: 96
                                                                                                                                                                                                                                                                                                                    CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
nes 26; Conservative
                                                                                                                                    APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                             ZIP: 63105
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                 USA
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VENTION: SERINE SUBSTITUTED MUTANTS OF
VENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
EQUENCES: 60
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100.0%; Pred. No. _
110e 0; Mismatches
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Pred. No. le-13;
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                                                       Matches
                                                                     Best Local
                                                                                  Query Match
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                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KORSMEYE TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                        TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: HOLLAND, DONALD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
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nes 26; Conserv
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                                                                                                                                                                     STRANDEDNESS
                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                LENGTH:
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               2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
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                                                                     Similarity
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                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                       Conservative
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                                                                                                                                                                                                amino acids
                                                                                                                                      peptide
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NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SERINE SUBSTITUTED MUTANTS OF BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.2%;
                                                                   93.2%;
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                                                                                                                                                                                                                                                                                              35, 197
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                                                                                                                                                                                                                                                                                  965458
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Pred. No. 1e-13;
                                                     0;
                                                                   Score 138; DB 2;
Pred. No. 1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUITE 1400
                                                     Mismatches
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                                                                                  DB 2; Length 204;
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RESULT

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US-08-733-505A-14
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; Patent No. 5965703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (314) 727-6092 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD
TITLE OF INVENTION: Acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 NLWAAORYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 7733 FO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               COUNTRY: U
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                     STATE:
                                                                                                                                                                   CITY: San Diego
                                                                                                                                                                                   ADDRESSEE: Campbell and Flores STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
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                                                                                                                                                                                                                                                                                                                                                                               Application US/08717123
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                                                                                                                                                   California
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7733 FORSYTH BLVD., SUITE 1400
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VUNTION: SERINE SUBSTITUTED MUTANTS OF
VENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                              United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                        Horne, William A.
                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.2%; Score 138; DB 2; 100.0%; Pred. No. 1e-13;
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    Mismatches

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                                                                                                                  ; MOLECULE TYPE: protein US-08-665-617-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-717-123-3
                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08665617
Patent No. 5663316
GENERAL INFORMATION:
                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                   TELEFAX: (352) 372-5800 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sallwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Xudong, Yin
TITLE OF INVENTION: GeI
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
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NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sallwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville
                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 32606
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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 2 NIWAAQRYGRELRRMSDEFEGSFK 25
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                                   Conservative
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                                                                                                                                                    linear
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                                                                                                                                                              single
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                                                 77.0%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                       us/08/665,617
                               Score 114; DB 1; L
Pred. No. 3.7e-10;
""""" tches 2;
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Pred. No. 2.9e-13;
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                                                               Length 166;
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RESULT 10
US-08-985-335-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P-ID
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS: 2:
SEQUENCE CHARACTERISTICS: 2:
LENGTH: 168 amino acids
                                                                                                                                                                                            Patent No.
GENERAL I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08717123 Patent No. 5965703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                 APPLICANT: Hillman, Jennifer
APPLICANT: Yue, Henry
APPLICANT: Lal, preti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEIN:
TITLE OF INVENTION: PROTEIN:
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Horne, William A. APPLICANT: Oltersdorf, Tilman
                                                                                                                                                                                                                                                                                                   103 NLWAAQRYGRELRRMSDEFVDSFK 126
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                                                                                                                                                                                                                                                                                                                                                   77.0%;
Local Similarity 91.7%;
nes 22; Conservative
                            STREET:
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STATE: Californ
STATE:
                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             2 NLWAAQRYGRELRRMSDEFEGSFK 25
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                                                                                                                                                                                            INFORMATION:
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              Palo Alto
                                                                                                                                                                                                                          Application US/08985335
CA
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                          E: Incyte Pharmaceuticals, 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States
                                                                                                                                                                              Hillman, Jennifer L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                   PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human BAD Polypeptides, Encoding Nucleic Acids and Methods of Use
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Pred. No. 3.8e-10;
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COUNTRY:

USA

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US-08-985-335-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Apprint No. 6080847
                                              ZIP: 94304
COMPUTER READABLE FORM:
CMEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: MAPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
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Best Local Similarity 91.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                        APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEI
TITLE OF INVENTION: PROLIF
TUTLE OF SEQUENCES: 9
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/9)
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 NLWAAQRYGRELRRMSDEFVDSFK 126
                    FILING DATE:
                                    APPLICATION NUMBER:
                                                                                                                                                                                                      COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                                                         STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NLWAAQRYGRELRRMSDEFEGSFK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i: 168 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08985335
                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                               Yue, Henry
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Pred. No. 3.8e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                   TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                               TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
             TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: COLLEY, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                         STRANDEDNESS:
                                                       TYPE: amino acid
                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 POI
CITY: Palo Alto
                                                                                                                             TELEPHONE:
                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NLWAAQRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                      94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Billings, Lucy
                                                                                                                                                                                                                                                                                                                                                                                                                CA
                                                                  168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 amino acids
                                                                                                                 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                  USA
SYNORAB01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                          linear
                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                     Diskette
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                                         single
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91.78;
                                                                                                                                                                                                                                 08/985,335
                                                                                                                                                                                                                                                                             US/09/410,372
                                                                                                                                                        36,749
ER: PF-0421 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No. 3.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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US-09-410-372-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.0%;
Best Local Similarity 91.7%;
Matches 22; Conservative
                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 7, Application US/09410372
Patent No. 6281334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASICED FOR WINDOWS Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION NUMBER: 08/985,335
APPLICATION NUMBER: 08/985,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 1683637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: COTLEY, Neil C.
TITLE OF INVENTION: PROTIETATION ASSOCIATION: PROLIFERATION
UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 NLWANGRYGRELRRMSDEFVDSFK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                               Local Similarity
mes 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NLWAAQRYGRELRRMSDEFEGSFK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Incyte Pharmaceuticals, Inc
3174 Porter Dr.
                                                                                                                                                                                                                                                          168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yue, Henry
                                                                 Conservative
                                                                                                                                                                               GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillman, Jennifer L.
                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                          650-855-0555
                                                                                                                                                                                                                             single
                                                                             77.0%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 114; DB 4; Length 168; Pred. No. 3.8e-10; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                          PF-0421 US
                                                                               Score 114; DB 4;
Pred. No. 3.8e-10;
                                                                                            Length 168;
                                                                 Indels
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RESULT 14

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US-08-333-565-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-661-479-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-333-565-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08661479 Patent No. 5834209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KORSME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS
SOFTWARE: Patentin Relac
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 31-OCT-1904
CLASSIFICATION: 435
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COmpatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DOS THE COMPATIBLE
COMPUTER: DOS THE COMPATIBLE
COMPUTER: DOS THE COMPATIBLE
COMPUTER: DOS THE COMPATIBLE
COMPUTER: COMPATIBLE
COM
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/661,479
APPLICATION NUMBER: US/08/661,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                STREET: 379 Lyt
CITY: Palo Alto
STATE: Californ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                     COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 NLWAAQRYGRELRRMSDEFEG 23
                                                                                                                                                                                                                                                           94301
                                                                                                                                                                                                                                                                                                                                California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KORSMEYER, Stanley J.
NVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                 379 Lytton Avenue
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IVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH

VENTION: REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                        Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.4%; Suc. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGULATOR
: 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                us/08/333,565
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Pred. No. 6.1e-11
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FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DUMBER: US 08/333,565
FILING DATE: 31.0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William REGISTRATION UNMBER: 30,223
REFERENCE/DOCKET NUMBER: 35.223
REFERENCE/DOCKET NUMBER: 15.726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2402
INFORMATION FOR SEO ID NO: 10:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
FYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: anino acids
TYPE: anino acids
TYPE: peptide
US-08-661-479-10

Ouery Match
Best Local Similarity 100.0%; Pred. No. 6.1e-11;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

OUER MATCHES 21; CONSERVATIVE 0; MISMATCHES 0; Gaps 0;

OUER MATCHES 21; CONSERVATIVE 0; MISMATCHES 0; Gaps 0;

OUER MATCHES 21; CONSERVATIVE 0; MISMATCHES 0; Gaps 0;

OUER MATCHES 22

DATE MATCHES 23

Search completed: September 20, 2002, 10:37:21

Job time: 409 sec
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Result
No.
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                       Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein -
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                     Score
                                                                                     48
47.5
47.5
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length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
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 Minimum Match 0%
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Gapop 10.0 , Gapext 0.5
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148
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28.146 Million cell updates/seo
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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pir3:*
pir4:*
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JC5575
D70760
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                                          oxaloacetate decar
oxoglutarate dehyd
hypothetical prote
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               Antho-RFamide prec
chlorocruorin chai
probable polyamine
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Ig kappa chain - h
annexin P35 - maiz
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floral homeotic pr
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neuropeptide Pol-R
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inter-alpha-trypsi
conserved hypothet
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### ALIGNMENTS

RESULT A55671

bad protein - mouse

C;Species: Mus musculus (house mouse)
C;Date: 03.Mar-1995 #sequence\_revision 03.Mar-1995 #text\_change 05.Nov-1999
C;Accession: A55671
R;Yang, E.: Zha, J.; Jockel, J.; Boise, I.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285.291, 1995
A;Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot A;Reference number: A55671; MUID:95136361
A;Accession: A55671
A;Accession: A55671
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-204 <XAN>
A;Cross-references: CB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779
C;Keywords: heterodimer

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 2 NIMAAQRYGRELRMXSDEFEGSFKGL 27  Qy 2 NIMAAQRYGRELRMXSDEFEGSFKGL 165  RESULT 2  JC5575  Itter-alpha-trypsin inhibitor heavy chain 2 - golden hamster C;Species: Mesocricetus auratus (golden hamster) C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000 C;Accession: JC5575, Pc4485  R;Nakatani, T; Suzuki, Y; Yamamoto, T; Sinohara, H.  J Biochem 122, 71-82, 1997 A;Fitle: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs sin inhibitor heavy chain family. J. Reference number: JC5574; MUJD:97420688 A;Accession: JC5575 A;Molecular type: mRNA A;Residues: 1-946 <nak> A;Residues: 1-946 <nak> A;Residues: 1-946 <nak> A;Residues: 1-946 <nak- #status="" 1-946="" 5-64;140-146;151-156;424-447;500-528;577-605="" <na2-="" <nak-="" a;residues:="" bonds:="" c;comment:="" complex="" component="" disulfide="" f;261-264,717-916="" ii="" in="" inhibitor="" inter-alpha-trypsin="" plasma="" predicted<="" th="" the="" three=""><th>2%; Score 138; DB 2; Length 204; .0%; Pred. No. 1.2e-12;</th></nak-></nak></nak></nak>	2%; Score 138; DB 2; Length 204; .0%; Pred. No. 1.2e-12;
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C:Accession: D70760

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go.; Connor, R.; Davids, R.; Devlin, K.; Peltwell, T.; Gentles, S.; Hamlin, N.; Holri Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, S37-544, 1998

A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987

A; Accession: D70760
                                                                         S38185
                                                                                                                                                                                                                                                                                                                                                                                                       G:Species: Mus musculus (house mouse)
C:Date: 15-Utl-1995 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
C:Accession: S3434
R:Chan, P.; Risler, J.L.; Raquence, G.; Saller, J.P.
Blochem, J. 306, 505-512, 1995
Blochem, J. 306, 505-512, 1995
A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: A:Reference number: S34353; MUID:95194326
A:Accession: S34354
A:Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical
C;Species: My
C;Date: 17-Ju
                          2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Sa
N.Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase;
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A;Residues: 1-946 (CHA>
A;Cross references: EMML:X70392; NID:9695633; PIDN:CAAA9842.1;
A;Cross references: EMML:X70392; NID:9695633; PIDN:CAAA9842.1;
C;Superfamily: inter-mlpha-trypsin inhibitor complex component
                 C; Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:Z74025; GB:AL123456; NID:g3261586; A;Experimental source: strain H37Rv C;Genetics:
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Species: Mycobacterium tuberculosis
Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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Best Local Similarity
Matches 10; Conser
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nes 9; Conser
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hes 9; Conservative
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Pred. No. 11;
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II
                                                yeast (Saccharomyces
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floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana N;Alternate names: homeotic protein APETALA3; MADS-box regulatory C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21 C;Accession: A42095; S52633; T47593 R;Jack, T.; Brockman, L.L.; Meyerowitz, E.M. Cell 68, 683-697, 1992
                                                                                                                                             RESULT
A42095
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A;Cross-references:
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C;Comment: This enzyme catalyzes
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A; Residues: 1-370 < ALJ>
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A; Residues: 1-370 <DOI>
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Gene 113, 67-74, 1992
Gene 113, 67-74, 1992
A; Title: Cloning, primary structure and regulation of the ARO4
A; Title: Cloning, primary structure and regulation of the ARO4
A; Reference number: JN0322;
A; Accession: JN0322
A; Accession: JN03
                                                                                                                                                                                                                                 A;Description: aldehyde-lyase; carbon-carbon lyase A;Pathway: aromatic amino acid biosynthesis; shikimate pathway A;Nathway: aromatic amino acid biosynthesis; shikimate pathway C;Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase C;Keywords: aldehyde-lyase; aromatic amino acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W:DOIgnon, F.; Biteau, N.; Aigle, M.; Crouzet, M. Yeast 9, 1131-1137, 1993
A.Title: The complete sequence of a 6794 bp segment A:Reference number: S38185; MUID:94078675
A:Accession: S38185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Cloning, primary structure, and regulation A;Reference number: A48651; MUID:93374850 A;Accession: B48651
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A;Residues: 1-370 <AIG>
A;Residues: 1-370 <AIG>
A;Cross-references: EMBL: 236118; NID: 9536664; PIDN: CAA85212.1;
R:Kuenzler, M.; Paravicini, G.; Egli, C.M.; Irniger, S.; Braus,
Gene 113, 67-74, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Cross-references: EMBL:Z36118; NID:g536664; PIDN:CAA85212.1; FR:Algle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; submitted to the Protein Sequence Database, August 1994
A;Reference number: S45940
A;Accession: S46130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGD:S0000453; MIPS:YBR249c
                                                     Score 52; DB
Pred. No. 8.4;
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#text\_change 21-Jul-2000

protein AP3

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A; Molecule type: DNA
A; Residues: 1-23 < SLO>
A; Residues: 1-23 < SLO>
A; Cross-references: EMBL: AL132971
A; Experimental source: cultivar Columbia; BAC clone T12E18
C; Genetics:
C; Genetics:
A; Map position:
A; Map position:
A; Matp position:

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A;Experimental source: petals, stamens
A;Mote: sequence extracted from NCBI backbone (NCBIN:82520, NCBIP:82521)
R;Okamoto, H; Yano, A; Shiratishi, H; Okada, K.; Shimura, Y.
Plant Nol. Biol. 26, 465-472, 1994
A;Title: Genetic complementation of a floral homeotic mutation, apetala3, with an A;Reference number: $52633; MUID:95036018
A;Accession: $52633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:NG, R.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G. Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483
A:Accession: C84338
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C;Superfamily: transcription factor squa; serum response factor DNA-binding C;Keywords: DNA binding; nucleus; transcription regulation C;Keywords: DNA binding; nucleus; transcription regulation F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>
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A; Accession: T47593
A; Status: preliminary
                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE004437; NID:g10581314; PIDN:AAG20071.1; GSPDB:GN00138 C;Genetics:
A;Gene: potA2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-63 < OKA>
A; Cross-references: GB: D21125
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A; Residues: 1-232 < JAC>
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A; Residues: 1-374 <STO>
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C:Accession: C84338
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C; Species: Halobacterium sp. NRC-1
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Matches 12; Conserv
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Pred. No. 7.3;
3; Mismatches
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A; Molecule type: DNA
A; Residues: 1-516 <STO>
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A; Accession: A81393
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A; Gene: F3N23.1
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Matches 12
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RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughas, B.; Huizar, L. Rature 408, 816-820, 2000
A; Authors: Hunter, J.J.; Jonkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.R.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Liuros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Recession: A96753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable threonine synthase [imported] - Arabidopsis thaliana
C:Species .Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 *text_change 31-Mar-2001
                                                                                                                                             A;Gene: rpoB; Cj0478
C;Superfamily: DNA-directed RNA polymerase
C;Keywords: nucleotidyltransferase
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A; Residues: 1-1378 <PAR>
A; Cross-references: GB:AL139075;
A; Experimental source: serotype (
                                                                                                                                                                                                                                                                                                                                                                                                                                           C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; B. Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A;Reference number: A81250; MUID:20150912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE005173; NID:g5903070; PIDN:AAD55628.1; GSPDB:GN00141
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35.3%;
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Pred. No. 63;
3; Mismatches
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7; Mismatches
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R;Klein, R.; Jaenichen, R.; Zachau, H.G. Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi A:Reference number: $40312; MUID:94080891
A:Accession: $40376
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                                                                                                                                                       Ig kappa chain - human
C;Specles: Homo sapiens (man)
C;Date: 06 Mar-1994 #sequence_revision 26-May-1995
C;Accession: S40376
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C;Accession: E83517

R;Stover, C. K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, I; Lory, S.; Olson, M.V.

Nature 406, 959-954, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholication number: AB2950; MUID:20437337

A;Accession: E83517
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A;Molecule type: DNA
A;Molecule type: CIL>
A;Residues: 1-127 cGLA>
A;Cross-references: GB:MC_003210; PIDN:CAC99167.1; PID:g16410491; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
                                                                                                                                                                                                                                                                                    S40376
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A:Molecule type: DNA
A;Residues: 1-453 <STO>
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                    4 WAAQRYGR--ELRRMSDE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KNLWAAQR-----YGRELRRMSDEFEGSFKGLK 28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 49.5; DE; Pred. No. 6.6; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49; DB
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                  genes
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                                                                                                                                                                                #text_change 21-Jan-2000
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                                                                      their
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                  hypermutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1:
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Fsihi, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         annexin p35 - maire
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Species: Zeamays (maize)
C;Accession: T02975
R;Battey, N.H; James, N.C.; Greenland, A.J.
Plant physiol: 112, 1391-1396, 1996
A;Title: CDNA isolation and gene expression of maize annexins p33 a A;Reference number: Z14796; MUID:97092863
A;Accession: T02975
A;Status: prelininary; translated from GB/EMBL/DDBJ
A;Residues: prelininary; translated from GB/EMBL/DDBJ
A;Residues: prelininary; translated from GB/EMBL/DDBJ
A;Residues: 1-314 CBATy-
A;Cross-references: EMBL:X98245; NID:g1370602; pIDN:CAA66901.1; pID
A;Experimental source: cultivar clipper; root tip
C:Superffamily: annexin repeat homology
F;14-85/Domain: annexin repeat homology -AXR->
                                                                                                          A; Cross-references: GB:M55177
C: Superfamily: ras transforming protein; translation elongation factor Tu C: Superfamily: ras transforming protein; translation elongation factor Tu C: Reywords: GTP binding; helongation factor Tu homology <ETU>F:11-24/Region: nucleotide-binding motif A (P-loop)
F:123-126/Region: GTP-binding MKXD motif
F:153-155/Region: GTP-binding SAK/L motif
F:23,24,42,123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys,
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
C36365
C36365
C36961es: Rhizomucor racemosus
C;Species: Rhizomucor racemosus
C;Species: Rhizomucor racemosus
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jan-2001
C;Accession: C36365
R;Casale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
Rol. Cell. Biol. 10, 6654-6663, 1990
A;Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which A;Recession: C36365; MJID: 91081774
A;Recession: C36365
                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <CAS>
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 1-134 <KUE>
A;Cross-references: EMBL:X72486; NID:9441440; PIDN:CAA51154.1; PID:9441441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: homonoglobulin bomology <IMM>
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Matches 10
   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AQRYGRE-LRRMSDEFEGSFK 25
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       32.49;
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Pred. No. 23;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pred. No. 9.7;
1; Mismatches
       Score 48;
Pred. No.
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рв
18;
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                                    Length 206
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Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316
A:Accession: F72289
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 cARN>
A:Residues: 1-220 cARN>
A:Cross-references: GB:AE001772; GB:AE000512; NID:94981693; PIDN:AAD36230.1; PID:9498170
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1154
C:Superfamily: yeast SOL3 protein
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F72289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oxidoreductase, sol/devB family - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Dete: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C;Accession: F72289
C;Accession: F72289
Garrett, M.M.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Search completed: September 20, 2002, 10:39:13 Job time: 485 sec
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                                                                                                                                                                                                           Query Match 32.4%; Score 48; DB 2;
Best Local Similarity 34.8%; Pred. No. 19;
Matches 8; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                               5 AAQRYGRELRRMSDEFEGSFKGL 27
| ::| ||:| :|: |:
111 ACEKYEREIRSATDQFDLAILGM 133
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||:||:||:||||
169 REIRRMNKEQEGRSKG 184
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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Perfect score:
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47.5
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54
53
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      BLOSUM62
Gapop 10.0 , Gapext 0.5
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148
1 KNLWAAQRYGRELRRMSDEFEGSFKGLK 28
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      BAD, HUMAN
ITHZ, MESAN
ITHZ, MOUSE
AROG, PEAST
AP3, ARATH
ARC, ARATH
ARC, ARATH
ARC, ARATH
ART, ARTEL
FMR1, ANTEL
FMR2, ANTEL
FMR1, ANTEL
FMR2, AN
ENV_SIVAT
LML1_CAEEL
NUOG_ECOLI
NUOG_SALTY
BIM_MOUSE
BIM_RAT
END8_ECOLI
SYM_THEMA
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o6137 mus musculu
o35147 rattus noru
o35247 homo sapien
p97279 mesocricetu
Q61703 mus musculu
P32449 saccharomyc
P35652 arabidopsis
Q61743 peudomonas
P22200 rhizomucor
Q9x0h bhermotoga
Q9mx8 solanum tub
Q9x705 arabidopsis
Q01133 calliactis
Q01133 calliactis
Q01133 calliactis
Q01133 calliactis
Q01133 calliactis
Q01137 capien
P21259 polyorchis
R016994 anthopleura
P10449 anthopleura
P19873 homo sapien
P21259 polyorchis
Q016994 anthopleura
P19873 homo sapien
P10499 bathopieura
P10490 anthopieura
P10490 ant
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                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Bcl12-antigonist of cell death (BAD) (Bcl-2 binding component
6) (Bcl-xL/Bcl-2 associated death promoter).
          MEDLINE-21109372;
                                                                     MEDLINE-98194755; PubMed
D'Agata V., Magro G., To
"Cloning and expression
the rat brain.";
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                      Hau S.Y., Kalpla A., Zhu L., Hsueh A.J.W.;
"Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
apoptosis in memmalian cells by 14-3-3 isoforms and Pll.";
Mol. Endocrinol. 11:1858-1867(1997).
                                                                                                                                                                                                      MEDLINE-98034386;
                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eucheria; Rodentia;
MCBI_TaxID=10116;
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PubMed=11161472;
U., Yu L.-Y., Su
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G., Travali S.,
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"Functional characterization of two splice variants their interaction with Bel-w in sympathetic neurons Mol. Cell. Meurosci. 17:97-106(2001).
-IP FUNCTION: Promotes cell death. Successfully compared to the control of the control of two splits of the control of two splits of the control of two splits of two sp
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binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the lew of heterodimerization of these proteins with MAX. Con reverse t death repressor activity of Bcl-x(L), but not that of Bcl-2 (B) similarity). Appears to act as a link between growth factor receptor signaling and the apoptoric pathways.

SUBUNIT: Forms heterodimers with the anti-apoptoric protein scolation factor x(L), Bcl-2 and Bcl-w, Also binds protein ScOMA10. The Scr-13/Sesr-137 phosphorylated form binds 14 3-3 proteins. SUBCELLULAR LCCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm (By similarity).

ALTERNATIVE PRODUCTS: 2 isoforms: alpha (shown here) and beta; produced by alternative splicing. They differ only in their Cthe (By

BC1-

are

terminal regions.

TISSUE SPECIFICITY: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the mw more

abundant form.

abundant form.

BAX How There is a domain is required by BIK, BID, BAK, BAD AND BAX How their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bel-2 family.

PMN: Phosphorylated on Ser-113 in response to survival stimuli. Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14·3·3 proteins. This interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bel-x(I) and the promotion of cell survival. Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the major site of protein kinase A (CAPK) phosphorylation (By SIMILARITY: CONTAINS A BCL-3 HOMOLOGY DOMAIN 3 (BH3). -

entities requires a license agreement (S or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss institute of Buoinformatics and the EMHL outsi the European Buoinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this Statement is not removed. Usage by and for con moved. Usage by and for commercial (See http://www.isb-slb.ch/announce/ collaboration . outstation

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SEQUENCE
                                                                                                                               MUTAGEN
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WITH 14-3-3 PROTEINS.
S->A: NO HETERODIKERIZATION WITH 14-3-3
PROTEINS. NO EFFECT ON HETERODIKERIZATION
WITH BOLZ NOR WITH PROTEIN PLI
SDAGGR -> ERRGRK (IN REF. 1).
MW; 7ANATIDAESCFFABI CRC64:
Score 138; DB; Pred. No. 1.7; Pred. No. 1.7
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PHOSPHORYLATION (BY CAPK AND PKB)
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PHOSPHORYLATION (BY CAPK AND PKB)
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BAD OR BBC6 OR BCL318.
-i- FUNCTION. Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-X(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

-i- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein S100Al0 (By similarity).

The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By similarity).

-i- SUBCELLULAR LOCATION outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.

-i- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.

-i- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.
                                                                                                                                                                                                                                       *Resik S.W.;

"Rationale for Bcl-xL/Bad peptide complex formation mutagenesis, and biophysical studies.";

Protein Sci. 9:2528-2534(2000).

-I- FUNCTION: Promotes cell death, Successfully comp
                                                                                                                                                                                                                                                                                                                     MEDLINE=21073561; PubMed=11206074; Petros A.M., Nettesheim D.G., Wang Mack J., Swift K., Matayoshi E.D.,
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Submitted (JAN-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ottilie S., Dlaz J.-L., Horne W., Chang J., Chang S., Fritz L.C., Oltersdorf ? "Dimerization properties of human BAD.";
J. Biol. Chem. 272:30866-30872(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PHOSPHORY MEDILINE-97083574; PubMed-8929532; Wang H.-G., Rapp U.R., Reed J.C.; "BcL-2 targets the protein kinase Cell 87:629-638(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Bone marrow;
MEDLINE-98049554; PubMed-9388232;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last anotation updat
Inter-alpha-trypsin inhibitor heavy chain H
chain H2) (HG2).
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MEDIINE-97420688; pubMed-9276673; Makatani T., Suzuki Y., Yamamoto T., Sinohara H.; Wakatani T., Suzuki Y., Yamamoto T., Sinohara H.; Pakatani T., Suzuki Y., Yamamoto T., Sinohara H.; Pakatani T., Suzuki Y., Yamamoto T., Sinohara H.; Pakatani Y., Sinohara H.; Pakatani Y., Sinohara H.; Pakatani Y., Sinohara H.; Sinohara H.; Publications for the evolution of the inter-alpha-trypsin heavy chain family.";
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                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                         Mesocricetus.
NCBI_TaxID-10036;
                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                        Mesocricetus
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SIMILARITY: CONTAINS 1 BCL-3 HOWOLOGY DO SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subsequent phosphorylation on Ser-99 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-118, a site within the BH3 domain, leadin to the release of Bcl-x(L) and the promotion of cell survival. Ser-99 is the major site of AKY/PKB phosphorylation, Ser-118 the major site of kinase A (CAPK) phosphorylation (by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: Phosphorylated on Ser-75 in response to survival stimuli
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AF021792; AAB72092.1;
AF031523; AAB88124.1;
BC001901; AAH01901.1;
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22; Conser
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91.7%;
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Chordata; Craniata; Vertebrata; I
Rodentia; Sciurognathi; Muridae;
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ITH2_MOUSE
Q61703;
15-JUL-1998
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CONFLICT
SEQUENCE
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SMART; SM(
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                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                           Glycoprotein.
SIGNAL
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                                                                                212
                                                                                                                        Local Similarity
mes 9; Conserv
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SIMILARITY: BELONGS TO THE ITIH FAMILY.
SIMILARITY: CONTAINS 1 VWFA DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
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                                                                         NVWIVELQGMRFLHVPDTFEGHFQGV 237
                                                                                                     NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                           Pro; IPR002035; vWFA.
PF00092; vwm; 1.
; SM00327; VWA; 1.
TE; PS50234; VWFA; 1.
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(GLONOROITIN 4-SULFATE, G
(BY SIMILARITY)
V-> Y (IN DEE
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Pred. No.
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5; Mismatches
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BY SIMILARITY.
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                       PRT;
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-> I (IN REF. 2).
CA8BF565458E7B2E
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(CROSS-LINK SI
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212 N

NVWITEPQGMRFLHVPDTFEGHFQGV NLWAAQRYGRELRRMSDEFEGSFKGL Query Match Best Local ( Matches

9; Conservative

5. Score 53; Pred. No.

Mismatches

12;

Indels

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Length 946;

27

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Chan P., Risler J.-L., Raguenez G., Salier J.-P.;

Chan P., Risler J.-L., Raguenez G., Salier J.-P.;

The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein with differential transcription in liver and brain.";

Blochem. J. 306:505-512(1995).

-I- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYMPHESIS AND DEGRADATION OF HYALURONAN WHICH ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
                                                                                                                                                                                                                                                                                                              This SNISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation: the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE
                              BINDING
                                                                                                                                        CHAIN
                                                                                                                                                                                                                                 InterPro; IPR002035; v
Pfam; PF00092; vwa; 1.
SMART; SM00327; VWA; 1
                                                                                                                                                                                                                                                                             EMBL; X70392; CAA49842.1; MGD; MGI:96619; Itih2.
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Mammalia; Eutheria;
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15-JUL-1999 (Rel.
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                                                                                                                                                                       Glycoprotein.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY:
SIMILARITY: BELONGS TO THE ITLH FAMILY.
SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: 1-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN H1 BIKUNIN. INTER-ALPHA-INHIBITOR (1-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-ILKE INHIBITOR (1-ALPHA-II) OF H2 AND BIKUNIN, AND PRE-ALPHA-ILHED HITHORY (1-ALPHA-I) OF H3 AND BIKUNIN TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BAAIN. PTM: HBAVY CHAINS ARE INTERLIKED WITH BIKUNIN VIA A CHONDROITIN PTM: HBAVE CHAINS ARE INTERLIKED WITH BIKUNIN VIA A CHONDROITIN SULPATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
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protease inhibitor;
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Metazoa; Chordata; C
Metazoa; Rodentia;
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VWFA;
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38, Last annotation updat
in inhibitor heavy chain F
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         BY SIMILARITY.

VWFA.

VWFA.

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N-LINKED (GLCNAG. . .) (

CHONDROITH 4 SULFATE, C

(BY SIMILARITY)
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                                                                                                                                        INTER-ALPHA-TRYPSIN
 40DB6716433ED9DC
                                                                                                                                                        SIMILARITY
                                                                                                                                                                                                    Signal;
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                                            .) (POTENTIAL).
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 CRC64;
                                                                                                                                          INHIBITOR HEAVY CHAIN
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P32449;
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"The complete sequence of a 6794 bp segment located on
of chromosome II of Saccharomyces cerevisiae. Finding
dUTPase in a yeast.";
Yeast 9:1131-1137(1993).
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MEDLINE-92225349; PubMed-1348717;

MEDLINE-92225349; PubMed-1348717;

Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.;

Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.;

"Cloning, primary structure and regulation of the ARO4 gene, encoding the tyrosine-inhibited 3-deoxy-p-arabino-heptulosonate-7-phosphate synthase from Saccharomyces cerevisiae.";

Gene 113:67-74(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota: Saccharomycotina: Saccharomycetes
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited (EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP Synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthasand OR YBR249C OR YBR1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCY-1993 (Rel.
01-FEB-1994 (Rel.
30-MAY-2000 (Rel.
         HSSP; P00886; 10R7.
SGD; S0000453; ARO4.
InterPro; 1PR001785; DAHP_synth_1: 1.
Pfam; PF00793; DAHP_synth_1: 1.
ProDom; PD005060; DAHP_synth_1: 1.
                                                                                                                                                              the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb·sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1993) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuenzler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS
                                                                                    EMBL; X61107; CAA43419.1; -.
EMBL; L20296; AAA65607.1; -.
EMBL; Z36118; CAA85212.1; -.
EMBL; S38185; S38185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94078675; PubMed=8256522;
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                                                                                                                                                                                                                                                                                    phosphate + phosphate - phosphoenolpyruvate + D-erythrose 4-
phosphate + H(2)O.

ENZYME REGULATION: INHIBITED BY TYROSINE.

PATHHAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE MITHIN
PATHHAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE MITHIN
THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).

INDUCTION: BY AMINO ACID STRANATION.

SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEAST
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28, Last sequence up
39, Last annotation
biosynthesis;
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synthase).
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RESULT 7
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                         WEDLINE-21015720; PubMed-11130713;

XX MEDLINE-21015720; PubMed-11130713;

XX Salamoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

XX Salamoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

XX Partmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,

XX De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,

XX Mincker P., Cattolico L., Waissenbach J., Saurin W., Ouetler F.,

XX Wincker P., Cattolico L., Waissenbach J., Saurin W., Ouetler F.,

XX Wincker P., Cattolico L., Waissenbach J., Saurin W., Ouetler F.,

XX Wincker P., Cattolico L., Waissenbach J., Saurin W., Ouetler F.,

XX Wincker P., Drzonek H., Erite H., Jordan N., Bangert S., Nyakatura G.,

XX Wincelmann R., Kranz H., Voss H., Holland R., Bardt P., Nyakatura G.,

XX Wincelmann R., Kranz H., Voss H., Holland R., Bardt P., Nordsiek G.,

XX Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Shionati B.,

XX Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Shionati B.,

XX Vezzi A., D'Angelo M., Scheen O., Bargues M., Terol J., Climent J.,

XX Waithelt J., Scharfe M., Scheen O., Burgues M., Terol J., Climent J.,

XX Mayarro P., Collado C., Perez Perez A., Ottenwaelder B., Duchemin D.,

XX Monfact A., Argiriou A., Flores M., Liguori R., Vitale D., Mewes H.-W.,

XX Mannhauft G., Hasse D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP3_ARATH
P35632; Q39003;
01-JUN-1994 (Rel. 29, Created)
101-JUN-1994 (Rel. 29, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Floral homeotic protein ApeTALA3.
AP3 OR AT3G54340 OR T12E18_30.
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"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
Genetics 15:1839-846(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxamoto H., Yano A., Shiraishi H., Okada K., Shimura Y.; "Genetic complementation of a floral homeotic mutation, apetala3, with an Arabidopsis thaliana gene homologous to DEFICIENS of Antirrhinum maine ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. LANDSBERG ERECTA;
MEDLINE-95036018; PubMed-7948893;
Okamoto H., Yano A., Shiraishi H.
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  Haase D., Sch
Kaul S., Town
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Schoof H., Rudd S.,
Town C.D., Koo H.L.,
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Pred. No. 2.4;
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  Zaccaria P.,
Tallon L.J.,
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                    Mewes H.-W.,
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InterPro; IFR002148; K-box.
InterPro; IFR002100; MADS-box.
InterPro; IFR002100; MADS-box.
InterPro; IFR002100; MADS-box.
InterPro; IRVOX, INTERPRO; INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; INTERPORT; INTERPO; INTERP
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EMBL, D21125; BAA04665.1; -
EMBL, AF115799; AAD51808.1; -
EMBL, AF115800; AAD51809.1; -
EMBL, AF115801; AAD51809.1; -
EMBL, AF115804; AAD51803.1; -
EMBL, AF115814; AAD51900.1; -
EMBL, AF115814; AAD51900.1; -
EMBL, AF115814; AAD51901.1; -
EMBL, AF115814; AAD51901.1; -
EMBL, AF115814; AAD51901.1; -
RPOB_CAMJE
Q46124; Q9PI31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS00065; MADS_BOX_2; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein;
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HSSP; P11746; 1MNM.
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-I- SUBCELLULAR LOCATION: NUCLEAR:
-I- TISSUE SPECIFICITY: EXPRESSED IN PETALS AND STAMENS.
-I- TISSUE SPECIFICITY: EXPRESSED IN PETALS AND STAMENS.
-I- MISCELLANEOUS: NUTATIONS IN AP3 CAUSE TRANSFORMATION
-INTO SEPALS AND STAMINA INTO CARRELS.
-I- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRAN
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-1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF FLOMER DEVELOPMENT:
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199
232 AA;
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3 157
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27341 MW;
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STRAIN-MCTC 11166;
MEDLINE-20159912; PubMed-10688204;
MEDLINE-20159912; PubMed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Fellwell T., Holtoyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last anotation update)
10-CCT-2001 (Rel. 40, Last anotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit).
RPOB OR CJ0478.
Campylobacter jejuni.
                                                                                                                                                                                                                                                  InterPro; IPR001572; RNA_pol_B.
Pfam; PF00562; RNA_pol_B; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {RNA}{(N).

-i* SUBONIT: THE ENZYME CONSISTS OF THE ENZYME WHICH IS COMPOSED OF 2 ALPHA BETA' CHAIN.
                                                                                                                                                                                                                                                                                                EMBL; AL139075; CAB75116.1; -. EMBL; X77304; CAA54509.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96084944; PubMed-7489896; Bustamante V.H., Puente J.L., San
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campylobacter
                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 338-1031 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                  Transferase;
                            3 LWAAQRYG--RELRRM----SDEFEGSFKGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBSTRATES.
CATALYTIC ACTIVITY: N nucleoside triphosphate -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
VWALEAYGAAHTLREMLTIKSDDVEGRESAYK
                                                           l Similarity
13; Conser
                                                                                                                                        proteome.
7 338
7 558
7 671
7 691
8 1378 AA;
                                                             Conservative
                                                                                                                                                                                                                                  Transcription; DNA-directed RNA polymerase;
                                                                                                                                                     347
558
671
691
                                                                              4 ω
0
                                                                                                                                          155915
                                                                          . 68;
                                                                                            . 88
                                                           Score 50; DB
Pred. No. 20;
3; Mismatches
                                                                                                                                      NDLANGVDAA -> MTWLMALMOP (IN REF. A -> R (IN REF. 2). C -> S (IN REF. 2). A -> R (IN REF. 2). A -> R (IN REF. 2). MW; AB7467C305028EB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sanchez-Lopez F.,
                                                                       NO ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF THE SIGMA CHAIN AND THE CORE ALPHA CHAINS, 1 BETA CHAIN, AN
                            28
                                                             10;
                                                                                        Length 1378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bobadilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BETA CHAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N diphosphate
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RESULT 9

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Query Match
Best Local S
Matches 10
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Q914GJ;
Q1-MAR-2002 (Rel. 01-MAR-2002 (Rel. 01-MAR
                                                                                                                                                                                                                                                                                                                             RAS3_RHIRA STAN
P22280;
01-AUG-1991 (Rel. 1
01-AUG-1991 (Rel. 1
30-MAY-2000 (Rel. 3
                                                                                                                                                                                                                                  Ras-like protein : RAS3.
Rhizomucor racemos Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
MEDILNB-20437337; PubMed-10984043;
STOVET C.K.; Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
BICKEY M.J., Brinkman F.S.L., Hufnagle W.O., Rowallk D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.K., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome seguence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the SWBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              opportunistic pathogen.',
Nature 406:959-964(2000).
-i- FUNCTION: Involved in DNA recombination (By similarity).
-i- SIMILARITY: BELONGS TO THE RAUC FAMILY.
   SERDIEMCE FROM N.A.
STRAIN+ACC 1245B:
MEDLINE-91061774: Pubmed-1701021:
Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., I
"Expression of a gene family in the dimorphic fungus
Which exhibits striking similarity to human ras genes
Mol. Cell. Blol. 10:654-6663 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA recombination protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombination;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
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    Created)
    Last sequence update)
    Last annotation updata

                                                                                                                                                                                                                                     Zygomycota;
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201
COILED COIL (POTENTIAL)
51539 MW; 1E7EA97E82EC5E4B CRC6
                                                                                                                                                                                                                            (Mucor circinelloides gomycota; Zygomycetes;
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5 ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49; DB
Pred. No. 8.3;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                             update;
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8.3;
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Mucorales; Muco
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                                                                        Linz
                                                Mucor
                                                                        .
स्व
                                                   racemosus
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Best Local S
Matches 10
                                                                                                            SEQUENCE FROM N.A.

STRAINMESS / DSM 3109;

WEDLINE-99287316; PubMed-10360571,

Melson K.E., Claycon R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

Haft D.H., Linher K.D., Garrett M.M.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Stewart A.M., Cotton M.D., Fratt M.S., Phillips C.A., Richardson D.,

Beidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

"Evidence St.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for Lateral gene transfer between Archaea and Bacteria from

genome sequence of Thermotoga maritima.",

Mature 399323-329(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THEMA
                                                -
                                                                                             <del>-</del>,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermotoga maritima.
Bacteria; Thermotogales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ++
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                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
   PUNCTION: TURNOLUSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-PHOSPHOGLUCONATE.

CATALTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + phospho-D-gluconate.

PATHWAY: SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.
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δÃ 밁

Thermotoga.

H(2)0

from

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6PGL_THEMA

09X0N8;

30-MAY-2000

30-MAY-2000

16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROW entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the BWBL the European Bioinformatics Institute. There are no restrict use by non-profit Institutions as long as its content in modified and this statement is not removed. Usage by and fo
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seg
16-CCT-2001 (Rel. 40, Last ann
6-phosphogluconolactonase (EC
PGL OR DEVB OR TM1154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M55177; AAA83379.1;
PIR; C36365; C36365.
HSSP; P01112; 1PLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENZYME REGULATION. ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE NUCLEOTIDE-EXCHANCE FACTOR (GEF) AND INACTIVATED BY A GIPASE-ACTIVATING PROTEIN (GAP).
SUBGELLULAR LOCATION: PLASMA MEMBRANE.
DEVELOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE SMALL
                                                                                                                                                                                                                                  RELRRMSDEFEGSFKG
                                                                                                                                                                                                 REIRRMNKEOEGRSKG 183
                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND YEAST
                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                       32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ras
                                                                                                                                                                                                                                    26
                    sequence update)
annotation update)
(EC 3.1.1.31) (6PGL
                                                                                                                                                                                                                                                                       Score 48; DB : Pred. No. 4.9; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTPASE SUPERFAMILY. RAS FAMILY.
                                                                                                            220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no restrictions
                    (6PGL)
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Best Local S
Matches 8
                      InterPro: IPR001926, BC_enzyme_beta.

Pfam; PF00291; PALP; 1.

PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.

Threonine blosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme; Chloroplast; Transi peptide.

Chloroplast; Transi peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOUNT STANDARD: PRT; 519 AA.

THRC_SOLTU STANDARD: PRT; 519 AA.

THRC_SOLTU STANDARD: PRT; 519 AA.

10)MTAR-2002 (Rel. 41. Created)
10)-MAR-2002 (Rel. 41. Last sequence update)
10)-MAR-2002 (Rel. 41. Last sequence update)
11-MAR-2002 (Rel. 41. Last sequence update)
11-MAR-2002 (Rel. 41. Last sequence update)
11-Mar-2002 (Rel. 41. Last shortetion update)
11-Mar-2002 (Rel. 41. Solanales)
11-Mar-2002 (Rel. 41. Solanales)
11-Mar-2002 (Rel. 41. Solanales)
11-Mar-2002 (Rel. 41. Solanales)
11-Mar-2002 (Rel. 41. Created)
11-Mar-200
                                                                                                                                                                                                                                This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this stratement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as its content is in may modified and this statement is not removed. Using by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license(135)-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Casazza P., Kaiger S., Willmitzer L., Mocijen R., Hegse H.;
"Isolation and characterization of a cORA encoding threonine synthase from Solanum tuborosum."
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

1- CATALYTIC ACTIVITY: O-Phospho-L-homoserine + H(2)O - L-threoning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4113;
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TIGR: TM1154: -.
InterPro: IPR000457: Glucosamine_iso.
Pfam: PF01182: Glucosamine_iso; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                methionine (SAM) (By similarity)
PATHWAY: Threenine blosynthesis; last step
SUBLUAT: Homodimer (By similarity),
SUBCELLULAR LOCATION: Chloroplast (By similarity),
SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACEKYEREIRSATDQFDLAILGM 133
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8; Conser
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220 AA; 25325 MW;
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Pred. No. 5.3
8; Mismatches
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g threonine synthase
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THRC_AF
RX MEDLINE-V. COLUMNIA.

RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,

RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,

RA Harris B., Duesterhoeit A., Stlekena W., Entlan K.-D., Terryn N.,

RA Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,

RA Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,

RA Harris B., Ansorge W., Pujdomenech P., Watson M., Schmidtheini T.,

RA Kreis M., Delseny M., Pujdomenech P., Watson M., Schmidtheini T.,

RA Kreis M., Delseny M., Pujdomenech P., Watson M., Schmidtheini T.,

RA Kreis M., Delseny M., Pujdomenech P., Watson M., Schmidtheini T.,

RA Kreis M., Delseny M., Pujdomenech P., Watson M., Schmidt P.,

RA Vos P., Hohelsel J., Zimmermann W., Wedler H., Ridley P.,

RA Vos P., Hohelsel J., Zimmermann W., Wedler H., Bridley P.,

RA Vos P., Hohelsel J., Zimmermann W., Wedler H., Berlup P.,

RA Vos P., Hohelsel J., Zimmermann W., Wedler H., Dirkse W.,

RA Vos P., Hohelsel J., Zimmermann W., Wedler H., Dirkse W.,

RA Langham S.-A., Hocklind H., Bastlaens II., Vent den Daele H.,

RA Vann Montagu H., Rogers J., Cronin M., Lamberth S., Van den Daele H.,

RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,

RA Berneiser S., Hempel S., Feldpausch M., Grand R., McLay K., Mayes R.,

RA Clark L., Doggert J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,

RA Clark L., Doggert J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,

RA Gabel C., Fuchs M., Fartmann B., Granderh M., Mueller-Auer S.,

RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,

RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,

RA Perter Perez A., Purnelle B., Bent E., Johnson S., Taron D., Jesse T.,

RA Gibbons T., Watse D., Lencke K., Mewes H.-H., Stocker S.,

RA Chefdor F., Cooke R., Berger C., Honfort A., Casacuberta E.,

RA Zarcaria P., Bevni M., Grander S., Harmon G., Edwards J.,

RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,

RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,

RA
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095785, 009144,
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, List sequence up
01-MAR-2002 (Rel. 41, List sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STPARIN-CV. Wassilewskija; MEDLIND-99418329; PubMed-10490396; MEDLIND-99418329; PubMed-10490396; Bartlem D., Tamaki Y., Nalto S.; Genomic nucleotide sequence of the Arabidopsis threonine synchase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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Query Match
Best Local Similarity
Whiches 12; Conserve
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CONFLICT
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InterPro; 1PR001926; PALP.
Pfam; PF00291; PALP.
PROSITE; PS00165; DEHYDRATAGE_SER_THR; 1.
PROSITE; PS00165; DEHYDRATAGE_SER_THR; 1.
PROSITE; PS00165; DEHYDRATAGE_SER_THR; 1.
Chloroplast; Transit peptide; 3D_structure.
                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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between the Swiss Institute of Bioinformatics and the Ep
the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
Nelson J., Spieth J., Kyan E., Andrews S., Geisel C., Layman D.
Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C.,
Antonoiu B., Zidanic M., Strong C., Sun H., Liamar B., Yordan C.,
Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
Granat S., Schödy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
Chen E., Marra M., Mattienssen R., McCombie W.R.;
                                                                                                                                                                                                                                                                     EMBL; AB027151; BAA77707.1; -. EMBL; AL050352; CAB43659.1; -. EMBL; AL161575; CAB79742.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomazeau K., Curien G., Dumas R., Biou V.;
"Crystal structure of threonine synthase from Arabidopsis thaliana.";
Protein Sci. 10:638-648 (201).
-1- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O - L-threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-adenosylmethionine-sensitive from higher plants."; FEBS Lett. 390:85-90(1996).
                                                                                               SEQUENCE
                                                                                                                                                       TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-adenosylmethionine.";
Biochemistry 37:13212-13221(1998).
                                                                                                                                                                                                                                                       EMBL; L41666; AAB04607.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11344332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Curien G., Dumas R., Ravanel S., Douce R.,
Curien G., Dumas R., Ravanel S., Douce R.,
"Characterization of an Arabidopsis thaliana cDNA encoding an
"Characterization of an Arabidopsis thaliana cDNA encoding an
"Characterization of an Arabidopsis thaliana cDNA encoding an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 41-526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=9748328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=8706836;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphate.
CCFACTOR: Pyridoxal phosphate.
ENZYME REGULATION: Allosterically activated
                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
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PYRIDOXAL PHOSPHATE.
A -> L (IN REF. 3).
A -> L 200 REF. 3).
                    Score 48; DB
Pred. No. 14;
6; Mismatches
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Antho-Framide neuropeptides precursor.
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Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
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TISSUE SPECIFICITY: NEURONS ASSOCIATED WITH SMOOTH MUSCLE FIBERS
                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by pon-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
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043521; 043522;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
BC12-11ke protein il (BC12 interacting mediator of cell death).
BC12-11ke protein il (BC12 interacting mediator of cell death).
                                                                                                                                                                                                                                                                     the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Bin: a novel member of the Bcl-2 family that promotes apoptosis.";
EMBO J. 17:384-395(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Peripheral blood, and Spleen; MEDLINE-98094360; PubMed-9430630;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                             InterPro; IPR000712; Bcl_2.
PROSITE; PS01259; BH3; FALSE_NEG.
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DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
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SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2
PROTEINS INCLUDING WCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES
NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
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# ALIGNMENTS

RESULT 1 D0919N2 DPT 0919N2 DPT 01-0C7-2000 (TTEMBLTel. 15. Created) DPT 01-DEC-2001 (TTEMBLTel. 19. Last sequence update) DPT 01-DEC-2001 (TTEMBLTel. 19. Last annotation update) DPT 01-DEC-2001 (TTEMBLTel. 19. Last sequence update) DE BAD. GN
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SQUERRIT RAPARACE CONTRACTOR CONT

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RA Colc S.T., BroSch R., Parkhill J., Garnier T., Churcher C., Harris [
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingsorth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Haminn N., Holroyd S.,
Hornsby T., Jogels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Ratter S., Seeger K., Skelton S., Squares S., Squares S.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G., R.,
TDECIPHERING THE BOLOGY OF Mycobacterium tuberculosis from the
Complete genome sequence.'
            Query Match
Best Local Similarity
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047148;
01-JUN-1998 (
01-MAY-2000 (
01-DEC-2001 (
                                                                                                                                             Chloroplast.
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SEQUENCE 50
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EMBL. 734025: CAA98415.1;
-Tuberculist; RY2014: Transposase_20.
Flam: PF0371: Transposase_20; I
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete Seque
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                                                                                                                                                                                                                                                                                                                                                        Kron K.A.;
"Phylogenetics of Rhododendroidese (Ericaceae)
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ 6
EMBL: U61331: AAC15245.2: ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATK.
Menziesia cillicalyx.
Chloroplast.
Eukaryota; Viridiplantae;
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Actinomycetales; Corynabacterineae; Mycobacteriaceae; Mycobacterium.
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InterPro; IPR002866; matK_N.
Pfam: PF0148: Intron_maturas2: 1.
Pfam: PF01824: MatK_N; 1.
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Spermatophyta: Magnollophyta: eudicottyledons; core eudicotts:
Astoridae: Ericales: Ericaceae: Menziesia:
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01-MAY-2000 (TERMBLrel. 13, Last sequence update)
01-DEC-2001 (TERMBLrel. 19, Last annotation update)
RIBOSOMAL MATURASE (FRAGMENT).
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Pred.
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Pred. No. 7.6;
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2.5;
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EMBL; A8012749; BAA25870.1; -
EMBL; A8012745; BAA25866.1; -
InterPro; IPR000442; Intron_m
InterPro; IPR000442; Intron_m
InterPro; IPR002866; MatK_N.
Pfam; PP01348; Intron_maturas
Pfam; PP01348; Intron_maturas
Pfam; PP01824; MatK_N; 1.
Chloroplast.
SEDOTENCE 506 AA; 60389 MM;
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062972;
01-AUG-1998
01-AUG-1998
01-DEC-2001
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063960;
01-AUG-1998
01-AUG-1998
01-DEC-2001
                                                                                                                                                                                                                               Chloroplast.

Chloroplast.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; Ericales; Ericaceae; Rhododendron.

pcB_TaxID-49169;
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Rhododendron farrerae.
Chloroplast.
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Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; Ericales; Ericaceae; Rhododendron.
NBI_TaxID-75582, 75580;
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YCF14 OR MATK.
                                                            "Investigation of Sectional Rhododendron(Ericaceae) base J. Jpn. Bot. 0:0-0(1998). EMBL; AB012729; BAA22850.1;
                                                                                                                                         Kurashige Y., Mine
Yukawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Kurashige Y., Mine M.,
Yukawa T.;
                        InterPro; IPR000442; Intron_
InterPro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                          Rhododendron ovatum.
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  Intron_maturas2;
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                                            Intron_maturse2
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Pred. No. 23;
5; Mismatches
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Best Local Similarity
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SEQUENCE 506
                                                                                                                  01-AUG-1998
01-AUG-1998
01-DEC-2001
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Rhododendron.
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01-AUG-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Kurashige Y.,
Yukawa T.;
                                      Rhododendron albiflorum.

Chloroplast.

Chloroplast.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Nateridae; Ericales; Ericaceae; Rhododendron.

(3: NCBL_TaxID-49161;
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InterPro; IPR002866; MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
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                                                                                                        RIBOSOMAL MATURASE.
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                   SEQUENCE FROM
                                    NCBI_TaxID=49161;
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Best Local
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Best Local :
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062977;
01-AUG-1998
01-AUG-1998
01-DEC-2001
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EMBL; A8012731; BAA25852.1; IPR000442; Intron_maInterPro; IPR002866; MatK_N.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Rhododendron.
UCBI_TaxID=4962B;
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01-AUG-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                              MATK.
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InterPro; IPR002866;
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        Chloroplast
                                        RIBOSOMAL
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 Eukaryota; Viridiplantae;
                   Rhododendron luteum
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                                                                                                                                                                                Local Similarity hes 12; Conserv
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12; Conserv
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 Streptophyta; Embryophyta; Tracheophyta
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5; Mismatches
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pred. No. 23;
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062978;
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01-AUG-1998 (Tremburel. 0
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062980;
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SEQUENCE 506 AA;
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J. Jpn. Bot. 0:0-0(1998).
EMBL; AB012735; BAA25856.1;
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Rhododendron canadense.
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InterPro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                   Kurashige Y., Mine
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InterPro; IPR002866; MatK_N.
Pfam; PF01148; Intron_maturas2; 1.
Pfam; PF011824; MatK_N; 1.
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                                                                              391
                                                                                                                                                                                                                                                                                           rukawa T.;
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                                                                           KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
                                                                                                                        l Similarity 37.1
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12; Conser
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(TrEMBLrel. 07,
                       PRELIMINARY;
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Pred. No. 23;
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Pred. No. 23;
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Best Local :
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062981;
01-AUG-1998 (TrEMBLrel. 07, C
01-AUG-1998 (TrEMBLrel. 07, L
01-DEC-2001 (TrEMBLrel. 19, L
                                                                                                           Chloroplast.
SEQUENCE 506 AA;
                                                                                                                                 Pfam; PF01348; Intron_maturas2;
Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                   "Investigation of Sectional Relationships in the Genus Rhododendron(Ericaceae) based on matk Sequences."; U. Jpn. Bot. 0:0-0(1998). EMBL; AB012738; BAA25859.1; -.
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Spermatophyta; Magnollophyta; eudicotyjeledons; core eudicots;
Asteridae; Ericales; Ericaceae; Rhododendron.
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Pfam; PF01824; MatK_N; 1.
Chloroplast.
SEQUENCE 506 AA; 60301 MW; (
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InterPro; IPR002866; MatK_N.
                                                                                                                                                                                                                                      Yukawa T.;
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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01-DEC-2001 (TrEMBLrel.
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J. Jpn. Bot. 0:0-0(1998).
EMBL: AB012737; BAA25858.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asteridae; Ericales;
NCBI_TaxID=49463;
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Asteridae; Eri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
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                       1 KNLWAA-----ORYGRELRRMSDEFEGSFK 25
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                                                                                                             60449 MW;
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Pred. No. 23;
5; Mismatches
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Last annotation update)
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                                                                                                             B138208746D99258 CRC64;
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Best Local :
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062983;
01-AUG-1998
01-AUG-1998
01-DEC-2001
                                              InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
Pfam; PP01348; Intron_maturas2; 1.
Pfam; PP01824; MatK_N; 1.
                                                                                                                                               Rhododendron(Ericaceae) based J. Jpn. Bot. 0:0-0(1998). EMBL; AB012740; BAA25861.1; -
  Chloroplast.
SEQUENCE 506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Chloroplast
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                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Kurashige Y., Mine M., Yukawa T.,
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta: eudicotyjiedons; core eudicots;
Asteridae; Ericales; Ericaceae; Rhododendron.
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InterPro; IPR002866; MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
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J. Jpn. Bot. 0:0-0(1998),
EMBL; AB012739; BAA28860.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RIBOSOWAL MATURASE.
                                                                                                                                                                                        "Investigation of Sectional Relationships in the Genus Rhododendron(Ericaceae) based on matK Sequences.";
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-75578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast.
SEQUENCE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01348; Intron_mat
Pfam; PF01824; MatK_N; 1.
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NCBI_TaxID=75577;
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  60393 MW;
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Pred. No. 23;
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DAAB47A759CFFC46 CRC64;
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Search completed: September Job time: 1664 sec

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Query Match

Score 52.5;

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506 AA;
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01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                    InterPro: IPR000442; Intron_maturse2.
InterPro: IPR002866; MatK_N.
Pfam: PP01348; Intron_maturas2; 1.
Pfam: PF01824; MatK_N; 1.
                                                                                                                                                                Rhododendron(Ericaceae) based
J. Jpn. Bot. 0:0-0(1998).
EMBL; AB012741; BAA25862.1; -.
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                                                                                                                                                                                                                                                                                                                           MATK.
                                                                                                                                                                                                                                                                                                                                    RIBOSOMAL MATURASE
                                                                                                                                                                                                                                                                                                                                                                                            062984
                                                                                                                                                                                                             Kurashige Y.,
Yukawa T.;
                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                  Chloroplast.
                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                        NCBI_TaxID-49622;
                                                                                                                                                                                                                                                                                                             Rhododendron ferrugineum (Alpenrose).
                                                                                                                                                                                                'Investigation of Sectional Relationships in the Genus
391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
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                   1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
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                                          Conservative
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Mine M., Kobayashi N., Handa T.,
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                                                     35.5%;
37.5%;
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                                                      Score 52.5;
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                                         Mismatches
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                                                              Length 506;
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OM protein protein search, using sw model GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

September 20, 2002, 10:35:59; ; Search time 228.86 Seconds
(without alignments)
13.104 Million cell updates/sec

Scoring table: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 KNLWAAQRYGRELRRMSDEFEGSFKGL (27)

Title: Perfect score:

US-09-544-664-56 143

Run on:

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

# Database :

A\_Geneseq\_032802:\*

| /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*
| /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA191.DAT:\*
| /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA192.DAT:\*
| /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA193.DAT:\*
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| /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA199.DAT:\*

Pred. Mo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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10	<b>∞</b> ₁	ರ ಚ ಈ ಬ	24	Result No.
138 138	138 138	138 138 138	143	Score
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51	51	51	51	51	51	51	51	51	51	51	72	72	73	73	84	84	98	93	93	102	102	102	102	113	114	114	114	114	114	114	138	138	138
35.7	35.7	35.7	35.7	35.7	35.7	35.7	35.7	35.7	35.7	35.7	50.3	50.3	51.0	51.0	58.7	58.7	60.1	65.0	65.0	71.3	71.3	71.3	71.3	79.0			79.7	79.7	79.7	٠.		96.5	96.5
682	242	241	236	232	232	186	186	181	171	125	20	18	16	16	16	16	16	26	26	59	59	59	65	23	168	168	168	168	268	166	567	204	204
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ABB52836	AAG25576	AAG54028	AAG54679	AAG54029	AAG25577	AAG54030	AAG25578	AAG25217	AAG25218	AAG25219	AAB70380	AAB70379	AAB37029	AAY05421	AAB37028	AAY05422	AAR95163	AAB70371	AAY96321	AAW61322	AAW61321	AAW61320	AAW61319	AAR95166	AAG67588	AAB48287	AAB70368	AAB13512	AAW55779	AAW32476	AAU00220	AAB70369	AAW58832
	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia		Arabidopsis thalia	Arabidopsis thalia				Arabidopsis thalia	BAD BH3 domain reg			Human BAD BH3 doma	Bcl2 polypeptide B	Mouse BAD BH3 doma	bcl-x(L)/bcl-2 ass	BAD BH3 consensus	Mammalian Bad Bcl-		Mutant BCL-XL/BCL-		Mutant BCL-XL/BCL-	$\sim$	Amino acid sequenc	Human Bad protein.		Human cell prolife	Human Bcl-xL/Bcl-2	BBC6 protein for r	Bad-DTTR apoptosis	Longer murine BAD	Murine BAD protein

### ALIGNMENTS

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AAB37056 standard; peptide; 27 Ş

AAB37056;

28-FEB-2001 (first entry)

Bcl2 polypeptide BH3 domain peptide #56.

RESULT TA AAB37056 XX AAB37056 XX AAB37056 XX AAB37056 XX Cytc XX Cyt Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Cell death agonist; Bed; apoptosis modulation; B cell imphoma/leukemia 2; cancer; proceate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.

Homo sapiens.

W0200059526-A1.

12-OCT-2000.

06-APR-2000; 2000WO-US09352

07-APR-1999; 9905-0128202.

(UYJE-) UNIV JEFFERSON THOMAS

Huang Z, Wang J, Zhang Z, Shan

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WPI; 2000-679325/66.

New peptide conjugates for modulating apoptosis or for inhibiting

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PIN PROPERTY OF STREET
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(C (R*)n Peptide where n = 1-10; X = C-0, when the R* y group is attached to the N-terminus of the applies, or a side chain of the peptide where the functional group of the side chain is NH2 or OR; or X = 0 or NH.

C the functional group of the side chain is NH2 or OR; or X = 0 or NH.

C side chain of the peptide, where the side chain functional group is COOH, or X = 0 or CNH2; on R = 2-18C alkyl or late (high functional group is COOH).

C side chain of the peptide, where the side chain six ly containing one or CONH2; on R = 2-18C alkyl or Love (high functional group is COOH).

C or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally composite that a 1-5C straight or branched chain alkyl group, or benzyl. The peptides a NAB3701-187058 represent reamples of alkyl group, or benzyl. The peptides a NAB3701-187058 represent analogues of a Rel -2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the call death agonist Bad. The peptides conjugate is useful for modulating apoptosis in the cells of a subject, or for corresing B cell lymphoma/Leukamia 2 (Bell-2) mediated blockage of a Rel -2 superfamily polypeptide corresponding to amino acids 72-97 of C useful for modulating apoptosis in the peptide conjugate is useful for treating a subject affilicted with a cancer cells of a subject affilicted with a cancer cellace on jugate is useful for treating a subject affilicted with a cancer cellace on jugate is useful for treating a conjugate is also useful for conjugate is necessarily. The peptide conjugate is also useful for creating a conjugate is also useful for conjugate is also useful for creating a conjugate is also useful for creating a conjugate is also useful for creating a subject affilicted with a cancer cells of an area of a conjugate is also useful for creating a conjugate is also useful for creating a conjugate is also useful for creating a subject affilicted with a cancer cells of a conjugate is also an 
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Best Local Similarity 100.0%;
Matches 27; Conservative (
                                                                                                                                                                                                                                                                               Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bc1-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; nor-small lung; renal; thyroid; neuroblastoga; melanomas; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
  Buang
                                                                                                                        06-APR-2000;
                                                                                                                                                                                                        WO200059526-A1
                                                                                                                                                                                                                                              Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                           Bcl2 polypeptide
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                                         (UYJE-) UNIV JEFFERSON THOMAS
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ting neurodegenerative disord
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Wang J,
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                                                                               9905-0128202
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  Zhang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide;
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  Shan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 143; DB 21;
Pred. No. 5.1e-15;
Mismatches 0;
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e chain of the peptide w
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Length

28;

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The invention relates to a peptide conjugate having the formula:

(R-X)n repetide where no conjugate having the formula:

(R-X)n repetide where no conjugate having the peptide where

the functional group of the side chain is NH2 or OH; or X-OON

CC when the R-X group is attached to the C-terminus of the peptide, or a

side chain of the peptide, where the side chain functional group is containing one

or convir, and R-2-18C alkyl or alkoxy, 2-14C alkylanyl containing one

or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

CC monosubstituted with a 1-5C straight or branched chain alkyl group,

CC phanyl optionally monosubstituted with a 1-5C straight or branched chain

CC alkyl group, or benzyl. The peptides ABB7001-B3705B represent analogues

CC of a Rel-2 superfamily polypeptide corresponding to makin acids 72-07 of

the BB3 domain of the cell death agonist Bad. The peptide conjugate is

CC useful for modulating apoptosis in the cells of a subject, or for

CC superior Bc-2-1 relates the peptide conjugate is useful for treating a

custing B cell lymphoma/leukenia 2 (Bcl-2) mediated blockage of

conjugate is also useful for the conjugate is useful for the conjugate is

conjugate is also useful for the conjugate is useful for creating a

conjugate is also useful for treating dancers, neuroblastoma, melanoma, or

conjugate is also useful for treating disorders characterized by

conjugate is also useful for treating disorders characterized of

conjugate is also useful for treating disorders characterized of

conjugate is also useful for treating disorders characterized by

conjugate is also useful for treating disorders acquired

conjugate is also useful for treating disorders characterized by
Claim 18; Page 19; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (pcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
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밁 ô Best Local Matches Query Match Best Local Cytostatio; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl 2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis wodulation; B cell lymphoms/leukemia 2; cancer: prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction. WO200059526-A1 Homo sapiens. 28-FEB-2001 AAB37001 1 KNLWAAQRYGRELRRMSDEFEGSFKGL 27 polypeptide ch 100.0%; l Similarity 100.0%; 27; Conservative 0 standard; peptide; (first entry) BH3 domain peptide 0: Score 143; DB 21; Pred. No. 5.3e-15; Mismatches 0; Indels 0 Gaps 0:

07-APR-1999;

9905-0128202

06-APR-2000; 2000WO-US09352

12-0CT-2000

(UYJE-) UNIV JEFFERSON THOMAS

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RESULT

AAB37002

XX

XX

XX

AAB3

AC AAB3

AC AAB3

AC BCL2

XX

BCL2

XX

Cytc

KW COstc

KW Costc

KW Costc

KW Tostc

KW 
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                                                                                                                                                                                                                                                                                                                                         Bcl2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 18; Page 17; 74pp; English.
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                                                       WO200059526-AI
                                                                                                        Homo sapiens.
                                                                                                                                                      stroke; myocardial infarction
                                                                                                                                                                                melanoma; lymphocytic leukemia; neurodegenerative disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB37002 standard; peptide;
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100.0%;
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Pred. No. 2.9e-14;
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The invention relates to a peptide conjugate having the formula:

((R.X)n peptide where a = 1-10; X - C-0, when the R-X group is attached to the N-terninus of the peptide, or a side chain of the peptide where to the functional group of the side chain is NHZ or OH; or X = 0 or NH.

Che when the R-X group is attached to the C-terninus of the peptide, or a side chain of the peptide, where the side chain is functional group is COH or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or CONH2; and R = 2-18C alkyl or the C-terninus of the peptide, or a side chain of the peptide, where the side chain functional group is COH or two double bonds, cyclobutyl. cyclopartyl, cyclohaxyl optionally composite the consumption of the conjugate or branched chain alkyl group, or benzyl. The peptides with a 1-SC straight or branched chain alkyl group, or benzyl. The peptides ABB7001-337058 represent examples of the geptide peptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist BAd. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukenia 2 (Bcl.-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 conjugate is custous affilicted with a cancer includes prostate conjugate is useful for treating a consumption of the conjugate is conjugate in the coll of concerts, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by cancer cells that conjugate is also useful for peptide conjugate is neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for period cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for period cancers, neuroblastoma, acquired conjugate is also useful for cancer characterized by cancer characterized by cancer a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18;
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Query Match
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Matches 26
Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; Bid Jomain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblasioma; neuroma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
                                                                                                                          Bcl2 polypeptide BH3 domain peptide #3.
                                                                                                                                                                                                                                AAB37003 standard;
                                                                                                                                                              28-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100
nes 26; Conservative
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                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                peptide;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                         80
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WO200059526-A1

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RESULT
AAB7037
ID AAB7
XX AAB7
XX AAB7
XX O2-M
OT 02-M
XX Shor
XX Shor
XX Inmun
KW Ecl-
KW Limmu
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(C (R.N)n peptide where n = 1-10; X = C=0, when the R-X group is attached cot the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = 0 or NH.

CC when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is containing one or CONH2; and R = 2-18C alkyleryl, cyclohexyl optionally or containing one or two double bonds, cyclobutyl, cyclohexyl, cyclohexyl optionally complexed with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ANB37001-B37058 represent examples of the peptide with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ANB37001-B37058 represent examples of a Bcl 2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist BH3. The peptides conjugate is useful for modulating apoptosis in the cells of a subject, or for the BH3 domain of the cell death agonist BH3. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for creversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of conjugates in cancer cells; it is also useful for inhibiting Bcl-2 (C function. In particular, the peptide conjugate is useful for treating a subject affilteed with a cancer cincarecterized by cancer cells that consumption or thyroid cancers, neuroblostoma, melanoma, or conjugate is also useful for treating disorders characterized by cancer cells that conjugate is also useful for creating a conjugate is also useful for creating conjugate is also useful for cancer colls that conjugate is also useful for creating disorders characterized by cancer cells that conjugate is also useful for creating disorders characterized by cancer colls that conjugate is also useful for creating disorders characterized by cancer characterized by cancer characterized by cancer characterized by cancer characterized b
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Matches 26
Bcl-XL/Bcl-2 associated cell death regulator; BAD: mutant; apoptosis; immunostlmulant; neuroprotective; nootropic; antischaemic; vulnerary; cyrostatic; antiviral; antiarthritic; antilinflamatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
                                                                                                                                                                                       AAB70370;
                                                                                                    Shorter murine BAD mutant amino acid sequence
                                                                                                                                                02-MAY-2001
                                                                                                                                                                                                                              AAB70370 standard; protein; 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                   26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 17; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-US09352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9908-0128202
                                                                                                                                                                                                                                                                                                                                                                                                                                     96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 138;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shan S,
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
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                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 27;
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28-MAY-1999;
WPI; 2001-138734/14.
                                                                                                                                                                                                       30-MAY-2000; 2000WO-US11864
                                                                                                                                                                                                                                                                                                       WO200110888-A1
                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
                                                                                                (APOP-) APOPTOSIS TECHNOLOGY
                                                                                                                                                                                                                                                       15-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                 lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        lmmunodeficiency disease; neurodegenerative disease; viral infection;
ischaemic cell death; reperfusion cell death; arthritis; infertility;
                                                                                                                                                       9908-0136783
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New mutant Bol \*Ku/Bol-2 Associated Cell Death Regulator polypeptide, useful for sorreuning for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or Serll3 -

Claim 7; Page 148-149; 157pp; English

The present invention describes an isolated or synthetic polypeptide

(1) comprising a less than full length amino acid sequence of a mutant

CC English and session than full length amino acid sequence of a mutant

CC fragment, which contains amino acid substitutions at Serila of a human

CC BAD (shorter murine BAD). (1) has immunostimulant neuroprotective,

conotropic, antilischaemic, vulnerary, cytostatic.

CC antiarthritic, antilischaemic, vulnerary, cytostatic.

CC antiarthritic, antilischaemic, vulnerary, cytostatics, antiviral,

CC con be used as an apoptosis inducer or inhibitor. BAD polypeptides and

CC polynucleotides can be used for screening candidate compounds and drugs

CC for activity that promote cell survival or apoptosis. Other uses include

CC for activity that promote cell survival or apoptosis. Other uses include

CC inducing or inhibiting apoptosis in a cell. Candidate compounds

CC inducing or inhibiting apoptosis in a cell. Candidate compounds

CC interior or the present candidate compounds

CC imphoproliferative conditions, arthritis, infertility, inflammation and

CC alimed shorter murine BAD mutant amino acid sequence from the present

Sequence 162

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Query Match
Best Local S
Matches 26
2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                      l Similarity 100.0%;
26; Conservative
                    96.5%; Score 138; DE
100.0%; Pred. No. 2.7
Live 0; Mismatches
                                                 DB 22;
                       2.2e-13;
3s 0;
                                              Length 162;
                       Indels
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98

AAR95168 AAR95168 standard; Protein; 204 Ą

06-JAN-1997 (first entry)

bcl-x(L)/bcl-2associated death promoter protein.

Epitope: murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypeptide; bcl-x; cell death; regulate; BH1: BH2: apoptotic cell death cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

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Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                               This sequence represents the murine hol-x(L)/hol-2 associated death promoter (Bad) gene. Bad is a 22.1 kb protein which interacts with bol-2 and bol-x protein and requilates cell death. It has bomology to the bol-2 related family clustered in the Bil and BEZ domain. Bad has been found to hybridise to bol-x(L) and bol-2 in yeast two-hybrid asseys and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of bol-x(L), but is much less effective at countering the death inhibitory activity of bol-x(L). Bad expression can accelerate apoptocic cell death induced by cytokine deprivation in an IL-3 dependent cell in the expressing bol-x(L), and its also counters the death repressor activity of bol-x(L). Bad competes with Bax for binding to bol-x(L). Bad may be used to identify agents which inhibit its binding to bol-2 or bol-x(L) to form beterodimers. Such agents may be used to treat neurodegenerative diseases, immunodeficiency diseases, and NICs sensesone or rischements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide encoding bol-x(L)/Rcl-2 associated death promoter useful to treat neophasia and apoptosis and to identify agents inhibiting its binding to bol-2 or bol-x(L) to form heteromultimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-251465/25.
N-PSDB; AAT29479.
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                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 1; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Korsmeyer SJ;
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          Murine BCL-XL/BCL-2 associated cell death regulator.
                                    07-OCT-1998 (first entry)
                                                                                                AAW61315 standard; Protein; 204
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                                                                                                                                                                                                                                                                                                                                         senescence or ischaemia.
                                                                                                                                                                                                                                                                                                          204 AA;
                                                                                                                                                                                                                                 96.5%; Silarity 100.0%; Conservative 0;
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191..192
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                                                                                                                                                                                                                               Score 138; DB 17;
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0; Mismatches 0;
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WM with item mouse, BCL-XL/BCL-2 associated cell death regulator; BAD protein; we serine substituted mutant; apoptosis; cancer; viral infection.

XX Mus Sp.

XX WOS817682-A1.

XX WOS817682-A1.
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Matches
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Best Local
07-0CT-1998
                            AAW61316 standard; Protein; 204
                                                             و
                                                                                           Similarity 100.
26; Conservative
(first entry)
                                                                                                  96.5%;
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                                                                                                 Score 138; DB 19
                                                                                           Mismatches
                            Ş
                                                                                                          DB 19;
                                                                                            0
                                                                                                         Length 204;
                                                                                            0;
                                                                                            Gaps
                                                                                            0;
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Sequence

204 AA;

Mutant BCL-XL/BCL-2 associated cell death regulator #1.
Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD

B 8

SXAXEXEX

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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell clearly registator) proteins, having an maino acid other than Ser at C position 112 and/or 135, relative to the murine BAD 204 as sequence. The position 112 and/or 135, relative to the murine BAD 204 as sequence. The CC present sequence represents a mutant BAD protein. Also described are: (1) CC fusion proteins of mutant BAD protein as are used to treat cor prevent diseases associated with reduced appropriate. For covering infection, appropriate, infertility, (2) CC inflammation and autoimmune disease, Polynucleotias expences encoding mutant BAD proteins are used to treat covering infection, appropriated expences encoding mutant BAD proteins and autoimmune disease, Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated animals for use as disease models or in drug screening. BAD correcting shosphorylated septencers inhibitors are potentially useful intreatment of excessive apoptosis such as alias, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is considered and non-composition of proteins and non-composition of proteins have considered and polynophorylated and baD, by usual immunoassays mutant BAD proteins have compositing activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not become the protein activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not the cycosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Mutant BCL-XL/BCL-2 associated cell death regulator #2.
                                                                        07-OCT-1998
                                                                                                                                                 AAW61317;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-261422/23.
N-PSDB; AAV27834.
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26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.5%; Score 138; DB 19; ilarity 100.0%; Pred. No. 2.8e-13; Conservative 0; Mismatches 0;
                                                                   (first entry)
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                                                                                                                                                                                                                    Protein;
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell clear for regulator) proteins, having an amino acid other than Ser at C position 112 and/or 156, relative to the murine BAD 204 as sequence. The position 112 and/or 156, relative to the murine BAD 204 as sequence. The constitution of the present sequence represents a mutant BAD protein. Also described are: (1) CC fragments of mutant BAD protein BAD 204 as rejuence represents a mutant BAD protein. Also described are: (2) Cf fusion proteins of mutant BAD proteins polypeptide that the configuration of discasses associated with reduced approbals, e.g. cancer viral infection, lymphoproliferation, arthritis, infertility, (2) Cf inflammation and autoimmune disease. Polynucleotist esquences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug streening. BAD creations phosphorylated such as AIDS, neurodegeneration, and inhibitors of serine phosphatase. Inhibitors are potentially useful intendents of ischaemic cell death. The apoptotic status of cells is aging or ischaemic cell death. The apoptotic status of cells is considered apoptotic status of cells is considered and non-considered apoptotic status of cells is considered and proteins have considered and promoting activity than wild-type BAD which can become phosphorylated on the specified Ser; forming a product that does not a heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family considered considering cells used to the considered considering and considered considering and considered considering activity than wild-type and that the does not a possible that decrease of the considering cell survival. The mutants with constanting cell survival. The mutants with constanting cell survival.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 60; 95pp; English.
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N-PSDB; AAV27835.
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Sequence
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       204 AA;
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Query Match 96.5
Best Local Similarity 100.
Matches 26; Conservative
140 nlwaaqrygrelrrmsdefegsfkgl 165
                               2 NIWAAGRYGRELRRMSDEFEGSFKGL 27
                                                                      96.5%; Score 138; DB 19;
100.0%; Pred. No. 2.8e-13;
sive 0; Mismatches 0;
                                                                        Indels
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Length 204;

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AAW61318 AAW61318 standard; Protein; ζ

AAW61318;

07-OCT-1998 (first entry)

Mutant BCL-XL/BCL-2 associated cell death regulator #3.

Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein

Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

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AAW58832
ID AAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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Best Local S
Matches 26
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                                                                                                           Murine BAD protein
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N-PSDB; AAV27836.
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      BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;
                                                                                                                                                                                                                       23-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW58832 standard;
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llarity 100.0%;
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ches 0;
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serine phosphorylation; post-translational modification; apoptosis; signal transduction regulator; phosphoserine phosphatase; senescence; immunodeficiency disease; neurodegenerative disease; infertility; cancer, viral infection; lymphoproliferative condition; arthritis; inflammation; autoimmune diseases.
                                                                                                                result from immunodeficiency diseases, senescence, neurodegenorative disease, ischaemic cell death, reperiosion cell death, inferrility and wound healing. Decreased apoptosis may result from cancer, viral
                                                                                                                                                                         This sequence represents a novel serine-phosphorylated protein, BAD (BCI-XI/BCI-2 associated cell death regulator). The serine residue is phosporylated in a post-translational modification and allows binding to the 14-3-3 protein which is a signal transduction regulator. Modulators of phosphorylated BAD, which act through inhibition/activation of a phosphoserine phosphatase, are useful for preventing/treating increased/decreased apoptosis in a cell. The increased apoptosis may
                                                                                                                                                                                                                                                                                                                                        Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                           Serine-phosphorylated Bcl-X-l/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with,
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Sequence
                                  Infection, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. Measuring the amount of phosphorylated BAD polypeptide and/or total phosphorylated compared to unphosphorylated BAD in a cell is useful for determining the apoptotic state of a cell.
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                                                                                                                                                                                                                                                                                                                                     Fig 8; 61pp;
  204 AA;
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2.8e-13;
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immunostimulant; neuroprotective; nootropic; antisichaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiviral; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; archititis, infertility;

lymphoproliferative

condition; inflammation;

autoimmune disease

Bc1-XL/Bc1-2 associated cell death regulator; BAD;

mutant; apoptosis;

NO:2.

Longer murine BAD mutant amino acid sequence SEQ ID

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RESULT

02-MAY-2001

(first entry)

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Chimeric -
                                                                  Mouse: Bad-DTTR; apoptosis; cancer; spinal muscular atrophy; diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alabiamer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Synthetic.
                                                Huntington's disease.
                                                                                                                                                                                        Bad-DTTR apoptosis-modifying fusion protein.
                                                                                                                                                                                                                                              31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                               AAU00220 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-138734/14
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                                                                                                                                                                                                                                           (first entry)
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RESULT 1
AAW32476
ID AAW3
XX
AC AAW3
XX
DT 15-J
XX
DE BBC6

AAW32476 standard;

Protein;

166

15

15-JAN-1998 AAW32476

(first entry)

BBC6 protein for regulating

cell death.

밁

Matches

Mismatches

Indels

0,

Gaps

0

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modifying fusion protein comprising Bad gene sequence fused via a short linker to diphtheria toxin translocation domain (DYTR). The functional apoptosis modifying fusion protein is capable of binding a target cell and integrating into or crossing a cellular membrane of the target cell and integrating into or crossing a cellular membrane of the target cell and the Bcl-XL domain, which targets the fusion protein to the target cell. The papoptosis modifying fusion protein comprises at least two domains: the DTR domain, which modifies an apoptocit response of the target cell. The fusion protein is useful for modifying cellular general papoptosis in a target cell, such as neuron, improve, cancer, neoplasm, macrophage, epithelial, stem, tumour or hyper-proliferative cell or an adipocyte. It is also useful for reducing apoptosis in a subject after transient ischaemic neuronal injury, or hyper-proliferative cell or an adipocyte. It is also useful for reducing apoptosis in a subject after transient ischaemic neuronal injury, or hyper-proliferative conditions through inhibition or enhancement of apoptotic cellular response, including neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, spinal muscular atcophy, stroke episodes and unregulated cell growth as in tumour's and effectively throughout the body and targeted to selective tissue and
                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric - Corynebacterium diptheriae Chimeric - Synthetic.
                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Youle RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200112661-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents the amino acid sequence of Bad-DTTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-AUG-1999;
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  Local Similarity hes 26; Conserv
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96.5%; Score 138;
Llarity 100.0%; Pred. No.
Conservative 0; Mismatch
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3..12
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  . 8.6e-13; ches 0;
                                        DB 22;
                                      Length 567;
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via a shor
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Search completed: September 20, 2002, 10:35:59 Job time: 427 sec
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                                                                                                                               Ouery Match 79.7%: Score 114; DB 18; Length 166; Best Local Similarity 91.7%: Pred. No. 1.1e-09; Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                 The present sequence represents a protein of 166 amino acids. The sequence is disclosed as being a protein called BBC6 which regulates cell death through interaction with BC1-2. The DNA may be used for the production of the recombinant protein, which can be used in unspecified therapeutic or diagnostic procedures, as a molecular weight marker, and to raise antibodies that can be used in unspecified diagnostic or therapeutic applications and to reduce or eliminate the biological activity of the BBC6 protein in vivo.
                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Column 11-12; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Isolated BBC6 gene - encodes a protein that regulates cell death through interaction with \ensuremath{\mathsf{Bcl-2}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-447980/41.
N-PSDB; AAT91561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BBC6 gene; cell death; cell cycle; Bcl2; human.
                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CLON-) CLONTECH LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-1996;
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Title: Perfect score:

Scoring table: Sequence:

Maximum

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length:

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on:

OM protein

27, Appl 18, Appl 18, Appl 10, Appl 40, Appl 50, Appl 170, Appl

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Post-processing: Minimum Match 0%
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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//cgn2_6/ptcdata/2/laa/6A_COMB.pep:*
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US-08-61-479-2

US-08-733-505A-1

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US-08-733-505A-1

US-08-65-617-2

US-08-65-617-2

US-08-65-335-7

US-08-985-335-7

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US-08-733-505A-3

US-08-733-505A-3

US-08-733-505A-3

US-08-733-505A-3

US-08-733-705A-3

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(without alignments)
8.719 Million cell updates/sec
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   Sequence
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2. Appli
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                                                                                                                           NAME/KEY: Protein
LOCATION: 1.204
COTHER INFORMATION:
OTHER INFORMATION:
US-08-333-565-2
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US-08-33-565-2

(Sequence 2, Application US/08333565

PATENT NO. 562865

CORNEAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED

TITLE OF INVENTION: REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
SOFTWARE: PATENTH US/08/333,565
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SOILD, WILLIAM M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
   Query Match 96.5%; S. Best Local Similarity 100.0%; Matches 26; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 326-240
TELEFAX: (415) 326-2422
TELEFAX: (415) 326-2422
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2IF: 9434.
COMPUTER READABLE FORM:
COMPUTER READABLE Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FR PC COS/MS-DOS
COMPUTER: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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of mouse BAD."
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US-08-718-738-18
US-08-718-738-18
US-09-721-844-18
US-09-721-843A-40
US-09-299-843A-40
US-09-359-161-7
US-08-997-362-17
US-08-997-362-17
US-08-997-362-94
US-08-873-970-94
US-09-09-855-99
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      Score 138; DI
Pred. No. 7e
0; Mismatches
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Query Match

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Query Match
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                                                                                                                               RESULT
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                                     Sequence 1, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tent No.
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726a-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KORSMEYER, Stabley J.
TIFLE OF INVENTION: REGULATOR
TIFLE OF INVENTION: REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                    140 NIWAAQRYGRELRRMSDEFEGSFKGL 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 11-JUN
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                                                                                                                                                                                                         2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
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of mouse BAD."
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                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Watches 26; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                CLASSIFICATION: 530
ATTORREY/AGENT INFORMATION:
ANAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                            MEDLIM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION NUMBER: US/08/733,505A
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREWN APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (314) 727-5188
TELECOMMUNICATION INFORMATION:
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                                                                                                FILING DATE:
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STATE: MI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 63105
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o. 5856445
                                                                                                                                                                                                                                   63105
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                                                                                                                                                                                                                                                                                                                                                              SERINE SUBSTITUTED MUTANTS OF BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.5%; Score 138; DB 2;
100.0%; Pred. No. 7e-14;
tive 0; Mismatches (
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                                                                                                                                                                                                                           CLASSIFICATION: 530
ACTORREY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R. 17
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEPAX: (314) 727-592
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5856445
GENERAL INFORMATION:
                                                                       Query Match
Best Local
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Best Local Similarity
                                                         Matches
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TELEPAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
                                                                                                                                      STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
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                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                     Local Similarity
                                                                                                                                                                                                  LENGTH:
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             2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
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                                                                                                                                                                                 i: 204 amino acids
amino acid
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7733 FORSYTH BLVD., SUITE 1400
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VENTION: SERIUE SUBSTITUTED MUTANTS OF
VENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                     Score 138;
Pred. No.
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Pred No.
                                                                                                                                                                                                                                                                                        965458
                                                         Mismatches
                                                                   7e-14;
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                                                                                 DB 2; Length 204;
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RESULT

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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-733-505A-14
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                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application Patent No. 5965703
GENERAL INFORMATION:
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Best Local Similarity
Matches 26; Conserva
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APPLICANT: KORSMEYER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (314) 727-6092 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                             COMPUTER READABLE FORM:
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APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF ESQUENCES: 15
CORRESPONDENCE ADDRESS:
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ADDRESSEE: HOWELL & HAFERKAMP, L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TELEPHONE: (314) 727-5188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                    STREET: 4370 La
CITY: San Diego
STATE: Californ
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CITY: ST. LOUIS
STATE: MISSOURI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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ZIP: 63105
                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/733,505A
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                                                                                                                                                      California
                                                                                                                                                                                   E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 amino acids
                                                                                                                               United States
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Pred. No. 7e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 204;
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APPLICATION NUMBER: US/08/717,123

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US-08-665-617-2
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US-08-717-123-3
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                                                      Query Match
Best Local 9
                                     Matches
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Best Local Similarity 96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 25;
                                                                                                                                                                                                                                  TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                         NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death NUMBER OF SEQUENCES: {\bf 2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 NLWAAORYGRELRRMTDEFEGSFKGL 165
                                               V Match 79.7%; Score 114; DB 1; Local Similarity 91.7%; Pred. No. 2.8e-10;
                                                                                                                                                                                               TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2421 N.W. CITY: Gainesville STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
2 NLWAAQRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  535-8949
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Pred. No. 2e-13;
                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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                                                                 Length 166;
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                                Indels
                                0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell; Cathryn A.
REGISTEATION NUMBER: 91,815
REFERENCE/DOCKET NUMBER: 91,915
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                           Sequence 1, Applic
Patent No. 6080847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.7%; Score 114;
Best Local Similarity 91.7%; Pred. No. 2.
Matches 22; Conservative 0; Mismatche
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Sequence 2, APP--
+ No. 5965703
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                 APPLICANT: Hillman, Jennife
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Oxley, Neil C.
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
UMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 535-89 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic TITLE OF INVENTION: Acids and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Horne, William A. APPLICANT: Oltersdorf, Tilman
                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 4370 La
CITY: San Diego
STATE: Californ
                                                                                                                                                                                                                                                                                                                                                                                                                                            2 NLWAAQRYGRELRRMSDEFEGSFK 25
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Palo Alto
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States
                                                                                                                                                                                                                                                   Hillman, Jennifer L.
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                                                                                                                        PROLIFERATION
                                                                                                                                            PROTEINS ASSOCIATED WITH CELL

 Mismatches

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2.8e-10;
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COUNTRY: U

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US-08-985-335-7
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                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 60808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.7%;
Best Local Similarity 91.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
                         SOFTWARE: FastSPO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/985,335 FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: SYNOF
CLONE: 358673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/98 FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                   APPLICANT: COTIEY, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
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MEDIUM TYPE: Diskett
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                                                                 ZIP: 94304
                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                            CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650-845-4166
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FastSEQ for Windows Version 2.0
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Pred. No. 2.
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; LIBRARY: GenBank
; CLONE: 1683637
US-08-985-335-7
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Patent No.
                                        TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
TYPE: amino acid
TYPANDEDNESS: single
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
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REGISTRATION NUMBER: 36,749
REFERENCE,DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for CURRENT APPLICATION DATA: OF APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                            NAME: Billings, Lucy J.
REGISTION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
            TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 NLWAAORYGRELRRMSDEFVDSFK 126
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CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                   FILING DATE:
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3174 Porter Dr.
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SYNORAB03
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                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                         Diskette
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91.7%;
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US-09-410-372-1
RESULT 14
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US-09-410-372-7
                                                                                                               Query Match
Best Local
                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09410372 Patent No. 6281334
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                                                                                                                                                                                                                                                                      TELEFAX: 650-845-4156
NFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/410,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION. PROLIFERATION
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yue, Henry APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
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nes 22; Conserv
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                                                                                                1 Similarity
22; Conser
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                                                                                                                                                                                                                                                                    168 amino acids
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3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                   650-845-4166
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                             79.78;
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                                                                                               Score 114; DB 4;
Pred. No. 2.8e-10;
0; Mismatches 2;
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Pred. No. 2.8e-10;
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                                                                                                                                                                                                                                                                                                                                               US-08-661-479-10
                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: SMITH, WILLIAM M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1572
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHAI: (415) 326-2422
INFORMATION FOR 580 ID NO: 10:
                                                                                                                                                                                                                                                                                                            Sequence 10, App
Sequence 10, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Appl. Patent No. 562285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 79.0
Best Local Similarity 100
Matches 21; Conservative
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-007-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: STREET: STREET: Palo Alto CITY: Palo Alto CTATE: California
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                                                                                                                                                                                                                                                                               APPLICANT:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                              COUNTRY:
  APPLICATION NUMBER:
                                                                                                                                                                                STREET:
                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                  379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Townsend and Townsend Khourie and Crew 379 Lytton Avenue
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WENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
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100.0%; pr
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Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
US/08/661,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 113;
Pred. No.
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Perfect score:
Sequence:
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                         US-09-544-664-56
143
                                                                                 September 20, 2002, 10:39:13 ; Search time 95.59 Seconds (without alignments) 27.141 Million cell updates/sec
     1 KNLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:

283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	æ	7	6	ψı	4	ω	, 2			Result No.
45 5	45.5	45.5	46	46	46	46	46	46.5	46.5	46.5	47	47	47	47.5	48	48	48	48.5	48.5	49	50	50	15	52	53	53	54	138	1 1 1 1 1 1	Score
31 8	31.8	31.8	32.2	32.2	32.2	32.2	32.2	32.5	32.5	32.5	32.9	32.9	32.9	33.2	33.6	33.6	33.6	33.9	33.9	34.3	35.0	35.0	35.7	36.4	37.1	37.1	37.8	96.5		Query Match Length
327	287	261	1378	1164	946	399	165	1140	435	314	5138	967	597	334	526	220	205	314	134	453	516	374	232	370	946	223	946	204		enath DB
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D97636	S43852	669510	A81393	T24806	IYHU2	T35440	259899	T09486	A44308	T02961	B96695	F82668	G82308	A39172	T08545	F72289	C36365	T02975	S40376	E83517	A96753	C84338	A42095	S38185	S54354	D70760	JC5575	A55671		IĐ
probable secreted (	neuropeptide Pol-R	conserved hypothet	DNA-directed RNA p	hypothetical prote	inter-alpha-trypsi	probable polyamine	chlorocruorin chai	hypothetical prote	Antho-RFamide prec		hypothetical prote	oxoglutarate dehyd	oxaloacetate decar	Antho-RFamide neur	threonine synthase	oxidoreductase, so	transforming prote	annexin P35 - maiz	Ig kappa chain - h	conserved hypothet	probable threonine	spermidine/putresc	floral homeotic pr	2-dehydro-3-deoxyp	inter-alpha-inhibi	hypothetical prote	inter-alpha-trypsi	bad protein - mous		Description

hypothetical	T19472	N	1263	31.5	÷	45
hypothetical	T22672	ı	1217	31.5	4.0	4
hypothetical prote	T23005	2	1199	31.5	45	43
env polyprotein -	VCLJG4	, 1-1	864	31.5	45	42
probable membrane	S52675	N	715	31.5	45	41
oxaloacetate decar	A28088		596	31.5	45	40
oxaloacetate decar	AE0909		591	31.5	45	39
0	AB0509		591	31.5	45	38
sodium ion pump ox	B44465	2	591	31.5	45	37
conserved hypothet	H95406		346	31.5	45	36
conserved hypothet	F83201		295	31.5	45	35
manganese-stabilzi	AG2287		273	31.5	45	34
photosystem II oxy	S06736		273	31.5	45	ω ω
NADH dehydrogenase	G83314		905	31.8	45.5	32
hypothetical prote	C71473		562	31.8	45.5	31
conserved hypothet	AF2859		327	31.8	45.5	0.6

#### ALIGNMENTS

nesury 1
A55671
A55671
bad protein - mouse
c;Species; Mus musculus (house Mouse)
c;Accession; A55671
R;Yang, E; Zha, J; Jockel, J; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
cell 80, 285-291, 1995
A;Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot
A;Reference number: A55671; MUID:95136361
A;Recession; A55671; MUID:95136361
A;Recession; A55671; MUID:95136361
A;Recession; A55671
A;Accession; A55671
A;Accession; B55671
A;Accession; B5 QY Best Local Query Match Best Local al Similarity 26; Conserv Conservative 96.5%; Score 138; DB 2; 1 100.0%; Pred. No. 9.4e-13; Live 0; Mismatches 0; Length 204; Indels 0, Gaps 0;

inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster c;Species: Mesocricetus auratus (golden hamster) c;Species: Mesocricetus auratus (golden hamster) gorden hamster) c;Date: 23-5ep-1997 #text\_change 20-Jun-2000 c;Accession: JC5575; Pc4485 f;Rinketanit, T; Surukit, Y; Yamamoto, T.; Sinchiara, H. J. Biochem, 122, 71-92, 1997 J. Biochem, 122, 71-92, 1997 A;Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs sin inhibitor heavy chain family.

A;Ritle: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs sin inhibitor heavy chain family.

A;Recession: JC5574; MUID:97420688

A: Molecuile type: nRNA
A: Rosidues: 1-946 < NANA
A: Rosidues: 1-948 < NANA
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C. Species: Mus musculus (house mouse)
C. Species: Mus musculus (house mouse)
C. Species: Naturily5 sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
C. Accession: $54354
C. Superfamily: Inter-alpha-trypsin inhibitor complex component II
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Ground protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)

Ground protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)

Ground Rv2014 - Mycobacterium tuberculosis

Ground Rv2014 - Mycobacterium tuberculosis

Ground Rv2014 - Mycobacterium tuberculosis (strain H37RV)

Rv2016 - St.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;

Rojandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skolton, S.; Squares, S.;

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skolton, S.; Squares, S.;

Rajandream, M.A.; Rogers, J.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A. Title: Dockphering the biology of Mycobacterium tuberculosis from the complete genome

A. Reference number: A70500; MUID:9839599

A. Accession: D70760
            RESULY 5
S38185
2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) ARO4 ~ yeast (Saccharomyces ce R;Alternate names: 3-deoxypyces cervisiae
C Species: Saccharomyces cervisiae
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A;Residues; 1-223 <COL>
A;Cross-references: G8:Z74025; G8:AL123456; NID:g3261586; PIDN:CAA98415.1; PID:e1299911
A;EXpertmental source: strain H37Rv
C;Genetics
A;Gene: Rv2014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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Best Local Similarity 58.8
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 34.0
9; Conservative
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9: Conservative
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Pred. No. 10;
5; Mismatches 1
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Pred. No. 3.2;
1; Mismatches
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A4205
A42
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A;Gene: SGD:AROd
A;Cross-references: SGD:S0000453; MIPS:YBR249c
A;Map position: 2R
C;Punction: Aldehyde-lyase; carbon-carbon lyase
A;Description: aldehyde-lyase; carbon-carbon lyase
A;Bascription: aldehyde-lyase; carbon-carbon lyase
A;Bascription: aldehyde-lyase; bikimate pathway
A;Rote: first steep in shikimate pathway
A;Rote: first steep in shikimate pathway
C;Superfamily: phospho-2-dehydro-3-deoxyhaptonatc aldolase
C;Keywords: aldehyde-lyase; aromatic amino acid biosynthesis;
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A:Molecuie type: DNA
A:Residues: 1 370 <AIG>
A:Residues: 1 370 <AIG>
A:Residues: 1 370 <AIG>
A:Residues: 1 370 <AIG>
A:Cross-references: EMBL::236118; NID::g536664; PIDN::CAA85212.1; PID::g536665; MIPS:Y
A:Cross-references: EMBL::236114; G.; Eg11, C.M.; Irnlger, S.; Braus, G.H.
A:Fulta: Cloning, Primary structure and regulation of the ARO4 gene, encoding the
A:Reference number: JN0322; MUID::92225349
A:Accession: JN0322
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RIA491e, M.; Baclet, M.C.; Barthe, C.; Elteau, M.; Crouzet, M.; Dolgnon, F.
submitted to the Protein Sequence Database, August 1994
A; Reference number: 845940
A;Accession: 946130.
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Best Local S
Matches 10
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Pred. No. 7.5;
5; Mismatches
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A;Map position: 3
A;Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
A;Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
A;Note: T12E18:30
A;Note: T12E18:30
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homology C;Superfamily: transcription regulation
C;Repwords: DNA binding nucleus; transcription regulation
C;Repwords: DNA binding domain homology <SRE>
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A; Residues; 1-32 < PLO>
A; Residues; 1-32 < PLO>
A; Cross references; EMBL; ALI32971
A; Experimental Source: cultivar Columbia; BAC clone T12E18
C; GenetLos;
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A;Experimental source: petals, Stamens
A;Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBIP:82521)
R;Okamoto, H.; Yano, A.; Shiraishi, H.; Okada, K.; Shimura, Y.
Plant Mol. Biol. 26, 465-472, 1994
A;Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabid A;Reference number: $52633; MUID:95036018
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C;GenetLus:
A;Gene: puck2
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A; Accession: T47593
A; Status: preliminary
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R;Bloecker, H; Mewes, H;W;Lemcke, K;; Mayer, K.F.X.; Quetier, F;; Salanoubat M.Mewes submitted to the Protein Sequence Database, March 2000
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A; Residues: 1-374 <STO>
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A;Accession: C84338
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A; Residues: 1-63 <OKA>
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Best Local Similarity
Matches 12; Conserv
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                                                             Matches
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les 10; Conserv
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; Pred. No. 6.5;
3; Mismatches
                                                           <u>,</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein PA1031 (imported] - Pseudomonas acruginosa (strain C;Specias: Pseudomonas acruginosa C;Date: 15-Sep-2000 *text_change 31-Dec-2000 C;Accession: E83517
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E83517
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A;Molecule type: DNA
A;Residues: 1-453 <STO>
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A.Reference number: A82950; MUID:20437337
A.Accession: E83517
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Nature 406, 959-964, 2000
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                     S40376
                                      RESULT
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A;Experimental source: strain PAO1
Ig kappa chain
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                                                                                                                                     4 WAAQRYGR--ELRRMSDE 19
                                                                                                 WASERQGREEELRRLASE 82
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Conservative

34.3%; 55.6%;

Pred. No. 25; 4; Mismatches Score 49; Pred. No.

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Indels

2

Gaps

1;

ВВ N

Length 453

an opportunistic pa

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C;Rccession: A96733
G;Rccession: A96733
G;Rccession: A96733
G;Rccession: A96734
G;Rccession: A96741; MUID: 21016719
G;Rccession: A96741; MUID: 21016719
G;Rccession: A96741; MUID: 21016719
G;Rccession: A96743
G;Rccession: A9674
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A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gross-references: GB:AE005173; NID:g5903070; PIDN:AAD55628.1; GSPDB:GN00141C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable threonine synthase [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 31-Mar-2001 *c.Species (C.Species) (C.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-516 <STO>
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163 NLFWAERFGKQYLQMNDLWVKHCGISHTGSFKDL 196
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Pred. No. 21;
7; Mismatches
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C;Becles: RhZmomcor racemosus
C;Becles: 28-Mar-1991 *sequence_revision 28-Mar-1991 *text_change 19-Jan-2001
C;Accession: C3636 *sequence_revision 28-Mar-1991 *text_change 19-Jan-2001
C;Accession: C3636 *sequence_revision 28-Mar-1991 *text_change 19-Jan-2001
C;Accession: C3636 *sequence_revision 28-Mar-1991 *text_change 19-Jan-2001
A;Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which exhit A;Reference number: A36365; MUID:91061774
A;Reference number: A36365; MUID:91061774
A;Accession: C3636 *sequence constant and con
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C:Capacies (6-Mar-1994 #sequence_revision 26-May-1995
C:Accession: $40376
C:Accession: $40376
R:Kilein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes
A:Reference number: $40312; MUID:94080891
A:Accession: $40376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: I-314 <BATY
A;Residues: I-314 <BATY
A;Residues: I-314 SATY
A;Cross references: EMBL:X98245; NID:g1370602; PIDN:CAA66901.1; PID:g1370603
A;Experimental source: cultivar clipper; root tip
C;Superfamily: annexin I; annexin repeat homology
F;14-85/Domain: annexin repeat homology <AXRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Battey, N.H.: James, N.C.: Greenland, A.J. Plant Physiol. 112, 1391-1396, 1996
A:71Itle: CDNA isolation and gene expression of maize A:Reference number: Z14796; MUID:97092863
A:Accession: T02975
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C:Date: 24-mar-1999 #sequence_revision 24-mar-1999 #text_change 21-Jul-2000
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A; Residues: 1-134 <KLE>
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Date: 06-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000;Accession: S40376
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Best Local
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47.6%; Pred. No. 21;
ative 4; Mismatches
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C; Superfamily:
                                                                                                                                                                                                                                   A; Accession: S71362
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A; Accession: S74307
A; Molecule type: protein
A; Residues: 40-54 <CUI>
                                                              A:Molecule type: mRNA
A:Residues: 'L',3-526 <CUR>
A:Cross-references: EMBL:L41666;
                                                                                                                                                      A;Experimental source: cultivar Columbia; BAC clone F27B13
R;Curien, G.; Dumas, R.; Ravanel, S.; Douce, R.
FEBS Lett. 30, 85-90, 1996
A;Title: Characterization of an Arabidopsis thaliana cDNA encoding
A;Reference number: S71362; MUID:96314555
                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-526 <BEV>
A; Cross-references: EMBL; ALO50352; GSPDB; GN00062; ATSP; F27B13.80
A; Cross-references: cultivar Columbia; BAC clone F27B13
                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: protein F27B13.80
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 07-Dec-1999
C;Accession: T08545; S71362; S74307
R;Bevan, M.: Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewe submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-220 <ARN>
A; Cross-references: GB: AE001772; GB: AE000512; NID: 94981693; PIDN: AAD36230.1; PID: 9498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Title: Evidence for lateral gene transfer between Archaea and Bacteria from A; Reference number: A72200; MUID:99287316 A; Accession: F72289
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: F72393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Accession: F72289
R;Nelson, K.E.; Clayton,
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F:123-126/Region: GTP-binding NXDL motif
F:133-155/Region: GTP-binding SAK/L motif
F:23.24,42,123,124,126,153/Binding site: Mg-GTP (Lys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 399, 323-329, 1999
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8; Conser
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                                                                 NID: 91448916;
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16;
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                                                                                                                                                                                                                                                                                                                                                                                                                          R.; Bancroft, I.; Mewes, H.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ser, Thr,
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Antho-RRamide neuropeptide 19 repeat precursor - sea anemone (Calliactis parasitica) C:Species: Calliactis parasitica C:Species: Calliactis parasitica C:Date: 07-Feb-1992 *sequence_revision 07-Feb-1992 *stext_change 21-Jul-2000 C:Accession: A39172
C:Accession: A39172
R:Darmer, D.; Schmutzler, C.; Diekhoff, D.; Grimmelikhuijzen, C.J.P.
Proc. Natl. Acad. Scil U.S.A. 88, 2555-2559, 1991
A:Title: Primary structure of the precursor for the sea anemone neuropeptide Antho-RFami A:Reference number: A39172; MUID:91172845
A:Accession: A39172
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-334 CDRP>
A:Cross-references: GB:M59166; NID:g156133; PIDN:AAA27878.1; PID:g156134
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A;Gene: A759:F27B13.80
A;Gene: A759:F27B13.80
A;Map position: 4
A;Map position: 4
A;Genome: nuclear
C;Keywords: carbon-oxygen lyase; chloroplast
F;1-39/Domain: transit peptide (chloroplast) #status predicted <TNP>
F;10-526/Product: threonine synthase #status experimental <MAT>
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Search completed: September 20, 2002, 10:39:13 Job time: 485 sec
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Query Match
Similarity 44.0%, Pred. No. 31;
Matches 11; Conservative 3; Mismatches 10;
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Best Local Similarity 35.3%;
Matches 12; Conservative (
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89 KRRYVPGRYGREFQGREFQGRE 113
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          BIM_MOUSE
BIM_RAT
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SYM_THEMA
ENV_SIVA1
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NUOG_SALTY
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23.237 Million cell updates/sec
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1. SUBUNNIT: Forms heterodimers with the anti-apoptotic proteins, Bel-x(I), Bel-2 and Bel-w. Also binds protein S100AN10 [By similarity). The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.

1. SUBCELIULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.

1. DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bel-2 family.

1. PTM: Phosphorylated on Ser-112 in response to survival stimuli. Subsequent phosphorylations. This interaction then facilitates the phosphorylations. This interaction then facilitates the phosphorylations at Ser-155, a size within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival.
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661337;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
BCl2-antagonist of cell death (BAD) (BCl-2 binding component
6) (Bcl-xL/Bcl-2 associated death promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Bad, a heterodimeric partner for Bc1-XL and Bc1-2, displaces Bax and promotes cell death.", cell 80:285-291(1895).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "14-3-3 proteins and survival kinases cooperate to inactivate BAD BH3 domain phosphorylation.";
Mol. cell 6:41-51(200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B., Greenberg M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Del Peso I., Gonzalez-García M., Page C., Herrera R., Nunez G.;
"Interleukin-3-induced phosphorylation of BAD through the protein
klnase Akt.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain, and Thymus;
MEDLINE-95136361; PubMed-7834748;
Yang E., Zha J., Jockel J., Boise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND MEDLINE-98022383; PubMed-9381178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20403302; PubMed=10949026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGENESIS OF SERINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 278:687-689(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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UVRA_STRCO
DPG1_XENLA
APJ_MOUSE
ADJ_HUMAN
APJ_MACMU
DHAP_MOUSE
Y030_NPVAC
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P73527
Q92507
Q91684
Q94V08
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Q97666
P47739
P41734
P11071
P51067
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Result No.

Score

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035147; 070256; 090HX1;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
BC12-antagonist of cell death (BAD) (BC1-2 binding component 6) (BC1-xL/BC1-2 associated death promoter).
                                                                                                                                                                                                                                   MEDLINE-98194755; PubMed-9535132; D'Agata V., Magro G., Travall S., Musco
                                                                                                                                                                                                                                                                                                                                                                    HSu S.Y., Kaipla A., Zhu L., Hsuch A.J.W.;
"Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
Mol. Endocrinol. 11:1858-1867(1997).
                               MEDLINE~21109372;
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                           "Cloning and expression the rat brain.";
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98034386; PubMed-9369453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is along as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUTAGEN
MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1096330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L37296; AAA64465.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000712; Bcl_2
PROSITE; PS01259; BH3; FALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NLWAAQRYGRELRRMSDEFEGSFKGL
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SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 100
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation.
147 161
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                                                                                                                                               243:137-140(1998).
                               PubMed=11161472;
                                                                                          (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22080
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Yu L.-Y., Sun Y.-F.,
                                                                                                                                                                                                       of the programmed co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          death promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY CAPK A)
PHOSPHORYLATION (BY CAPK A)
PHOSPHORYLATION (BY CAPK A)
S-A: NO PHOSPHORYLATION.
S-A: NO PHOSPHORYLATION.
S-A: NO PHOSPHORYLATION.
S-A: NO PHOSPHORYLATION.
BCL-X(L)
BCL-X(L)
BCL-X(L)
BCL-X(L)
                                                                                       ALPHA
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Pred. No.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
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                                                                                          AND
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                                                                                                                                                                                                   cell death regulator BAD
Saarma M.,
                                                                                                                                                                                                                                   Cavallaro S.;
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; Murinae; Rat
Lindholm
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DINA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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ITEMENTIAL PRODUCTS: 2 isoforms; alpha (Shown here) and by alternative splicing. They differ only in the reproduced by alternative splicing. They are the service some specific specifi
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-i- FUNCTION: Promote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bel-2 family.

PTM: Phosphorylated on Ser-113 in response to survival stimuli. Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14-33 proteins. This interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bel-x(L) and the promotion of cell survival. Ser-137 is the major site of AKT/PKB phosphorylation. Ser-156 the major site of protein kinase A (CAPK) phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS A BCL-3 HOMOLOGY DOMAIN 3 (BH3). SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: Expressed in all tissues tested, brain, liver, spleen and heart. In the brain, restric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the meaburdant form.
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CONFLICT MUTAGEN VARSPLIC use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). MUTAGEN EMBL; AF003523; AAC53374.1; -. EMBL; AF031227; AAC15100.1; -. EMBL; AF279910; AAF91427.1; -. EMBL; AF279911; AAF91428.1; -. This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extended the European Bioinformatics Institute. There are no restrained the European Bioinformatics Institute. MOD\_RES MOD\_RES Apoptosis; PROSITE InterPro; PS01259; IPR000712; 205 Phosphorylation; 137 113 166 156 137 29 Ã, внз; 137 113 205 156 137 34 22228 BCL\_2 FALSE\_NEG ¥. Alternative splicing WITH 14-3-3 PROTEINS. S->A: NO HETERODIMERIZATION WITH -> EELTYSVEFLPVRAIAMEGWPLLWSFQSFPHTLPPTPP EVAMFPLRYWTALRRLC (IN ISOFORM BETA). S->A: NO EFFECT ON HETERODIMERIZATION PHOSPHORYLATION (BY CAPK AND PKB) SIMILARITY). WITH BCL2 NOR WITH PROTEIN P11. PROTEINS SIMILARITY). LPRPKSAGTATOMRQSASWTRIIQSWWDRNLGKGGSTPSQ PHOSPHORYLATION (BY CAPK AND PHOSPHORYLATION (BY CAPK AND PKB) DAGGR -> ERRGRK (IN REF. 7AFA71DAE9CF4A81 CRC64; NO EFFECT ON HETERODIMERIZATION There are no restrictions on ng as its content is in no REF. 1). EMBL outstation PKB) collaboration (BY (BY (BY

Query Match Best Local

Local Similarity

96.5%; 50. 100.0%; Pr

Score 138; I Pred. No. 1

В .2e-13; 0 Length

Mismatches

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Gaps

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Conservative

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NLWAAQRYGRELRRMSDEFEGSFKGL

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MEDLINE=97083574; Pu
Wang H.-G., Rapp U.R
"Bcl-2 targets the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAD_HUMAN STANDARD; PRT; 168 AA. 092934; 014803; 01-NOV-1997 (Rel. 35, Created) 16-007-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) 01-dara-dagonist of cell death (BAD) (Bcl-2 binding 5) (Bcl-3L)Fcl-2 associated death promoter). BAD OR BBC6 OR BCL216.
binding to Bcl.x(L), Bcl.2 and Bcl.w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl.x(L), but not that of Bcl.2 (By similarity). Appears to act as a link between growth factor. receptor signaling and the apoptotic pathways.

1. SUBUNIT: Forms beterodimers with the anti-apoptotic proteins, Bcl.x(L), Bcl.2 and Bcl.w. Also binds protein $100A10 (By similarity). The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By similarity).

1. SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.

1. TISSUE SPECIFICITY: EXPRESSED IN AWIDE VARIETY OF TISSUES.

1. DOMAIN: Intact BH3 domain is required by BHK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl.2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mack J.
Fesik S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          שייים אומים של Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae. NCBL_TaxID=9806;
                                                                                                                                                                                                                                                                                                                                                                         "Rationale for Bcl-xL/Bad peptide complex mutagenesis, and biophysical studies."; Protein Sci. 9.2328-2534 (2000).
-1- FUNCTION: Promotes cell death. Success
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Petros A.M., Nettesheim D.G., Wang Mack J., Swift K., Matayoshi E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 103-127.
MEDLINE=21073561; PubMed=11206074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
TISSUE-Bone marrow;
MEDLINE-98049554; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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Takayama S., Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A human protein that interacts BAD.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INE=97083574: PubMed=8929532;
H.-G., Rapp U.R., Reed J.C.;
-2 targets the protein kinase
87:629-638(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLWAAQRYGRELRRMSDEFEGSFKGL 166
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***. Diaz J.-L., Horne W., Chang J.,

**Weeks S., Fritz L.C., Oltersdorf

**Lion properties of human BAD.**;

Chem. 272:30866-30872(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S., Reed J.C.;
(OCT-1997) to
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Zhang H., Thompson C.
                                                                                                                                                                                                                                                                                                                                                                            Successfully
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h Bcl-2
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2 NLWAAQRYGRELRRMSDEFEGSFK 25

Matches Query Match Best Local

Similarity

79.78;

Conservative

0;

Pred. No. 4e-); Mismatches Score 114;

4e-10; DB ۲,

Length 168;

N

0;

Gaps

0

밁

103

NLWAAQRYGRELRRMSDEFVDSFK 126

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Apoptosis;
                                                                                                                                                                                       EMBL;
EMBL;
                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities reguires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE
                      CONFLICT
                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÷
                                                                       MOD_RES
                                                                                                                                      PROSITE.
                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                   PTM: Phosphorylated on Ser-75 in response to survival stimults Subsequent phosphorylation on Ser-99 promotes heterodimerizate with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-118, a site within the B43 domain, lead to the release of Bcl-x(L) and the promotion of cell survival Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 major site of protein kinase A (CAPK) phosphorylation (by Similarity).

SIMILARITY: CONTAINS 1 BCL-3 HOMOLOGY DOMAIN 3 (BH3).
                                                                                                                                                               603167
                                                                                                                                                                          1G5J; 07-FEB-01
                                                                                                                                                                                     U66879; AAB36516.1; -. AF021792; AAB72092.1; -. AF031523; AAB88124.1; -. BC001901; AAH01901.1; -.
                                                                                                                                      PS01259;
                                                                                                                                                 IPR000712; Bc1_2
                                                                                              Phosphorylation;
110 124
75 75
168
                                                118
                       64
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ĀΑ;
                                                                                                                                      вн3;
                                                118
18392
                       91
                                                                        99
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WW;
                                  PHOSPHORYLATION
SIMILARITY),
PHOSPHORYLATION
SIMILARITY),
PHOSPHORYLATION
SIMILARITY).
                                                                                                                         3D-structure
                                                                                                                                      LNEG
PQLLPRGDGGRRRDGGGAQ
69FD8D27DDEE3241 (
                         AGAVEIRSRHSSYPAGTEDDEGMGEEPS
                                                                                                            внз
                                                (BY
                                                                       (BY
                                                                                                YB)
Q (IN REF.
CRC64;
                                                                       CAPK
                                                                                                 CAPK
                                                CAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                          heterodimerization
                                                AND
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                                                                        PKB)
                                                PKB)
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                         RWGCGDPES
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                                                (BY
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RESULT
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15-7UL-1998 (Rel. 36, Created)
15-7UL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update inter-alpha-trypsin inhibitor heavy chain H chain H2) (HC2).
                                                                                                                                                                                                                                                                                                                                                                                                                            MESAU
Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.; Whiteular Cloning and sequencing of cDNAs encoding three precursors of the inter-alpha-trypsin inhibitor in Syrian implications for the evolution of the inter-alpha-trypsin
                                                                                                    TISSUE-Liver;
                                                                                                                                                        Mesocricetus,
NCBI_TaxID=10036;
                                                                                                                                                                                                   Eukaryota;
Mammalia;
                                                                                MEDLINE=97420688; PubMed=9276673;
                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           Mesocricetus
                                                                                                                                                                                                                                                               ITIH2.
                                                                                                                                                                                                :; Metazoa;
Eutheria;
                                                                                                                                                                                                                                           auratus
                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                           (Golden hamster)
                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                  on update)
                                                                                                                                                                                                                                                                                                    precursor
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                    heavy-chain
hamster:
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RESULT 5
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Best Local &
Matches
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A TOTEET ALDBA "CRY9SIA" INDIBITION AND ITS FELATED PROTEINS IN SYFIAN

TOTEET ALDBA "CRY9SIA" INDIBITION AND OTHER MATRIX PROTEIN.

A BINDING PROTEIN BETWEEN HYALIFROMA AND OTHER MATRIX PROTEIN.

COLLIZATION, SYNTHESIS AND DEGRADATION OF HYALIFROMAN WHICH ARE

ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY

SIMILARITY).

COLUMN INTER ALPHA INTERIFF AND DEGRADATION OF HYALIFROMAN WHICH ARE

ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY

SIMILARITY).

COLUMN INTER ALPHA HALFING (11, 12 OR H3) AND ONE LIGHT CHAIN,

BIKUMIN. INTER ALPHA HALFING (1 ALPHA I) IS COMPOSED OF H1, H2

AND BIKUMIN, AND PRE-ALPHA INTERITOR (1 ALPHA I) OF H3 AND BIKUMIN,

AND PRE-ALPHA INTERITOR (P-ALPHA I) OF H3 AND BIKUMIN,

A SULLATE BRIDGE TO THE TIESTE C-TERMINAL ASPARTATE (BY

SIMILARITY).

ELONGS TO THE ITST C-TERMINAL ASPARTATE (BY

SIMILARITY).

ELONGS TO THE ITST HAMILY.
ITH2_MOUSE
Q61703;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                     CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein.
SIGNAL
PROPEP 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its year of the swiss on the subject of the statement of the subject of the swisses of the sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Plasma;
MEDLINE-97018241; PubMed-8864857;

 J. Blochem.
 {2}

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                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro:
                                                                                                                                                212
                                                                                                                                                                                         N
                                                                                                                                                NVWIVELQGMRFLHVPDTFEGHFQGV 237
                                                                                                                                                                                         NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00092; vwa; 1.; SM00327; VWA; 1.
TE; PS50234; VWFA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protease
                                                                                                                                                                                                                                Similarity 34.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002035; vWFA.
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595
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                                                                                                                                                                                                                                                                                                                                        Ą,
                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140-146; 151-156; 424-447; 500-528 AND 577-605
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118
263
445
578
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702
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                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
CHONDROITIN 4-SULFATE,
                                                                                                                                                                                                                                5
                                                                                                                                                                                                                              Score 54; DB Pred. No. 3; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
V -> Y (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTER-ALPHA-TRYPSIN
                                                                                                                                                                                                                                                                                                                                                          -> Y (IN REF. 2).
-> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                        CA8BF565458E7B2E CRC64;
                                         946
                                                                                                                                                                                                                                                                       DB 1; Length 946;
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                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                                                Indels
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
CROSS-LINK S
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212 N

NLWAAQRYGRELRRMSDEFEGSFKGL 27

Query Match Best Local Matches

Similarity

37.1%;

Conservative

5 Score 53; Pred. No.

Mismatches 묘 1;

0;

Gaps

0

Length 946;

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SEOURNCE FROM N.A.

CSTRAIN-CSTBL/GN: TISSUE-Liver:

C STRAIN-CSTBL/GN: TISSUE-Liver:

X MEDLINE-S194326; PubMed-7534067;

X Chan P., Risler J.-L., Raguenez G., Salier J.-P.;

A Chan P., Risler J.-L., Raguenez G., Salier J.-P.;

A Chan P. Risler J.-L., Raguenez G., Salier J.-P.;

The three heavy-chain precursors for the inter-alpha-inhibitor

T shally in mouse: new members of the multicopper oxidase protein

The three heavy-chain precursors for the multicopper oxidase protein

The three heavy-chain precursors for the multicopper oxidase protein

The three heavy-chain precursors in liver and brain.*;

LE BLOCHEM. J. 306:505-512(1995).

LE 
                                                CARBOHYD
CARBOHYD
BINDING
                                                                                                                        DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002035; Pfam; PF00092; vwa; 1 SMART; SM00327; VWA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2).
   SEQUENCE
                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                  Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X70392; CAA49842.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
Mammalia; F
                                                                                                                                                                                                                                                                                                                          Serine protease inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:96619; Itih2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
SIMILARITY: BELONGS TO THE ITH FAMILY
SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN. TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN. PTM. HEAVY CHAINS ARE INVERLINED WITH BIXUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: I ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED ONE OR THO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN. BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                  PS50234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lus (Mouse).
; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
   946
                                                   703
308
118
118
263
445
702
A,
                                                   946
468
118
263
445
702
                                                                                                                                                                                                                      18
54
702
   105927
                                                                                                                                                                                                                                                                                                                                                                                                                          VWFA
   X.
                                                                                                                                                                                                                                                                                                                       Repeat; Signal; Multigene family;
                                                N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
CHONDROLTIN 4-SULFATE,
                                                                                                                                              VWFA.
                                                                                                                                                                         BY SIMILARITY
                           (BY SIMILARITY
                                                                                                                                                                                                                         INTER-ALPHA-TRYPSIN
   40DB6716433ED9DC
   CRC64;
                                                                                                                                                                                                                         INHIBITOR HEAVY CHAIN
                                                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
CROSS-LINK S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF H1,
                                                   SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H2
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SQ

SEQUENCE

370 AA;

39749 MW;

594ED48F24175979 CRC64;

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EMBL; X61107; CAA43419 1; -.
EMBL; L20296; AAA65607.1; -.
EMBL; L20296; AAA65607.1; -.
EMBL; C30118; CAA85212.1; -.
PFR; S38185; S30185.
HSSP; PO08665; LOR7.
SCD; S0000455; ARO4.
InterPCD, IEPRO1795; DAHP_Synth_1; 1.
PFONDOM; PD005060; DAHP_Synth_1; 1.
PFCDOM; PD005060; DAHP_Synth_1; 1.
Aromatic amino acid biosynthesis; Lyase; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1993 (Rel. 27, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAY-2000 (Rel. 29, Last annotation update)
19-MAY-2000 (Rel. 39-Last annotation update)
19-Mospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-Inh
(EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase)
Synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate
ARO4 OR YREA/45C OR YREA/101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUJILOVIC G., BOHL F.M., BOHL T.M.;
Submitted (ANG-1994) TO the EMHL/GenBank/DDBJ databases.
Submitted (ANG-1994) TO the EMHL/GenBank/DDBJ databases.
1- PUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOSNOLPYRUVATE (PEP)
AND D-ERVTHROSE-4-PHOSPHATE (PAP) GIVING RISE TO 3-DEOXY-D-
ARBHING-HEFFULGOSMANE-7-PHOSPHATE (DAHP)
1- CARALFYIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
1- POSPHATE + PHOSPHATE - PHOSPHATE + POSPHORDED BY UNATE + D-ERVTHROSE 4-
1- PHOSPHATE + H(2)O.
1- ENZYME REGULATION. IMHERITED BY TYROSIME.
1- PANTHWAY: PIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE MITHIN
1- PANTHWAY: PIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE MITHIN
1- PANTHWAY: PIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE MITHIN
1- PANTHWAY: PIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE FAMILY.
1- INDUCTION: BY AMINO ACID STARVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doignon F., Biteau N., Aigle M., Crouzet M.; "The complete sequence of a 6794 bp segment located on the of chromosome II of Saccharomyces cerevisiae. Finding of a dUTPase in a yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDILINE-9225349; PubMed=1348717;
MEDILINE-9225349; PubMed=1348717;
Kuonzler M., Peravicini G., Egli C., Irniger S., Braus G.H.;
Ruonzler M., Peravicini G., Egli C., Irniger S., Braus G.H.;
Ruonzler M., Peravicini G., Egli C., Irniger S., Braus G.H.;
Ruonzler M., Peravicini G., Egli C., Irniger S., Braus G.H.;
Ruonzler M., Peravicini G., Egli C., Irniger S., Braus G.H.;
Ruonzler M., Peravicini G., Egli C., Irniger S., Braus G.H.;
Ruonzler M., Erniger M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: rungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AROG_YEAST
P32449;
                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288C;
MEDLINE=94078675; PubMed=8256522;
MEDLINE=94078675; PubMed=8256522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dUTPase in a yeast.";
Yeast 9:1131-1137(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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RA Salanoubat W., Lencke K., Rieger M., Ansorge M., Onseld M.,
Ra Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Ra Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Ra Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Ra Mincker P., Cattolico L., Weissenbach J., Sauxin W., Quetter P.,
Ra Mincker P., Cattolico L., Weissenbach J., Sauxin W., Quetter P.,
Ra Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Bences V.,
Ra Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Bences V.,
Ra Wurmbach E., Drzonek H., Brite H., Jordan N., Bangort S.,
Ra Wezzi A., D'Angelo M., Pallaviccin A., Toppo S., Simionati B.,
Ra Wezzi A., D'Angelo M., Pallaviccin A., Toppo S., Simionati B.,
Ra Conrad A., Horrischer K., Kauer G., Loehnert T. H., Nordsiek G.,
Ra Conrad A., Horrischer K., Kauer G., Ottenwaelder B., Duckemin D.,
Ra Reichelt J., Schaffe M., Schoen O., Bargues M., Terol J., Climent J.,
Ra Reichelt J., Schaffe M., Schoen O., Bargues M., Terol J., Climent D.,
Ra Reichelt J., Schaffe M., Schoen D., Bargues M., Terol J., Witale D.,
Ra Ade Haan M., Maarse A.C., Alcarza J.-P., Cottet A., Casacuberta E.,
Ra Mannhaupt G., Haase O., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
Ra Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
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p3562; 03003; Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
16-CCT-2001 (Rel. 40, Last anotation update)
16-CCT-2011 homeotic protein APETALA3.
AP3 OR AT3654340 OR T12E16-30.
AP3 OR AT3657440 OR T12E16-30.
AP3 OR T12E16-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. LANDSBERG ERECTA;
MEDLINE-95036018; Pubbecd-7948893;
Okamoto H., Yano A., Shirasahi H., Okada K., Shimura Y.;
"Genetic complementation of a floral homeotic mutation, aperala3,
with an Arabidopsis thaliana gene homologous to DEFICIENS of
Antirthinum majus.";
Dlapt Def Tarabura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purugganan M.D., Suddith J.I.;

"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";

Genes of Arabidopsis thaliana.";
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Jack T. Brockman L., Meyerowitz E.M.;
"The homeotic gene APETALA3 of Arabidopsis
box and is expressed in petals and stamens.
cell 68:683-997(1992).
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STRAIN=VARIOUS STRAINS;
MEDLINE=99126449; PubMed=9927474;
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RESULT 8
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Matches 12
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InterPro: IPR002100; MADS-box.
Plam; PF01486; K-box; 1.
Pfam; PF00319; SRP-TP; 1.
PP1MTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS00366; MADS_BOX_2; 1.
PROSITE; PS00366; MADS_BOX_2; 1.
PROSITE; PS00366; MADS_BOX_2; 1.
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Q914U3;
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-I- SUBUNIT: FORMS AN HITERODINER WITH PISTILLATA.
-I- SUBCELLULAR LOCATION: NUCLEAR.
-I- TISSUE SPECIFICITY: EXPRESSED IN PETALS AND STAMENS.
-I- MISCELLANEOUS: MUTATIONS IN AP3 CAUSE TRANSFORMATION INTO SEPALS AND STAMINA INTO CARPELS.
-I- SIMILARIY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANFACTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Developmental protein.
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HSSP; P11746; IMNM.
TRANSFAC; T01776; ...
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D21125; BAA0665.1;
L; A2711579; AAD5188.1;
L; A2711590; AAD51889.1;
L; A27115800; AAD51891.1;
L; A27115804; AAD51893.1;
L; A27115814; AAD5193.1;
L; 
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27341 MW;
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Pred. No. 1.7;
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K-BOX.
A -> R (IN REF. 2).
669070319F9857C3 CRC64;
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RASSJEHRA
AD PAZSA
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DE RASS-11
GN RASS-1
GN RASS-
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Best Local :
Matches 10
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P22280;
01-AUG-1991
01-AUG-1991
30-MAY-2000
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01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA recombination;
DOMAIN 16
SEQUENCE 453 AA;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizomucor
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                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE
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(Rel.
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PRODENCE FROM N.A.

IC STRAIN-ATCC 15692 / PAO1;

IC STRAIN-ATCC 15692 / PAO1;

IX MEDILINE-20437337; PubMed-10984043;

IX MEDILINE-20437337; PubMed-10984043;

IX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.

IX Hickey M.J., Brithman F.S.L., Huffnsgle W.O., Kowalik D.J., Lagrou

IX Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.

IX Garber R.L., Goltry L., Folger K.R., Kas A., Larbig K., Lim R.N.

IX Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.N.

IX Brith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

IX Brith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

IX Relizer J., Saier M.H., Hancock R.E.M., LOTY S., Olson M.V.;

IX Relizer J., Saier M.H., Hancock R.E.M., LOTY S., Olson M.V.;

IX Complete genome sequence of Pseudomonas aeruginosa PAO1, an

IX PROPORTINISTIC pathogen.*;

IX Nature 406.959-94(2000).

IX PROPORTINISTIC PATRON. IN PROPORTINISTIC PATRON.

IX PROPORTINISTIC PATRON. IN PROPORTINISTIC PATRON. I
STRAIN-ATCC 1216B;
MEDLINE-91061774: Pubmed-1701021;
Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.
"Expression of a gene family in the dimorphic fungus Mucor
which exhibits striking similarity to human ras genes.";
Mol. Cell. Biol, 10:6654-6663(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMB1 outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in o way modified and this statement is not removed. Usage by and for commercial entities requires a license greement (See http://www.isb-sib.ch/snnounce/or send an email to license@ibb-sib.ch).
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InterPro; IPR003798; DUF195.
Pfam; PF02646; DUF195; 1.
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 WAAQRYGR--ELRRMSDE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WASERQGREEELRRLASE
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; Fungi; Zyg
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41, Last
41, Last
protein
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Zygomycota; Zygomycetes; Mucorales; Muco
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201 COILED COIL (POTENTIAL).
51539 MW; 1E7EA97E82EC5E4B CRC64;
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51 A
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Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB Pred. No. 7.3; 4; Mismatches
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D.J., Lagrou M.,
n S., Yuan Y.,
K., Lim R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                       Mucoraceae;
                                                                                 racemosus
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RESULT 10
6PGL_THEMA
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Best Local S
Matches 10
                                                                                          STRAIN-MSSB / DSM 3109;
MEDILINE-99287316; PubMed-10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Elsen J.A., White O.G.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
"Evidence for lateral gene transfer between Archaea and Bacteria (Togenome sequence of ThermoLoga maritima.";
Nature 399:323-329(1999).

1- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
6-phosphoglucomolactonase (EC 3.1.1.31) (6PGL).
PGL OR DEVB OR TM1154.
Thermotoga mar::---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the TRMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                       Thermotoga maritima.
Bacteria; Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP: P01112: 1PLL.
InterPro: IPR003577; Ras.
InterPro: IPR001806; Ras_trnsfrmng
                                                              -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone +
                                                                                                                                                                                                                                                                                                                   Bacteria; Thermotogales; Thermotoga
NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00071;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND TNACTIVATED BY A GTPASE-
ACTIVATING PROTEIN (GAP).
SUBCELLULAR LOCATION: PLASMA MEMBRANE.
 phospho-D-gluconate.
PATHWAY: SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.
SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS GERMLING AND YEAST.
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                                                                                  PHOSPHOGLUCONATE.
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10; Conservative
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16 23 GTP (BY SIMILARITY).

63 67 GTP (BY SIMILARITY).

12 125 GTP (BY SIMILARITY).

12 125 GTP (BY SIMILARITY).

38 46 EFFECTOR REGION (PROBABLE).

202 202 FARNESYL (BY SIMILARITY).
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Pred. No.
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4.3;
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SEQUENCE
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THREONINE SYNTHASE,
PYRIDOXAL PHOSPHATE (BY SIMILARITY).
114C0979CD231464 CRC64;

CHLOROPLAST (BY SIMILARITY)

AA;

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Query Match
Best Local Similarity 34.0
"Atches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EUropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EUROPAN BIOInformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Casazza P., Kaiser S., Willmitzer I., Hoei
"Isolation and characterization of a cDNA
from Solanum tuberosum.";
Submitted (AUG-1998) to the EMBL/GenBank/I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000457; Glucosamine_iso. Pfam; PF01182; Glucosamine_iso; 1. Hydrolase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                          -: PA/THWAY: Threonine biosynthesis; last step.
-: SUBUNIT: Homodimer (By similar)
-: SUBCELLULAR LOCATION: Chloroplast (By similarity).
-: SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; eudicotyledons; c
Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Threonine synthase, chloro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; TM1154;
TRANSIT 1 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                    Threonine biosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme;
                                                                                                                                                               EMBL; AF082894; AAF74984.1;
                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 ACEKYEREIRSATDQFDLAILGM 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphate. Pyridoxal phosphate (By similarity) CORCYNCIOR: Pyridoxal phosphate (By similarity) ENZYME REGULATION: Allosterically activated by methionine (SAM) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _SOLTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQRYGRELRRMSDEFEGSFKGL
                                                                                                           Pro; IPR001926; B6_enzyme_beta
PF00291; PALP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE001772; AAD36230.1;
                                                                                 PS00165; DEHYDRATASE_SER_THR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteome.
25325 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chloroplast precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O-phospho-L-homoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the EMBL/GenBank/DDBJ databases.
O-phospho-L-homoserine + H(2)O -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9B0FD07EE01E60C3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      519 AA
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encoding three
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by S-adenosyl.
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RX MEDILINE-2008348B; PubMed=1061719B;
RX MEDILINE-2008348B; PubMed=1061719B;
RA Mayer K.F.X., Schueller C., Wanbutt R., Murphy G., Volckaert G.,
RA Mayer K.F.X., Schueller C., Wanbutt R., Murphy G., Volckaert G.,
RA Molt P., Duesterhoeft A., Stiakema M., Entian K.-D., Terryn N.,
RA Rohl T., Duesterhoeft M., Brandt P., Grivell L.A., Rieger M.,
RA Welchselgortner M., de Simone V., Obermaler B., Mache R., Mueller M.,
RA Welchselgortner M., de Simone V., Obermaler B., Mache R., Mueller M., Ratson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Reichert B., Robles J., Zimmermann M., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F.,
RA Wan der Schweren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Wan den Es, Brandt A., Petters S., van Stoveren M., Dirkse W.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Weitzenegger T., Bothest R., Van den Daele H.
RA Wen Montagu M., Rogers J., Cronin A., Ouail M., Bray-Allen S.,
RA Meljanch D., Majaret C., Gielen J., Villare G., Koetter P.,
RA Messenet O., Ouigley F., Clabauld G., Mendlein A., Felber R.,
RA Mendler M., Rathann B., Granderath K., Denner D., Herrl A.,
RA Mendler M., Witale D., Liguori R., Plravndi E.,
RA Heljnen L., Schwarts S., Schmidt W., Lecharny A., Aubourg S.,
RA Pitshan D., Haase D., Lencke K., Mewes H., W., Stocker S.,
RA Peter Perez A., Purnelle B., Bent E., Hohse M., Habermann K.,
RA Mendler M., Weitsen R., Stoker S.,
RA Mendler M., Weitsen R., Stoker S.,
RA Mendler
        PART REPORTED TO THE PROPERTY OF THE PROPERTY 
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Best Local Similarity
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ATABIADOPSIS thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid Spermatophyta; Magnollophyta; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-cv. Wassilewskija;
MEDLINE-99418329; PubMed-10490396;
Bartlem D., Tamaki Y., Naito S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Threonine synthase, chloroplast precursor (EC AT4G29840 OR F27B13.80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THRC_ARATH
Q9S7B5; Q39144;
01-MAR-2002 (Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bartlem D., Tamaki Y., Naito S.,
"Genomic nucleotide sequence of the Arabidopsis threonine synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (In) Plant Gene Register PGR99-108
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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E., Dante
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Pepin K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.2.99.2) (TS)
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δõ

2 NLWAAQRYGRELRRMSD------EFEGSFKGL

27

Matches

Conservative

6;

Score 48; DB Pred. No. 12; 6; Mismatches

1; 8;

Length 526 Indels

8 Gaps

1.

Query Match Best Local Similarity

33.6%;

BINDING CONFLICT

526 AA;

57776

₹.

THREONINE SYNTHASE.

PYRIDOXAL PHOSPHATE.

A -> L (IN REF. 3).

-> L (IN REF. 3). B27787A57B882AD0 CRC64;

PROSITE: PS00165; DEHYDRATASE\_SER\_THR: 1.
Threonine bicsynthesis; Lyase; Pyridoxal phosphate;
Chloroplast; Transit peptide: 3D-structure.
TRANSIT 1 40 CHLOROPLAST.
TRANSIT 1 40 THREONINE SYNTHASE.
CHAIN 41 526 THREONINE SYNTHASE.
BINDING 203 203 PYRIDOXAL PHOSPHATE.
BINDING 203 203 A -> L (IN REF. 3).

Allosteric enzyme.

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EMBL; AB027151; BAA77707.1; -.
EMBL; AL050352; CAB4569.1; -.
EMBL; AL161575; CAB79742.1; -.
EMBL; L41666; AAB04607.1; -.
PDB; 1EXY; 02-AUG-01.
InterPro; IPR001926; PALP.
Pfam; PF00291; PALP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C., Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma F., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy M., Haseqawa A., Hameed A., Lodhi M., Johnson A., Chen E., Marra M., Martiensen R., McCombie W.R.;

'Sequence and analysis of chromosome 4 of the plant Arabidopsis thallana.'
                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                        - - ENZYME REGULATION: Allosterically activated up to 20-fold by sadenosyl-methionine (SAM).
- PATHMAY: Threonine biosynthesis; last step.
- SUBURLIT: Homodimer.
- SUBCELLULAR ICCATION: Chloroplast.
- SUBLIARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thomazeau K., Curien G., Dumms R., Biou V., "Crystal structure of threonine synthase from Arabidopsis thaliana.", protein Sci. 10:638-648(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Curien G., Job D., Douce R., Dumas R.;
"Allosteric activation of Arabidopsis threonine synthase S-adenosylmethionine.";
Biochemistry 37:13212-13221(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-adenosylmethionine-sensitive from higher plants."; FEBS Lett. 390:85-90(1996).
                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed-11344332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Curien G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed-9748328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *Characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8706836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 2-526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 402:769-777(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphate.
COFACTOR: Pyridoxal phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: 0-phospho-L-homoserine + H(2)0 - L-threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6836;
Dumas R., r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ravanel S., Douce R.;
an Arabidopsis thaliana cDNA encoding an
-sensitive threonine synthase. Threonine synthase
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172 NLFWAERFGKQFLGMNDLWVKHCGISHTGSFKDL

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Ol-JUN-1994 (Rel. 29, Last sequence update)
Ol-JUN-1902 (Rel. 41, Last annoration update)
Anthor RFamide neuropetides precursor.
Calliactis parasitica (Sea anemone).
Calliactis parasitica (Sea anemone).
Sukaryota; Mecazoa; Condaria; Anthozoa; Zoantharia; Actiniaria; Myaantheae; Igormathiidee; Calliactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE-9,1172845; PubMed=1706527;

Darmer D. Schmutzler C. Diskhoff D., Grimmelikhuijzen C.J.P.;

"Primary Structure of the precursor for the sea anemone neuropeptide
antho-RFamide (<Glu-Gly-Aug-be-HH2);

Proc. Natl. Acad. Sci. U.S.A. 88:2555-2559(1991).

"FOCCINATION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT

"FURCHISQUIAK STRANSPESS."
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p1R; A39172; A39172;
InterPro; IPR002544; FARP.
Pfam; PF01581; FARP; 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuropeptide; Amidation;
SIGNAL 1 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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       Repeat;
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Query Match Best Local

Similarity

32.98;

Score 47; Pred. No.

DB 1;

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DT 16-007
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RETISSUE-Peripheral blood, and Spleen:

RX MEDLINE-98094365; pubmed-9430650;

RX MEDLINE-98094365; pubmed-9430650;

RA O'Connor L., Strasser A., O'Railly L.A., Hausmann G., Adams J.M.,

RA O'Connor L., Strasser A., O'Railly L.A., Hausmann G., Adams J.M.,

RA O'Connor L., Strasser A., O'Railly that promotes apoptosis.",

RA O'Connor L., Strasser A., O'Railly that promotes apoptosis.",

RA O'Connor L., Strasser A., O'Railly that promotes apoptosis.",

RA O'Connor L., Strasser A., O'Railly that promotes apoptosis.",

RA O'Connor L., Strasser A., O'Railly that promotes apoptosis.",

RA O'Connor L., Strasser A., O'Railly that promotes apoptosis.",

REPHOJ. 17.384-395(1998)

C1 - FUNCTION: INDUCES APOPTOSIS. ISOFORM BIML IS MORE POTENT THAN

LSOFORM BIMEL.

C2 - SEGUENT'S FORUS HETERODINERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2

PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BAD BHRF-1. DOES

NOT HETERODINERSIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,

BAX OR BAK (BY SIMILARITY)

C3 - SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOPLASMIC MEMBRANES

C4 - SEGUENTIARITY PROAPOPTOTIC SHOWN HERE) AND

C5 - STATILARITY PROADOUCED BY ALTERNATIVE SPLICING.

C6 - STATILARITY BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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043521; 04
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16-OCT-2001 (Rel. 40, Last squence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last squence update)
16-OCT-2001 (Rel. 40, Last squence upda
                                       Apoptosis;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                      MIM; 603827,
                                                                                                                                                                                                                                                                    EMBL; AF032457; AAC39593.1; -. EMBL; AF032458; AAC39594.1; -.
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                                            PS01259; BH3; FALSE_NEG.
s; Alternative splicing; Membrane.
148 162 BH3.
42 101 MISSING (IN )
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216994;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 41, Last annotation update)
201-MAR-2002 (Rel. 41, Last annotation update)
Antho-Reamide neuropeptides type 2 precursor.
Anthopleure elegantissima (Sea ancmone).
Eukaryota; Metazob; Conidaria; Anthozoa; Zoantharia; Actiniaria;
Mynantheae; Actiniidae; Anthopleura.
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MEDLINE-9054550; PubMed-1429603;

Schmutzler C., Darmer D., Diekhoff D., Grimmelikhuijzen C.J.P., '.

'Identification of a novel type of processing sites in the precursor for the sea anemone neuropeptide Antho-Remaide (Glu-Gly-Arg-Phe-NA);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuropeptide;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 From Anthopleura elegantissima.";
J. Biol. Chem. 267:22534-22541(1992).
-I- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT NEUROMUSCULAR SYNAPSES.
-I- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M99170;
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Query Match 32.5%; Score 46.5; DB 1; Length 429; Best Local Similarity 52.4%; Pred. No. 16; Matches 11: Conservative 3: Mismatches 6; Indels 1: Gaps Qy 5 AAQRYGRELR-RMSDEFEGSE 24
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5 AAQRYGRELR-RMSDEFEGSF 24 | |:||||: | ||:| | 209 AQGRFGRELQGREFQGRF 229

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Search completed: September 20, 2002, 11:04:35 Job time: 1632 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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3: sp_tungi:* 4: sp_tungi:* 5: sp_luman:* 5: sp_laretebrate:* 6: sp_marman1:* 7: sp_marman1:* 9: sp_bage:* 10: sp_plart:* 11: sp_rodent:* 12: sp_virus:* 13: sp_vertebrate:* 14: sp_unclassified:* 15: sp_urvirus:* 16: sp_arvirus:* 17: sp_archeap:* 17: sp_archeap:*	Database : SPTREMBL_19:* 1: sp_archea:* 2:	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Total number of hits satisfying chosen parameters: 562222	Searched: 562222 segs, 172994929 residues	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Title: US-09-544-664-56 Perfect score: 143 Sequence: 1 KNLWAAQRYGRELRRWSDEFEGSFKGL 27	Run on: September 20, 2002, 11:03:47 : Search time 172.19 Seconds (without alignments) 27.126 Million cell updates/sec	OM protein - protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

RESULT Q10843 ID Q AC Q DT 0	Oy Oy	S D P P P P P P P P P P P P P P P P P P	
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A Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
A Gordon S.V., Eighmeiter K., Gas S., Barry C.E. III, Tekaia P.,
A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Hanlin N., Holroyd S.,
A Rutter S., Osborne J., Quali M.A., Rajandram M.A., Rogers J.,
A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
A Sulston JE., Taylor K., Whitchead S., Barrell B.G.;
Theolphering the biology of Mycobacterium tuberculosis from the complete genome sequence.;
The Taylor T., Adaptis J.,
E. Nature 39:5:537-544 (1999).
E. Nature 39:5:537-544 (1999).
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Cole S.T., Brosch I
Gordon S.V., Eiglme
                                                                                                         Chloroplast.
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SEQUENCE 5
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NCBL_TaxID=49154;
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Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
EMBL: U6131; AAC15245.2; -.
InterPro: IPR002462; Intron_maturse2.
InterPro: IPR002462; Matk_N.
Pfem: PF01348; Intron_maturas2; 1.
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InterPro; IPR000442; Intron_maturse2
InterPro; IPR002866; MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
                                                                                        Rhododendron(Ericaceae) base
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EMBL; AB012729; BAA25850.1;
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Yukawa T.;
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Chloroplast.

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Rhododendron.
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Yukawa T.;
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RESULT
062977
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062975
   OCCUPATION NO SOCIAL STREET
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Best Local S
Matches 12
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Best Local
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                                                                                     062977
062977;
062977;
01-AUG-1998 (TrEMBLrel. 0
01-AUG-1998 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
RIBOSOMAL MATURASE.
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J. Jpn. Bot. 0:0-0(1998).
EMBL, A8012731; BAA255521; -.
InterPro: IPR002442; Intron_maturse2.
InterPro: IPR002866; Matk_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01348; Intron_maturas2; 1.
Ffam; PF01844; Matk_N; 1.
Chloroplast, Matk_N; 1.
SEQUENCE 506 AA; 60491 NW; 3CCC930385B12DBC CRO
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062975;
01-AUG-1998 (Tremblrel. 07,
01-AUG-1998 (Tremblrel. 07,
01-DEC-2001 (Tremblrel. 19,
Chloroplast.
Eukaryota; Viridiplantae;
                                                                         MATK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhododendron(Ericaceae) based on matk 
J. Jpn. Bot. 0:0-0(1998).
EMBL: AB012732; BAAS563.1; -...
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK.N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01348; Intron_maturas2; 1.
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Kurashige Y., Mine M.,
Yukawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyjedons; core eudicots;
Asteridae; Ericales; Ericaceae; Rhododendron.
                                             Rhododendron luteum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast.
SEQUENCE 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhododendron ponticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Investigation of Sectional Relationships in the Genus
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                                                                                                                                                                                                                                                                                                                                                                                1 KNLWAA------QRYGRELRRMSDEFEGSEK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                             ch 36.7%; l Similarity 37.5%; 12; Conservative
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12; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60449 MW;
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                                                                                                                      07,
07,
Streptophyta;
                                                                                                                      Created)
Last sequence up
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Pred. No. 20;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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Pred. No. 20;
                                                                                                                                                                                                                 PRT;
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   Embryophyta;
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   Tracheophyta;
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RESULT 11
062980
ID 062980
AC 062980
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Best Local Similarity
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Best Local Similarity 37.1
Matches 12; Conservative
                                                                                                                         Matches
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062978;
01-AUG-1998 (TIEMBLITEL C
01-AUG-1998 (TIEMBLITEL O
01-DEC-2001 (TIEMBLITEL 1
 062980;
062980;
01-AUG-1998
                                                                                                                                                                         Chloroplast.
506 AA:
                                                                                                                                                                                               "Investigation of Sectional Relationships in the Rhododendron(Ericacees) based on matk Sequences. J. Jpn. Bot. 0:0-0(1998).

EMBL: AB012735; BAA28656.1; -.
EMBL: AB012735; BAA28656.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR000486; Matk_M.
Pfam; Pp01348; Intro_maturas2; 1.
Pfam; Pp01348; Intro_maturas2; 1.
Chiarrollaf; Rotk_N; 1.
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Kurashige Y., Mine M.,
                                                                                                                                                                                                                                                                                                                                              Ebkaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Nhododendron.
                                                                                                                                                                                                                                                                                                                                                                                Chloroplast
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InterPro; IPR002866; MatK_N.
Pfam; PP01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhododendron(Ericaceae) base
J. Jpn. Bot. 0:0-0(1998),
EMBL; AB012734; BAA25855.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Kurashige Y., Mine M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; wagnollophyta; eudicotyledons; Asteridae; Ericales; Ericaceae; Rhododendron. NCBI_TaxID-49467; [1]
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-49465;
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                                                                                                                                                                                                                                                                                            lukawa T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
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                                                                                                   1 KNLWAA-----
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                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                 MATURASE
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 (TrEMBLrel.
                                                                                                                        Conservative
                       PRELIMINARY;
                                                                                                                                                                              60350 MW;
                                                                                                                                36.7%;
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 07,
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19,
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pred. No. 20;
5; Mismatches
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Last sequence update)
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ed on matK Sequences
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Pred. No. 20;
5; Mismatches
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                       PRT
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                       506
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                                                                                                                                                                                                                                                                                                   T., Takayanagi
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                                                                                                                                                                              CRC64;
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Best Local S
Matches 12
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Best Local
                                           Matches
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062981;
01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                        Chloroplast.
Confrence 506 AA; 60449 MW;
                                                                                                                                                                                                                                                                              Chloroplast.
Chloroplast.
Thervota; Viridiplantae;
                                                                                                                    InterPro: IPR000442: Intron_maturse2.
InterPro: IPR002866; MatK_N.
Pfam: PP01348: Intron_maturas2; 1.
Pfam: PP01824; MatK_N; 1.
                                                                                                                                                                Rhododendron(Ericaceae) based J. Jpn. Bot. 0:0-0(1998). EMBL; AB012738; BAA25859.1; -.
                                                                                                                                                                                                            SEQUENCE FROM N.A. Kurashige Y., Mine M., Yukawa T.;
                                                                                                                                                                                                                                                                                                                        RIBOSOMAL MATURASE.
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SEQUENCE 506
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Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnollophyta; eudicottyledons; core eudicots;
Asteridae: Ericales; Ericaceae; Rhododendron.
                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; Asteridae; Ericales; Ericaceac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhododendron(Ericaceae) based on matl
J. Jpn. Bot. 0:0-0(198),
EMBL: ABD12737; BAA25858 1: -
InterPro: IPR002462: Intron_maturse2
InterPro: IPR002866: MatK_N.
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Chloroplast.
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                                                                                                                                                                                                 *Investigation of Sectional Relationships
                                                                                                                                                                                                                                                       NCBI_TaxID-75576;
                                                                                                                                                                                                                                                                                                            Rhododendron pentaphyllum.
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Yukawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Investigation of Sectional
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                    1 KNLWAA------ORYGRELRRMSDEFEGSFK 25
                                                              Match
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KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK
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                                           l Similarity
12; Conserv
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                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA; 60301 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Intron_maturas2;
                                                   36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.7%;
                                                                                                                                                                                                                                                                    Ericaceae; Rhododendron
                                                                                                                                                                                                                      Kobayashi N., Handa T.,
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19,
                                                                                                                                                                                                                                                                           Streptophyta, Embryc
yta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score 52.5; r; Pred. No. 20; 5; Mismatches
                                         Score 52.5; I
Pred. No. 20;
5; Mismatches
                                           5,
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Best Local Similarity
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01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
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506 AA;
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01-AUG-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
RIBOSOMAL MATURASE.
                                               Pram; PF01348; Intron_maturas2; Pfam; PF01824; MatK_N; 1.
                                                                                              Rhododendron(Ericaceae) based on math

J. Jpn. Bot. 0:0-0(1984);

EMBL; AB012740; BAA25861.1; -.

InterPro; IPR000442; Intron_maturse2

InterPro; IPR002866; Matk_N.

Pfam; PF01348; Intron_maturas2; 1.
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Spermatophyta; Magnollophyta; eudicotyjtedons; core eudicots;
Asteridae: Ericales; Ericaceae; Rhododendron.
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Pfam; PF01824; MatK_N;
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
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J. Jpn. Bot. 0:0-0(1998).
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Kurashige Y., Mine M.,
Yukawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyjedons; core eudicots;
Asteridae; Ericales; Ericaceae; Rhododendron.
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                                      Chloroplast
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-75578;
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    50393 MW;
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Pred. No. 2
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    DAAB47A759CFFC46 CRC64;
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Search completed: September 20, Job time: 1665 sec

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Query Match

36.78;

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Query Match
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01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                          InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; Matk_N.
Pfam; PP01348; Intron_maturas2; 1.
Pfam; PP01824; Matk_N; 1.
                                                                                                                                                                       Rhododendron(Ericaceae) based on matk
J. Jpn. Bot. 0:0-0(1998).
EMBL; AB012741; BAA25862.1; -
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SEQUENCE FROM N.A.
Kurashiqe Y., Mine M., Kobayashi N.,
                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eu
Asteridae; Ericales; Ericaceae; Rhododendron.
                                                                                                                                                                                                                                                                                                                  Chloroplast.
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                                                                                                      SEQUENCE
                                                                                                                  Chloroplast
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391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
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                                            Conservative
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                     ORYGRELRRMSDEFEGSFK 25
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Pred. No. 20;
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                                     September 20, 2002, 10:28:52; Search time 228.86 Seconds

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12:019 Million cell updates/sec
US-09-544-664-1
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Perfect score: 1	138
Sequence: 1	1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
Scoring table: B	BLOSUM62 Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 747574

747574 seqs, 111073796 residues

Searched:

Minimum DB Maximum DB Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries seq length: 0 seq length: 2000000000

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Database :
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1: /SIDS1/gcgdata/h
2: /SIDS1/gcgdata/h
3: /SIDS1/gcgdata/h
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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138	138	138	138	138	138	138	138	138	138	138	Score	
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204	204	204	204	204	162	28	27	27	26	26	Match Length	
19	19	19	19	17	22	21	21	21	21	21	DB.	
AAW61318	AAW61317	AAW61316	AAW61315	AAR95168	AAB70370	AAB37055	AAB37056	AAB37003	AAB37002	AAB37001	ID	
Mutant BCL-XL/BCL-	Mutant BCL-XL/BCL-	Mutant BCL-XL/BCL-	Murine BCL-XL/BCL-	bcl-x(L)/bcl-2 ass	Shorter murine BAD	Bcl2 polypeptide B	Bcl2 polypeptide B	Bcl2 polypeptide B	Bcl2 polypeptide B	вс12 polypeptide в	Description	

Arabidopsis thalia	AAG52445	21	516	36.2	50	45	
Arabidopsis thal	AAG25576	21	242	37.0	51	44	
Arabidopsis thal	AAG54028	21	241	•	51	43	
	AAG54679	21	236		51	42	
Arabidopsis	AAG54029	21	232	•	51	41	
Arabidopsis	AAG25577	21	232	37.0	51	40	
S	AAG54030	21	186	•	51	39	
thal	AAG25578	21	186		51	38	
is that		21	181		51	37	
thal	AAG25218	21	171	•	55	36	
psis tha	AAG25219	21	125		51	3 5	
ain	AAB70380	22	20	•	72	34	
BAD BH3 domain reg	AAB70379	22	18		72	ω ω	
Bcl2 polypeptide B	AAB37029	21	16		73	32	
Human BAD BH3 doma	AAY05421	20	16	•	73	31	
Bcl2 polypeptide B	AAB37028	21	16		84	30	
Mouse BAD BH3 doma	AAY05422	20	16		84	29	
bcl-x(L)/bcl-2 ass	AAR95163	17	16		86	28	
nse	AAB70371	22	26		93	27	
Mammalian Bad Bcl-	AAY96321	21	26		93	26	
Mutant BCL-XL/BCL-	AAW61322	19	59	•	102	25	
BCL-	AAW61321	19	59	73.9	102	24	
	AAW61320	19	59	•	102	23	
Mutant BCL-XL/BCL-	AAW61319	19	59	•	102	22	
bcl·x(L)/bcl-2 ass	AAR95166	17	23	•	113	21	
acid sequen	AAG67688	22	168	•	114	20	
	AAB48287	22	168		114	19	
Human BAD mutant a	AAB70368	22	168	•	114	18	
Human cell prolife	AAB13512	21	168	•	114	17	
	AAW55779	19	168	•	114	16	
BBC6 protein for r	AAW32476	18	166	•	114	15	
	022	22	567	•	138	14	
ger muri	03	22	204		138	13	
Murine BAD protein	AAW58832	9	204	100.0	138	12	

## ALIGNMENTS

RESULT	LT 1
AAB3	AAB37001
ID	AAB37001 standard; peptide; 26 AA.
×	
AC	AAB37001;
×	
DT	28-FEB-2001 (first entry)
XX	
DE	Bcl2 polypeptide BH3 domain peptide #1.
×	
ΧZ	Cytostatic; neuroprotective; anti-HIV; vi
KΨ	cardiant; Bcl-2 superfamily; BH3 domain;
KW	apoptosis modulation; B cell lymphoma/leu
Χ¥	colorectal; gastric; non-small lung; rena
X	melanoma; lymphocytic leukemia; neurodege
æ	stroke; myocardial infarction.

irucide; cerebroprotective; cell death agonist; Bad; cell death agonist; Bad; ukemia 2; cancer; prostate; al; thyroid; neuroblastoma; enerative disorder; AIDS;

Homo sapiens.

12-OCT-2000.

WO200059526-A1.

06-APR-2000; 2000WO-US09352

99US-0128202.

07-APR-1999;

(UYJE-) UNIV JEFFERSON THOMAS.

Huang Z, Wang J, Zhang Z, Shan S, Ľ.

2 ;

WPI; 2000-679325/66.

New peptide conjugates for modulating apoptosis or for inhibiting B

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The invention relates to a peptide conjugate having the formula:

(C (R*X)n*peptide where n = 1-10; X = C-0, when the R*X group is attached to the *t-terminus of the peptide, or a side chain of the peptide where c the functional group of the side chain is NH2 or OH; or X = 0 or NH.

CC when the R*X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH.

CC or COOH2: and R = 2-16c alkyl or alkoy, 2-14c alkylenyl containing one or two double bonds, cyclobutyl. cyclobertyl. cyclobertyl one of the peptide or a cook of the peptide of a cook of the peptide of a cook of the peptide of a l-5C straight or branched chain alkyl group, phenyl potionally monosubstituted with a 1-5C straight or branched chain cook of the peptide of the conjugate The peptides represent examples of the peptide of the conjugate and the conjugate is cook of the peptide of the conjugate and the conjugate is useful for modulating apoptosis in the cells of a subject, or for cook of the coll that the peptide conjugate is useful for modulating apoptosis in the cells of a subject. The peptide conjugate is conjugate afflicted with a cancer characterized by cancer cells that conjugate is subject afflicted with a cancer interactive discovers a guitable conjugate is acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is acute or chronic lymphocytic and non-lymphocytic leukemi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/Leukenia 2; cancer; prostate colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphomytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
                                                                                                                                                                    07-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB37002 standard; peptide;
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                                                                                  (UYJE-) UNIV JEFFERSON THOMAS.
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Wang J,
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RESULT

ANB37003

ID AOB3

XX AAB3

XX AAB3

XX CACC

XX CCYCC

XX CCYCC

KW MELIO

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XX WOZC

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(R.Y)n repetide where n = 1-10; X = C=0, when the R.X group is attached to the N-terminus of the peptide, or a side chain of the peptide where certain the functional group of the side chain is NH2 or OH; or X = 0 or NH, creaminus of the peptide, or a side chain functional group is COOH or COOHIZ; and R = 2-18C alkyl or alkoxy. 2-14C alkylenyl optionally consumptionally monosubstituted with a 1-5C straight or branched chain a side yield or peptide with a 1-5C straight or branched chain of the peptide with a 1-5C straight or branched chain a side yield yie
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Best Local Similarity luv.
Matches 26; Conservative
                                                                                  06-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; Bil domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/Leukemia 2; cancer; prostate; apoptosis modulation; D cell lymphoma/Leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bcl2 polypeptide BH3 domain peptide #3.
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Pred. No. 1.4e-14;
; Mismatches 0;
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ANB37056
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AC AA
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(C (R*)n*peptide where n = 1.0; X = C=0, when the R*X group is attached to the N*-terminus of the apptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = 0 or NH.

CC when the R*X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R = 2.10c alkyl or alkoxy, 2.14C alkylay() containing one or two double bonds, cyclobutyl, cyclopentyl, cyclopentyl, cyclobexyl potionally come of the consubstituted with a 1.5C straight or banched chain alkyl group, or benzyl in the peptides AhagyOOL-BYOSB represent analogues of the peptide portion of the conjugate The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amhan acids 72-97 of the BH domain of the cell death agonist Bad. The peptide conjugate is conjugate is useful for medulating apoptosis in the cells of a subject, or for creversing B cell lymphomalethemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 subject afflicted with a cancer characterized by cancer cells that consumption in particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that conjugate is also useful for treating disorders and apoptosis, e.g. neurobject leakens. The apptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurobject disorders acquired conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurobject disorders characterized by conjugate is also useful for treating disorders characterized by the conjugate is also useful for treating disorders characterized by conjugate is also useful for treating disorders characterized by the conjugate is also useful for treating disorders disorders.
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Best Local Similarity
Matches 26; Conser
                                                                                                                                                                                                                                                        Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bci-2 superfamily; BH3 domain; cell death agonist; BH3; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; neunoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
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CC (RAyn. repetide where n = 1-10; X = C=0, when the RAY group is attached to the N-terminus of the peptide, or a side chain of the peptide where to the functional group of the side chain is NH2 or OH; or X = C of the functional group of the side chain is NH2 or OH; or X = O or NH.

CC when the RAY group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R = 2-18c alxyl or atknoy, 2-14C alxylaryl containing one or town double bonds, cyclobutyl, cyclopentyl, cyclopentyl, cyclopentyl, optionally composition of the C-terminus of the peptide, or a cyclopentyl optionally monosubstituted with a 1-5C straight or branched chain alxyl group, or benzyl optionally monosubstituted with a 1-5C straight or branched chain alxyl group, or benzyl optionally monosubstituted with a 1-5C straight or branched chain alxyl group, or benzyl optionally monosubstituted with a 1-5C straight or branched chain alxyl group, or benzyl management of the conjugate or the peptide conjugate is useful for management of the conjugate is not a subject or for the peptide conjugate is useful for treating apoptosis in cancer cells: It is also useful for Inhibiting Bel-2 subject afflicted with a cancer characterized by cancer cells that cancer chronic lymphocytic and non-lymphocytic leukemia. The apptide conjugate is assisted apoptosis, e.g. neurodegenerative disorders acquired increased apoptosis, e.g. neurodegenerative disorders acquired infarction.
  Query Match
Best Local S
Matches 26
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                                                                                                         Sequence
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ch 100.0%; Score 138; DB 21; 1 Similarity 100.0%; Pred. No. 1.4e-14; 26; Conservative 0; Mismatches 0;
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Indels
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AAB37055 standard; peptide;

28-FEB-2001 (first entry)

BC12 polypeptide BH3 domain peptide

RESULT
AAB37055
TD AAB
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XX
XX
AC AAB
AC AAB
AC BC1:
XX
XX
Cyt
KW Carr
KW Carr
KW Carr
KW Colt
KW melli
KW mel Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprote cardiant; Bc1-2 superfamily; BH3 domain; cell death agonist; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; proclorecta; gastric; non-small lung; renal; thyroid; neurobia melanoma; lymphocytic leukemia; neurodegenerative disorder; a stroke; myocardial infarction. cerebroprotective; ncer; prostate; neuroblastoma;

12-OCT-2000 WO200059526-A1

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RESULT
AAB70370
IO AAB7
XX
AC AAB7
XX
OZ-P
XX
DY O2-P
XX
ZX
XX
DY Shor
XX
EGL-
XW Lmmu
KW Lmmu
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KW Lmmu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a peptide conjugate having the formula:

(C (R-)n repetide where n = 1-10; X = C-0, when the R-X group is attached to the N-terninus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or 0; or NH, considering the peptide where the side chain is NH2 or 0; or NH, considering the peptide or considering the peptide, where the side chain (inctional group is attached to the C-terninus of the peptide, or a side chain of the peptide, where the side chain (inctional group is considering one or two double bonds, cyclobuty). cyclopenty), cyclopenty), cyclopenty, cyclopenty,
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 26
Bcl-XL/Bcl-2 associated cell death regulator: BAD; mutant; apoptosis; immunostimulant; neuroprotective; nootropic; antistohaenic; vilnorary; cyrostatic; antivital; antiarbiritic; antiarbiranatory; wond healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
                                                                                                                                                   02-MAY-2001
                                                                                                                                                                                            AAB70370;
                                                                                                                                                                                                                               AAB70370 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide conjugates for modulating apoptosis or for inhibiting cell jymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CYJE-)
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                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Page 19; 74pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                (first
                                                                                                          BAD
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                                                                                                          mutant
                                                                                                                                                                                                                               protein;
                                                                                                                                                entry)
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                                                                                                          amino
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Pred. No. 1.5
); Mismatches
                                                                                                     acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                       SEQ
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Claim 7; Page 148-149; 157pp; English
                                                                                                                New mutant
useful for
                                                          Serll3 -
                                                                                                                                                                                                 WPI; 2001-138734/14.
                                                                                                                                                                                                                                                                                                              (APOP-) APOPTOSIS TECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                        28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WC200110888-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                             BCL-XL/BC1-2 Associated Cell Death Regulator polypeptide, screening for candidate compounds which induce or inhibit comprises amino acid substitutions at Serils, Seriss or
                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US11864
                                                                                                                                                                                                                                                                                                                                                                        9905-0136783
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The present invention describes an isolated or synthetic polypeptide (I) complising a less than full length amino acid sequence of a mutant (I) complising a less than full length amino acid sequence of a mutant (I) complising a less than full length amino acid sequence of a mutant (I) thick contains amino acid substitutions at SerilB of a human for the sequence of the contains amino acid substitutions at SerilB of a human contains a murine BAD) contains a murine BAD (Anger murine BAD) or SerilJ of a murine BAD (Anger murine BAD) or SerilJ of a murine BAD (Anger murine BAD) or SerilJ of a murine Can be used as an apoptosis inducer or inhibitor. BAD polypeptides and crus series and series and containt of the series include containt of the series and containt of the ser Sequence 162 Ą

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RESULT
AAR95118
ID AAR9
XX AAR9
AC AAR9
XX 06-J
XX BC1-
XX ED11
KW POLY
KW CYEC
                                                                                                                                                      Matches
                                                                                                                                                             Query Match
Best Local
                                                                 AAR95168;
                                                                                 AAR95168
                                                                                                                       98
                                                                                                                               1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                ~1
                                                                                                                      nlwaaqrygrelrrmsdefegsfkgl 123
                                                                                                                                                      100.
Similarity 100.
26; Conservative
                                                                                standard; Protein;
                                                                                                                                                           0.09;
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                                                                                                                                                      Score 138; E
Pred. No. 1.1
0; Mismatches
                                                                                                                                                     DB 22;
..le-13;
gs 0;
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                                                                                                                                                      Indels
                                                                                                                                                                    162;
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ρý 밁

06-JAN-1997

(first

entry)

bcl-x(L)/bcl-2 associated death

promoter protein.

Epitope; murine: bcl-x(1)/bcl-2 associated death promoter; Bad; spolypeptide; bcl-x; cell death, regulate; BHI; BHI; apoptotic cel cytokine deprivation; IL-3 dependent cell line; Kmmunodeficiency; cell death; ncy; AIDS: stroke;

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This sequence represents the murine bcl-x(L)/bcl-2 associated death (CC promoter (Bad) gene. Bad is a 22.1 kD protest which interacts with bcl-2 and bcl-x protests and regulates cell death. It has homology to to the bcl-2-related family clustered in the BHI and BH2 domain. Bad that been found to hybridise to bcl-x(L) and bcl-2 in youst two-hybrid castalys and in vivo in manmallan cells. Overexpressed Bad counters the countering the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-x(L). Bad expression can acclerate apoptotic cell the structure of bcl-x(L), but is much less effective at 1.3 dependent cell line expressing bcl-x(L), and its also counters the cell death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad any be used to learning sense which inhibit its binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be used to learning sense which inhibit its binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be used to learning sense which inhibit its binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be used to learning sense sense yet and the sense of the sense of
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local !
                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleoride encoding bci-x(L)/bci-2 associated death promotor useful to treat neoplasia and apoptosis and to identify egents inhibiting its binding to bci-2 or bci-x(L) to form heteromultimers
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             Murine BCL-XL/BCL-2 associated cell death regulator
                                                   07-OCT-1998 (first entry)
                                                                                            AAW61315;
                                                                                                                                  AAW61315 standard;
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                               140 alwaagrygreirrmsdefegsfkgl 165
                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                     1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
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DB; AAT29479.
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ilarity 100.0%;
Conservative 0
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191..192
/notes "BH2 conserved amino acids"
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147..149
                                                                                                                                  Protein; 204
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                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                           Score 138; DB 17;
Pred. No. 1.4e-13;
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                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                      204;
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                                                                                                                                                                     RESULT
AAW61316
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Best Local
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N-PSDB; AAV27833.
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                                                                            07-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                  AAW61316;
                                                                                                                                                     AAW61316 standard; Protein;
                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                 1 Similarity
26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                     204 AA;
                                                                         (first entry)
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                                                                                                                                                        204
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Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
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New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection

The present invention describes mutant BAD (BCI-XL/BCI-2 associated cell classified regulator) procesns, having an amino acid other than Ser at C position 112 and/or 136. relative to the murine BAD 204 as sequence. The C present sequence is the murine BAD protein. Also described are: (1) CC fusion proteins of mutant BAD protein able to decrease cell viability; (2) CC fusion proteins of mutant BAD protein able to decrease cell viability; (2) to resease intracellular delivery, mutant BAD proteins are used to treat C or prevent diseases associated with reduced apoptosis, e.g. concerviral inferention, hymphoproliferation, arthritis, infertility.

CC viral inferction, hymphoproliferation, arthritis, infertility.

CC inflammation and autoimmune disease. Polymputeotide sequences encoding that BD proteins can be used similarly by gene therapy or to produce transgenic enimals for use as disease models or in drug screening. BAD communed to service application of the second of the second in the specific fear are used to screen for enhancers and inhibitors of serime-phosphatase. Inhibitors are potentially useful in treatment of excessive applications such as ADDs, neurodepeneration, againg or ischemic cell death. The appoints such as ADDs, neurodepeneration, againg or ischemic cell death. The appoints status of cells is considered and non-phosphorylated by measuring relative amounts of phosphorylated and non-phosphorylated by measuring relative amounts of phosphorylated and non-phosphorylated with BCL 2 or BCL-XL but instead binds to 14-3-3 family corrections in the cytosol. thus promoting cell survival. The mutants with the companies of the cytosol. Thus promoting cell survival. The mutants with the companies with BCL 2 or BCL-XL but instead binds to 14-3-3 family contents in the cytosol. Thus promoting cell survival. The mutants with

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100.0%; Score 138; DB 19; ilarity 100.0%; Pred. No. 1.4e-13; Conservative 0; Mismatches 0;
                                Length 204;
    Indels
    0;
    Gaps
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0

Mutant BCL-XL/BCL-2 associated cell death regulator #1

B 9

Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

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AAW61317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell classes) required by metalis, having an amino acid other than Ser at CC position 112 and/or 136, relative to the mutine BAD 204 as sequence. The position 112 and/or 136, relative to the mutine BAD 204 as sequence. The CC present sequence represents a mutant BAD protein Aiso described are: (1) CC fusion proteins of mutant BAD protein able to decrease cell viability; (2) Cf fusion proteins of mutant BAD protein able to decrease cell viability; (2) concerving infertion; hyphoproliferation, arthritis, infertility.

CC prevent diseases associated with reduced apoptosis, e.g. cancerviral infertion and autolemnue disease. Polynucleotide sequences encoding mutant BAD proteins can be used stainarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD contents can be seed in treatment of excessive applicate such as AIDs, neurodespencration, additional intentment of excessive applicate such as AIDs, neurodespencration, adjing or ischmenic cell death. The apoptotic status of cells is content death. Phe apoptot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 26
Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD
                                                        Mutant BCL-XL/BCL-2 associated cell death regulator #2.
                                                                                                                                                                                 AAW61317;
                                                                                                                        07-DCT-1998
                                                                                                                                                                                                                                         AAW61317 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-261422/23
N-PSDB; AAV27834.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                              tch 100.0%; Score 138; DB 19; al Similarity 100.0%; Pred. No. 1.4e-13; 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 AA;
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                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            death result invention describes mutant BAD (BCL-XL)RGCL-2 associated cell death resultator) proteins intended cell and the protein and protein and the protein BAD (A) as sequence. The position of the protein and the protein all the protein BAD (A) as sequence. The protein and the protein BAD (A) as sequence. The protein and a protein all the control of the protein and the protein all the control of the protein and the protein all the control of the protein and the protein all the control of the protein and the protein at specified sequences encoding unitarit BAD proteins are glasses models of in drug acreening BAD (A) as a protein and the protein at specified sequences are potentially useful in treatment of excessive appotentials unitarity are protein all the protein and the protein activity and the protein all the protein all the protein and the protein activity than wild type BAD which can become of phosphorylated and the protein activity than wild type BAD which can become phosphorylated and the protein activity than wild type BAD which can become of phosphorylated and protein activity than wild type BAD which can become phosphorylated and protein activity than wild type BAD which can become of phosphorylated and protein activity than wild type BAD which can become of phosphorylated and protein activity than wild type BAD which can become of phosphorylated and protein activity than wild type BAD which can become of phosphorylated and protein activity than wild type BAD which can become of phosphorylated and protein activity than wild type BAD which can become of the protein and the protein and protein and protein and protei
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Best Local Similarity 100.0%; Fred. No. 1.4e-13;
Matches 26; Conservative 0; Mismatches 0;
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Synthetic.
Murine; mouse; BCL-XL/BCL-2 associated cell death regulator;
                                                        Mutant BCL-XL/BCL-2 associated cell death regulator #3
                                                                                                                    07-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 60; 95pp; English.
                                                                                                                                                                             AAW61318;
                                                                                                                                                                                                                                     AAW61318 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09817682-A1.
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                                                                                                                                                                                                                                     Protein;
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EXEX EXACX B
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                                                                                                                                                                                                                                                       The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell clearly regulator) proteins, having an amino acid other than Ser at CD position [12] and/or 136, relative to the mutine BAD 204 as sequence. The CD position [12] and/or 136, relative to the mutine BAD 204 as sequence. The CD present sequence represents a mutant BAD protein. Also described are: [1] CC fusion proteins of mutant BAD protein able to decrease cell viability; [2] CC fusion proteins are used to treat cor prevent diseases associated with reduced apoptosis, e.g. concer, curial infection, lymphoproliferation, arthritis, infertility.

CC viral infection and autoimmune disease. Polymucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transpents animals for use as disease models or in drug screening. BAD cortains phosphorylated at specified Ser are used to screen for enhancers and inhibitors of service phosphatuse. Thibitors are potentially useful in treatment of excessive apoptosis such as ADDs, neurodegeneration, caping or ischaemic cell death; The apoptosis such as ADDs neurodegeneration of determined by measuring relative amounts of phosphorylated and non-phosphorylated and hop-phosphorylated and product that does not phosphorylated with BCL-2 or BCL-XL but instead blands to 14-3-3 family corporations in the cyclosol, thus promoting cell survival. The mutants with the cyclosol, thus promoting cell survival. The mutants with constituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 60-61; 95pp; English
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BAD protein
                      Murine BAD protein.
                                            23-JUL-1998
                                                                  AAW58832;
                                                                                                                                                                                                                                                      Sequence
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                                                                                        AAW58832 standard;
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                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                            1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
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DB; AAV27836.
                                                                                                                                                 nlwaaqrygrelrrmsdefegsfkgl 165
                                                                                                                                                                                                                                                       204 AA;
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(larity 100.0%;
Conservative 0
Bc1-XL/Bc1-2 associated cell death regulator; 14-3-3;
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                                                                                                                           02-MAY-2001
                                                                                                                                                                       AAB70369
                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                   murine BAD mutant amino
                                                                                                                                                                                                                                                                            26; Conservative
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                                                                                                                                                                       protein;
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serine phosphorylation; post-translational modification; apoptosis; signal transduction requilator; phosphosesine phosphatase; sensescenc immunodeficiency disease; neurodegenerative disease; lifertility; cancer, viral infection; lymphoproliferative condition; arthritis; inflammarion; autoimmune diseases.
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Serine-phosphorylated BcJ-X-1/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with, e.g. cencer and immunodeficiency diseases

This sequence represents a novel serine-phosphorylated protein, RAD (BCL XI/BCL 2 associated cell death regulator). The serine residue is phosporylated in a post translational modification and allows binding to the 14-3-3 protein which is a signal translation and allows binding to the 14-3-3 protein which is a signal translation expending the phosphorylated BAD, which act through inhibition/activation of a phosphosetine phosphatase, are useful for preventing/treating increased/apercased apoptosis may result from immunodeficiency diseases, senescence, neurodegenerative disease, isohaemic cell death, reperfusion cell death, infertility and wound-healing. Decreased apoptosis may result from cancer, viral infearchm, upphoproliterative conditions, arthritis, infertility. Inflammation and aucoimmuse diseases. Measuring the amount of phosphorylated compared to unprosphorylated BAD polypeptide and/or total phosphorylated compared to upprosphorylated BAD polypeptide and/or total phosphorylated compared to upprosphorylated BAD polypeptide and/or total phosphorylated compared to upprosphorylated BAD polypeptide and/or total

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.0%; Score 138; DB 19;
.0%; Pred. No. 1.4e-13;
0; Mismatches 0;
                       Length
    indels
                        204;
0;
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acid sequence SEQ ID NO:2

BC1-XL/Bc1-2 associated cell death regulator, BND; mutent; speptiests; immunostinulant; netroprocective; nootropic; antikisheemic; vulnerat;; cycosiatic; antiviral; antiarthitic; antifiliammatory; would healing; cycosiatic; antiviral; antiarthitic; antifiliammatory; would healing; immunosippressive; apoptosis inducer; apoptosis inhibitor; infection; immunosippressive; apoptosis inducer; apoptosis inhibitor; infection; immunosipressive; apoptosis inducer; apoptosis inhibitor; infection; immunosipressive; apoptosis inducer; apoptosis inhibitor; infection; immunosipressive; infection; immunosipressive; infection; infection; alcolimande diseases.

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an isolated or synthetic polypeptide (I) comprising a less than full length amino acid sequence of a mutant (B1) tamprising a less than full length amino acid sequence of a mutant (B1) tamprising a less than full length amino polypeptide (BAD) or its fragment, which contains antho acid substitutions at Seril8 of a human BAD, Seril5 of a mutant BAD (Longer murine BAD) or Seril3 of a mutant BAD (Anger murine BAD) or Seril3 of a mutant BAD) or Seril3 of a mutant BAD, antiritie, antirities, and antiarthritic, antirities, and antiarthritic, antirities, and antiarthritic, antirities, and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and con be used as an apoptosis inducer or inhibitor. BAD polypeptides are polymucleotides can be used (or screening candidate compounds and drugs for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds inducing or inhibiting apoptosis in a cell. Candidate compounds (dentified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischaemic cell canthomic diseases. The present sequence represents a specifically coloration and autoinmune diseases. The present sequence represents a specifically cells and colorative conditions, arthritis, infertiley, infarmation and autoinmune diseases. The present sequence represents a specifically cells and colorative conditions.
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Best Local S
Matches 26
                                                                                       Mouse, Bad-DTR: apoptosis, cancer; spinal muscular attrophy; diphtheria toxin receptor bidding domain; DTR: neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischematc neuronal injury; stroke; spinal cord injury; nunchigion's disease.
                                                                                                                                                                                                                                                                                                                                                                                               Bad-DTTR apoptosis-modifying fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU00220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Synthetic.
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al Similarity 100.0%;
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pred. No. 1,4e-13;
Mismatches 0;
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modifying fusion protein comprising gade sequence of Bad-DTTR apoptosis-
modifying fusion protein comprising gade gene sequence fused via a short
linker to diphtheria toxin transiocation domain (DTTR). The
transicational apoptosis-modifying fusion protein is capable of binding a
cutarget cell and integrating into or crossing a cellular membrane of the
transic cell and integrating into or crossing a cellular membrane of the
transic cell and the spotosis-modifying fusion protein comprises at least
two domains: the DTR domain, which targets the fusion protein to the
transic cell. The fusion protein is useful for modifying
of the target cell. The fusion protein a target cell, such as neuron,
full transic cell. The fusion protein is useful for modifying
cell, thibiting or enhancing) apoptosis in a target cell, such as neuron,
full transic cell. The fusion protein is useful for reducing
cell, the protein cell or an adipocyte. It is also useful for reducing
the protein cell cell or an adipocyte. It is also useful for reducing
cells in a subject after transient ischemic neuronal injury,
cell apoptosis in a subject after transient ischemic neuronal injury,
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cell activity spinal cord injury ornditions through inhibition or enhancement
cell activity spinal cord injury ornditions through inhibition or enhancement
cell activity spinal cord injury. The fusion protein can be delivered
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cell scancers. The apoptosis of the cell grave has a considered to selective tissue a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel fusion protein for modifying apoptosis in target cell and reducting apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response of cell.
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 59-61; 65pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Corynebacterium diptheriae Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Youle RJ, Liu X, Collier RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARD ) HARVARD COLLEGE.
(USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-FEB-2001
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DB; AAS00248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US22293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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BXBXBXB
                                                         RESULT 15
AAW32476
                                                                                                          δ
                                                                                             g
                                                AAW32476 standard;
                15-JAN-1998
                                                                                         1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
[[[[[[]]]]]]]]]]]]]]]]
161 nlWaaqrygrelrrmsdefegsfkgl 186
               (first entry)
                                                 Protein;
                                                 166
                                                 B
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BBC6 protein for regulating cell

death

Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0

0 ;

Score 138; DB 22; Pred. No. 4.3e-13; ; Mismatches 0;

Indels Length 567;

0; Gaps

0

Sequence

567 AA;

Chimeric -

Mus sp

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Search completed: September 20, 2002, 10:35:56 Job time: 424\ sec
                                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.6%; Score 114, DB 18, Best Local Similarity 91.7%; Pred. No. 6.1e-10; Matches 2; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a protein of 166 amino acids. The sequence is disclosed as being a protein called BRG6 which regulates' cell death through interaction with Bcl-2. The DNA may be used for the production of the recombinant protein, which can be used in unspecified therapeutic or dispressive procedures, as a molecular weight marker, and to relies antibodies that can be used in unspecified disprostic or therapeutic applications and to reduce or eliminate the biological activity of the BBC6 protein in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Column 11-12; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated BBC6 gene - encodes a protein that regulates cell death through interaction with Bc1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-447980/41.
N-PSDB; AAT91561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xudong Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CLON-) CLONTECH LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-SEP-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BBC6 gene; cell death; cell cycle; Bcl2; human.
                                                                                                                                                                                                                                                                                                                                                    166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0665617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0665617.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Title: Perfect score: Sequence:

US-09-544-664-1 138

NLWAAQRYGRELRRMSDEFEGSFKGL

26

OM protein -

protein search, using sw model

Copyright

GenCore version (c) 1993 - 2000

4.5 Compugen

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September 20, 2002, 10:30:32;

; search time 75.64 Seconds (without alignments) 8.396 Million cell updates/sec

on

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_AA:\*
1: /cgn2\_6/ptodata/2
2: /cgn2\_6/ptodata/2
3: /cgn2\_6/ptodata/2
4: /cgn2\_6/ptodata/2
5: /cgn2\_6/ptodata/2
6: /cgn2\_6/ptodata/2

/cgn2\_6/ptodata/2/iaa/5a\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/5a\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/5a\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6a\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6a\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

231628 seqs, 24425594 residues Gapop 10.0 , Gapext 0.5

Searched. Scoring table:

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COMPUTER: US
COMPUTER TABABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: PlopsyMS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING NUMBER: BC-DOS/MS-DOS
OPERATION NUMBER: US/08/333,565
FILING DATE: 31-0CT-994
CLASSIFICATION INFORMATION:
NAME: SMITH, WILLIAM MS
REGISFRATION NUMBER: BO, 22
REPERRENCE/DOCKET NUMBER:
REPUBLICATION OF BO, 22
REPERRENCE/DOCKET NUMBER:
REPUBLICATION OF BO, 22
REPERRENCE/DOCKET NUMBER:
REPUBLICATION OF BO, 22
REPUBLICATION OF BO, 23
REPUBLICATION OF B
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US-08-333-565-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application Patent No. 5622852
GENERAL INFORMATION:
Query Match 100.0%; score 138; DB i: Length 204; Best Local Similarity 100.0%; pred No. 4e-14; Hatches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KORSMYER, Stanley J.
TITLE OF INVENTION: Bol-X/Bol-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CTIT: Palo Alto
COUNTRY - US
COLUMNY - US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2, Application US/08333565
o. 5622852
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US-08-497-312-19
US-08-1718-738-18
US-08-218-738-18
US-08-218-738-18
US-08-133-848-40
US-08-133-848-40
US-09-133-318-40
US-09-133-1113-74
US-08-937-161-7
US-08-937-362-170
US-08-937-362-170
US-08-937-362-170
US-08-937-362-94
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18. Appl
18. Appl
18. Appl
18. Appl
29. Appl
20. Appl
                  Gaps
                  0;
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Result No.

Score

US-08-33-566-2
US-08-61-33-500A-1
US-08-733-500A-1
US-08-733-500A-1
US-08-733-500A-1
US-08-733-500A-1
US-08-733-500A-1
US-08-733-7
US-08-733-7
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US-08-733-500A-1
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US-08-733-1
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US-08-733-1
US-08-733-1
US-08-7

Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5,

% Query Match

Length

В

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ф

1 NLWAAGRYGRELRRMSDEFEGSFKGL 26 !!!!!!!!!!!!!!!!!!!!!!!!! 140 NLWAAGRYGRELRRMSDEFEGSFKGL 165

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RESULT 3
US-08-733-505A-1
                                                                                                                                                                                                                                                                                                                     : NAME/KEV: Protein
: LOCATION: 1.204
: OTHER INFORMATION: /note= *Deduced amino acid sequence
: OTHER INFORMATION: of mouse BAD.*
US-08-661-479-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-08-661-479-2
                                                  Sequence 1, Application US/08733505A Patent No. 5856445 GENERAL INFORMATION:
                                                                                                                                                                                                                                  Overy Match 100.0%; Score 138; DB 2; Length 204; Best Local Similarity 100.0%; Pred. No. 4e-14; Matches 26; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS;
LENGTH: 204 pmino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   general information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPART TYPE: Ploppy disk
COMPARTIE: BM PC COMPATIBLE
OPERATING SYSTEM: PC-DGS/MS-OOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/661.47^
EILING DATE: 11-UNN-^^CCASSIFTY**
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BCL-KL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICAMY: KORSHEYER, Stanley J.
TITLE OF INVENTION: BEDL'A/BEL'2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: SO
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend Khourle and Crew STREET: 379 Lytton Avenue CITY: Pala Alco
STRYEE. California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08661479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-1995
N: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 08/333,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L5726A-000700
                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                         Gaps.
                                                                                                                                                                                                                                    0;
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; TYPE: amino acid
: STRANDEDNESS:
; TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-733-505A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-733-505A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/733
PILING BATE:
CLASSIFICATION: 530
ATTORNET/AGENT INFORMATION:
NAME: BOLLAND, DOWALD R.
RECISTRATION NUMBER: 35,197
REFERENCE/DOCKST NUMBER: 9654
TELEPONNUMICATION INFORMATION: 1140 727-518
TELEPONE: (314) 727-592
INFORMATION FOR SED ID NO: 1.
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08733505A Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 138; DB 2
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 25; Conservative 0; Mismatches
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
ANAME: HOLLAND, DONALD R.
REGISTRATION MUMBER: 35,197
REFERENCE/DOCKET MUMBER: 9654
TELECONMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                  COMPUTER HEADABLE FORM:
COMPUTER TEADABLE FORM:
MEDIUM TYPED BE FLOPPY disk
MEDIUM TYPED FLOPPY disk
MEDIUM TYPED FLOPPY DISK
MEDIUM TYPED FLOPPY
MEDIUM TORMAN:
MEDIUM TORMAN TORMAN
CORRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICAMY: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BCI-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR NUMBER OF SEQUENCES: G.
CORRESPONDENCE, ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: FAtentin Meabase #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 7733 FOR CITY: ST. LOUIS STATE: MISSOURI COUNTRY: USA
                                                                                                                                                                                                                                                                                                                               ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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HER: 965458
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RESULT 5
US-08-733-505A-13
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Best Local Similarity 100.0%;
Matches 26; Conservative (
                                                         Matches
                                                                       Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                              TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM WC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR NUMBER OF SEQUENCES: 60
                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
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STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                      Similarity
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7733 FORSYTH BLVD., SUITE 1400
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ilarity 100.0%;
Conservative
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                                                                                                                                                          linear
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                                                                                                                                          peptide
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NO: 12:
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Pred. No.
                                                                      Score 138; DB 2
Pred. No. 4e-14;
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                                                         Mismatches
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RESULT

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US-08-717-123-3
                                                                                                                                                                                                                                                                                                                        Patent No. 5965703
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                            Sequence
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Best Local
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAPERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village brive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: HOLLAND, DONALD R
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: BEGL-XL/BGL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                    TITLE OF INVENTION: Human BAD Polypeptides, TITLE OF INVENTION: Acids and Methods of Us
                                                                                                                                                                                                                                                                                      APPLICANT: Horne, William A. APPLICANT: Oltersdorf, Tilme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PRICOLINI Release #1.0, Version #1.25
JRREWT APPLICATION DATA:
                                                                                                            COUNTRY: U
ZIP: 92122
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5, 5965703
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26; Conserv
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    204 amino acids
amino acid

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(14) 727-6092
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Pred. No. 4e-14;
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MOLECULE TYPE: protein US-08-665-617-2
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Best Local Similarity 96.2
Marches 25; Conservative
                               Query Match
   Matches
                                                                                                                                                                                 TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PACENTEN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/665,617
APPLICATION NUMBER: US/08/665,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
                                                                                                                                                                                                                              NAME: Saliwanchik, David R. REGISTION NUMBER: 31.794
REGISTOR TO NUMBER: CL
REFERENCE/DOCKET NUMBER: CL
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 2444 CITY: Gainesville STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT
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                 Local
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                 Similarity
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2421 N.W. 41st Street, Suite A-1
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91.7%;
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Score 114; DB 1; Length 166; Pred. No. 1.8e-10; 0; Mismatches 2; Indels
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Pred. No. 1
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les 0;
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1 NIWAAQRYGRELRRMSDEFEGSFK 24

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; MOLECULE TYPE:
US-08-717-123-2
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Patent No.
                                                                                                                                                                                                              Sequence 1
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS;
ENGTH: 168 amino acids
                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                             APPLICANT: COTLEY, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                          NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                              APPLICANT:
                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 NEWAAQRYGREERRMSDEFVDSFK 124
                                                                                                                                                                                                                                                                                                              103 NLWAAQRYGRELRRMSDEFVDSFK 126
                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 20-SE CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                               l Similarity 91.7
22; Conservative
                                                                                                                                                                                                                  , Application US/08985335
6080847
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amino acid
Palo Alto
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: United States
            E: Incyte Pharmaceuticals, Inc
3174 Porter Dr
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                                                                                                                            Lal, Preeti
Shah, Purvi
                                                                                                                                                               Yue, Henry
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91.7%;
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Pred. No. 1.8e-10;
0; Mismatches 2;
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US-08-985-335-7
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Best Local Similarity 91.7%;
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INFORMATION FOR SEQ ID NO: 1:
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APPLICANT:
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LIBRARY: SYNOF
CLONE: 358673
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                              APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 9
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TITLE OF INVENTION: PROTEI
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
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CITY: Palo Alto
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amino acid
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Pred. No. 1
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RESULT 12
US-09-410-372-1
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Best Local Similarity
                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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INFORMATION FOR SEQ
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
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TITLE OF INVENTION: PROTEI
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            TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                   SEQUENCE CHARACTERISTICS:
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TONE: 1683637
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CITY: Palo Alto
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                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/410,372
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                                        STRANDEDNESS:
                                                                                                                    TELEFAX:
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3174 Porter Dr.
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SYNORAB01
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91.7%;
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Pred. No. 1.8e-10;
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LIBRARY:

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В
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                                                                                Query Match
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Best Local Similarity
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                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
                                                                                                                                           LIBRARY: GenBa
                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Corley, I
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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103 NLWAAQRYGRELRRMSDEFVDSFK 126
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                                                      Local Similarity
les 22; Conserv
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                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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                          1 NLWAAQRYGRELRRMSDEFEGSFK 24
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                                                     Conservative
                                                                                                                                                GenBank
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91.7%;
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91.7%;
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                                                                Score 114; DB 4;
Pred. No. 1.8e-10;
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Pred. No. 1
                                                   Mismatches
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                                                                           Length 168;
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RESULT

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RESULT 15
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                                                                                                                                                                                                                                                                                                           Patent No. 5834209
GENERAL INFORMATION:
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 326-240
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Bcl-x/Bcl TITLE OF INVENTION: REGULATOR
                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
  APPLICATION NUMBER:
                                                                                                                                    COUNTRY:
                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/333,565 FILING DATE: 31-OCT-1994 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: California
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JENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
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100.0%; Pr
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Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
REGULATOR
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100.0%; Pred. No. 2.
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US/08/661,479
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FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-CCT-1994
ATTORNEY/ASENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 15726A-000700
TELECOMMUNICATION UNMBER: 15726A-000700
TELECHONE: (415) 326-2420
TELECHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENCTH: 23 amino acids
TYPE: TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-661-479-10
                                                                                                      밁
Search completed: September 20, 2002, 10:37:18 Job time: 406 sec
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Best Local Similarity 100.
Matches 21; Conservative
                                                                                                   81.9%; Score 113; DB 2; Length 23; 100.0%; Pred. No. 2.8e-11; ative 0; Mismatches 0; Indels
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Result
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Maximum DB :
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Listing first 45 summaries
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Match Length
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000
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JC5575
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NADH dehydrogenase	hypothetical prote	hypothetical proce	_			. –	env polyprotein -	probable membrane	oxaloacetate decar		oxaloacetate decar	sodium ion pump ox	conserved hypothet	conserved hypothet	chlorocruorin chai

## ALIGNMENTS

bad protein - mouse C:poecies: mus musculus (house mouse) C:Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999

RESULT A55671

C:Accession: A55671

C:Accession: A55671

R:Yang, E:; Zha, J:; Jockel, J:; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.

Cell 80, 285-291, 1955

A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot A:Peference number: A55671; MUID:95136361

A:Accession: A55671

A:Status: preliminary; not compared with conceptual translation A:Status: preliminary; not compared with conceptual translation A:Molecule type: mRNA

A:Residues: 1-204 cYAN2

A:Cross-references: GBL137296; NID:g639778; PIDN:AAA664465.1; PID:g639779

C:Keywords: heterodimer

000000 Match 100 0% Score 138: DB 2: Length 204:
Hest Local Similarity 100.08; Prod. No. 7.1e-13; Best Local Similarity 100.08; Prod. No. 7.1e-13; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NLWAAQRYGRELRRWSDEFEGSFKGL 26
RESULT 2
ישל בארט inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-199/ #text_change zv-uun-zuvv C:Accession: JC5575; PC4485
R; Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.
J. Biochem. 122, 71-82, 1997
sin inhibitor heavy chain family.
A; Reference number: JC5574; MUID:97420688
A;Accession: JC5575
A, Molecule type: mRNA
A;Residues: I-946 <nak> A;Cross-references: DDBJ:D89286; NID:g1694689; PIDN:BAAl3939.1; PID:g1694690</nak>
A; Experimental source: liver
A; Accession: PC4485
A; Molecule type: protein
C; Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3
that the complexes play important role for panceatic cancer.
C;Superfamily: inter-alpha-trypsin innibitor complex component if
TO CAPAPAPAPASAUROCOLIGE DO CY

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RESULT
S38185
2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces ce. N;Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; DAHP synthase; C;Species: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X70392; NID:g695633; PIDN:CAA49842.1; PID:g695634
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.
Biochem, J. 366, 505-512, 1995
A;Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in A;Reference number: S54353; MUID:95194326
A;Accession: S54354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Spectes: Mus musculus (house mouse)
C.Date: 15-7ul-1995 #sequence_revision 01-Sep-1995 #text_change
C.Accession: $54334
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: D70760
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C;Accession: D70760
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
R;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc
Ralandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:Z74025; GB:AL123456; NID:g3261586; PIDN:CAA98415.1; A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-223 <COL>
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C.Species: Mycobacterium tuberculosis
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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Conservative
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Best Local
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                                                                                                                                                        NVWI IEPQGMRFLHVPDTFEGHFQGV 237
                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                          9; Conserv
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                                                                                                                                                                                                                                                           38.4%;
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                                                                                                                                                                                                                                                         Score 53;
Pred. No.
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Pred. No.
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                                                                                                                                                A42095
                                                                                                                                                                    RESULT
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A;Pathway: aromatic amino acid biosynthesis; shikimate pathway
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A;Map position: 2R
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A; Residues: 1-204,208-370 <KUE>
A; Cross-references: EMBL:X61107
R; Kuenzler, M.; Balmelli, T; E;
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C;Comment: This enzyme catalyzes
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A; Residues: 352-370 <KU2>
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9, 1131-1137, 1993
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phosphoenolpyruvate and D-erythr

biosynthesis; carbon-carbon lyase;

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Gene 113, 67-74, 1992
A;Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the A;Reference number: JN0322; MUID:92225349
A;Accession: JN0322
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A;Residues: 1-370 <AIG>
A;Cross-references: EMBL:Z36118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:YBR2
A;Kuenzier, M.; Paravicini, G.; Egli, C.M.; Irniger, S.; Braus, G.H.
A; Title: Cloning, primary structure, and A; Reference number: A48651; MUID: 93374850 A; Accession: B48651
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J. Bacteriol. 175, 5548-5558, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:L20296; NID:g311101; R;Aljinovic, G.; Pohl, F.M.; Pohl, T.M. submitted to the Protein Sequence Database, A; Reference number: S45906
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                                                                                                                 C.M.; Paravicini, G.; Braus,
                                                        and regulation of
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floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana N;Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3 C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000 C;Accession: A42095; S52633; T47593 R:Jack, T.; Brockman, L.L.; Meyerowitz, E.M. Cell 68, 683-697, 1992
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A:Title: The homeotic gen
A:Reference number: A4205
A:Accession: A42095
A:Scatus: preliminary
A:Molecule type: mRNA
A:Residues: 1-232 - JAC-
A:Residues: T-232 - JAC-
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A:Reference number: 224469
A:Recession: 747593
A:Status: preliminary
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R:Okamoto, H.; Yano, A.; Shiraishi, H.; Okada, K.; Shimura, Y.
Plant Mol. Biol. 26, 465-472, 1994
A:71tle: Genetic complementation of a floral homeotic mutation, apetala3, with A:Reference number: $52633; MUID:95036018
A:Accession: $52633; MUID:95036018
A:Accession: $52633; MUID:95036018
A:Reference type: DMA
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R;Bloecker, H.; Mewes, H.W.; Lencke, K.; Mayer, K.F.X.; Quetier,
submitted to the Protein Sequence Database, March 2000
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A;Experimental source: petals, stamens
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C;Genetics:
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A; Residues: 1-374 <STO>
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                                                                   840376
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Ig kappa chain -
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197
ELRRLSDAVEGSF
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probable threonine synthase [imported] - Arabidopsis thaliana
probable threonine synthase [imported] - Arabidopsis thaliana
probable (2-Pate: 02-Mar-2001)
probate: 02-Mar-2001 stext_change 31-Mar-2001
probate: 02-Mar-2001 stext_change 31-Mar-2001
probate: 02-Mar-2001
probate: 02-Mar-2001
probate: 02-Mar-2001
probate: 02-Mar-2002
probate: 02-Mar-2003
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probate: 02-Mar-2003
probate: 02-Mar-2001
probate: 02-Mar-2002
probate: 02-Mar-2002
probate: 02-Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Complete genome sequence of Pseudomonas A;Reference number: A82950; MUID:20437337 A;Accession: E83517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein PA1031 [imported] - Pseudomonas aeruginosa (strain PA0
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                     A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1031
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-453 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE005173; NID:g5903070; PIDN:AAD55628.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE004535; GB:AE004091; NID:g9946936; PIDN:AAG04420.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-516 <STO>
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Best Local S
Matches 12
                                                                                                                                Matches
                                                                                                                                                                                       Query Match
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65
                                                                                                                                                              Local
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                                                           3 WAAQRYGR--ELRRMSDE 18
WASERQGREEELRRLASE 82
                                                                                                                           1 Similarity
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                                                                                                                           Conservative
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                                                                                                                           Score 49; DB
Pred. No. 23;
4; Mismatches
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Pred. No. 19;
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                                                                                                                                                 . 23;
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Folger, K.R.; Kas,
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A.; Larbig,
                                                                                                                                Gaps
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annexin P35 - maize

C:Species: Zee mays (malze)
C:Species: Zee mays (malze)
C:Species: Zee mays (malze)
C:Accession: T03978
R:Bettey, N.H.; James, N.C.; Greenland, A.J.
Plant Physiol. 112, 1391-1396, 1996
A:Title: CDNA isolation and gene expression of maize annexins P33 and P35.
A:Reference number: Z14796; MUID:97092863
A:Accession: T02975
A:Reference number: Z14796; MUID:97092863
A:Accession: T02975
A:Residus: pretimnary; translated from GB/EHBL/DDBJ
A:Molecule type: mRNA
A:Residus: 1-314 CBAT?
A:Residus: 1-314 CBAT?
A:Experimental source: cuitivar clipper; root tip
C:Superfenally: annexin repeat homology
F:14-85/Domain: annexin repeat homology <AXR>
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A:Title: Expressed human immunoglobulin chi genes and A:Reference number: $40312; MUID:94080891

A:Reference number: $40312; MUID:94080891

A:Recession: $40376

A:Recession: $40376

A:Residues: preliminary; translation not shown

A:Residues: preliminary; translation not shown

A:Residues: 1-134 KLE>

A:Cross-references: EMBL:X72486; NID:9441440; PIDN:CJ

C:Superfamily: immunoglobulin v region; immunoglobulin

C:Reywords: heterotetramer; immunoglobulin

F:34-113/Domain: immunoglobulin homology <IMM>
Cransforming protein homolog MRAS3 - Rhizomucor racemosus
Cranecies: Rhizomucor racemosus
Richaele, W.L.; McConnell
D. G.; Wans, S.Y.; Lee, Y.J.; Linz, J.E.
Rol. Cell
Biol
D. G.; Wans, S.Y.; Lee, Y.J.; Linz, J.E.
Rol. Cell
Biol
D. G.; Wans, S.Y.; Lee, Y.J.; Linz, J.E.
A.; Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which A.; Accession: C36365
A.; Accession: C36365
A.; Accession: C36365
A.; Status: preliminary
A.; Residues: preliminary
A.; Residues: 1-206 C3As>
A.; Cross-references: GB:M55177
C.; Superfamily: ras transforming protein; translation elongation factor Tu homology
C.; Keywords: GTP binding; nucleotide binding; P-loop
F:11-126/Domain: translation elongation factor Tu homology <FUD
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C:Species: Of-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: $40376
C:Accession: $40376
R:Ktein, R.; Jachichen, R.; Zachau, H.G.
buf. J. Immunol. 23, 3246-3271, 1999
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Best Local Similarity 38.3
Matches 13; Conservative
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Best Local
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54 AEAYGKELLRALGDEIHGKFE 74
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hes 10; Conservative
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47, 68;
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Pred. No. 7.8;
1; Mismatches
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Pred. No. 19;
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                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-526 cBPD>
A; Cross references: EMBL:AL050352; GSPDB:GN00062; ATSP:F27B13.80
A; Cross references: EMBL:AL050352; GSPDB:GN00062; ATSP:F27B13.80
A; EXpertmental source: cultivar columbia; BAC clone F27B13
R; Curlen, G; Dumas, R; Ravanel, S; Douce, R.
R; Curlen, G; Dumas, R; Ravanel, S; Douce, R.
F2BS Lett. 390, 85-90, 1996
A; Title: Characterization of an Arabidopsis thaliana cDNA encoding an S-adenosylmethi
A; Reference number: S71362; MUID:96314555
A; Accession: S71362;
                                                                                                                                                                                                                                                                                                                                                                                                                              threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana kalternate names: protein r27B130 C:Opecies; Arabidopsis thaliana (mouse-ear cress) C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 07-Dec-1999 C:Accession: 708545: 871362; 874017 R;Bevan, M; Zimmerman, W; Gruenore, A; Wambutt, R.; Bancroft, I.; Mewe submitted to the Protein Sequence Database, May 1999 A;Reference number: Z16442 A;Accession: 708545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
A; Gene: TM1154
C; Superfamily: yeast SOL3
                                                                                                                           A; Molecule type: mRNA
A; Residues: 'L', 3-526
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                                                                     A:Cross-references: EMBL:L41666;
A:Accession: S74307
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Matches
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NID: 91448916; PIDN: AAB04607.1; PID: 91448917

I.; Mewes,

H.W.;

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A; Molecule type; DNA
A; Residues: 1-220 <ARN>
A; Residues: 1-220 <ARN>
A; Cross-references: GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AAD36230.1; PID:g498
A; Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                      Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A:Reference number: A72200: MUID:99287316
A:Recession: F72289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oxidoreductase, sol/devB family - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Dete: 11-Jun-1999 *sequence_revision 11-Jun-1999 *text_change 21-Ju1-2000
C:Accession: F72289 *sequence_revision 11-Jun-1999 *text_change 21-Ju1-2000
C:Accession: F72289 *sequence_revision 11-Jun-1999 *text_change 21-Ju1-2000
C:Accession: F72280 *sequence_revision 11-Jun-1999 *text_change 21-Ju1-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;17-24/Region: nucleotide-binding motif A (P-loop)
F;13-125/Region: GTP-binding NKXD motif
F;153-155/Region: GTP-binding SKK/L motif
F;23,24,42,123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 RELRRMSDEFEGSFKG 25
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8; Conservative
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34.8%; Score 48; DB
34.8%; Pred. NO. 15;
Live 8; Mismatches
                                                                                                                                            protein
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Pred. No. 14;
2; Mismatches
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                                                       Length 220;
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oxaloacetate decarboxylase, alpha chain VC0550 [similarity] - Vibrio cholerae (strain NI c;Species: Vibrio cholerae c;Date: 18 Aug-2000 *sequence_revision 20-Aug-2000 *text_change 02-Feb-2001 c;Accession: G82308 c;Seatorin: G82308 c;Seatorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Genetics:
A:Gene: ATSP:P27B13.80
A:Gene: ATSP:P27B13.80
A:Map position: 4
A:Genome: nuclear
A:Genome: nuclear
C:Keywords: carbon-oxygen lyase; chloroplast
C:Keywords: carbon-oxygen lyase; chloroplast
F:1-39/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:40-526/Product: threonine synthase #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type; DNA
A; Residues; 1-597 (HEIX
A; Residues; 1-597 (HEIX
A; Cross-references; GB: AE004141; GB: AE003852; NID: g9554976; PIDN: AAF93718.1; GSPDB: GN00:
A; Experimental source; serogroup 01; strain N16961; biotype El Tor
C: Genetics:
A; Gene: VC0550
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C; Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/bio
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Search completed: September 20, 2002, 10:39:02
Job time: 474 sec
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Best Local Similarity 35.3%;
Matches 12: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Owery Match 34.1%; Score 47; DB 2; Length 597; Best Local Similarity 47.4%; Prod. No. 60; Matches 9; Conservative 4; Mismatches 6; Indels
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Q9x507 Q9wv08 P35414 O97666 P11071 P51067 P33310 Q93310 Q94zq5 P5257 P12904

escherichia salmoneila saccharomyc mus musculu

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed.
is derived by analysis of the total score distribution.

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                  BAO, RAT

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RASS_REARIA

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         of1337 mus musculi
o55147 rattus norv
o5524 homo sapien
p97273 mas musculiu
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(6170) mas musculiu
(6170) mas pusculomonas
p22280 ritomucor
05610 seabstopsis
o25280 ritomucor
05610 seabstopsis
o24521 homo sapien
p10412 seabstopsis
o24521 homo sapien
p10412 campylobact
p2124 campylobact
p2125 pylorchis
021134 campylobact
p2125 pylorchis
021136 ximon sapien
p10813 caenorhabdi
p33602 eschorichia
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p33602 sapien
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5 anthopleura
3 homo sapien
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             TISSUB-EASTAIN, and Thymus; 184748; MEDLING-953651; PubMed; 1948; Yang E. Zhan J. Jookel J. Boise L. Yang E. Zhan J. Jookel J. Boise L. Padd, a heterodimeric partner for B promotes cell death; cell 81:28-29.(1955).
"14-3-3 protedins and survival kinases cooperate to inactivate BAD by BH3 domain phosphorylation.";

Wol. Cell 6:41-51(2000).

1- FUNCTION: Promotes cell death. Successfully competes for the binding to Bel-K(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reperse the death repressor activity of Bcl-x(l), but not that of Bcl-2, appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

1- SUBJNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(l), Bcl-2 and Bcl-w. Also binds protein 5100AlO (By similarity). The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.

1- SUBJNIT: Forms heterodimers with the anti-apoptotic proteins.

1- SUBJNIT: Forms heterodimers with the anti-apoptotic proteins.

1- SUBJNIT: Forms heterodimers with the Bcl-2 family.

1- SUBCELGUAR LOCATION: Outers mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.

1- DAMAIN: Intact BH3 domain is required by BIK, BLD, BAK, BAD AND PAR Anti-apoptotic members of the Bcl-2 family.

1- SUBJNIT: Anti-apoptocic members of the Bcl-2 family.

1- SUBJNIT: Anti-apoptocic members of the Bcl-2 family.

1- SUBJNIT: Anti-apoptocic members of the Bcl-2 family.

1- Subsequent phosphorylation on Ser-135 promotes heterodimerization with 14-3-9 proteins. This interaction then facilitates the phosphorylation at Ser-155, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival.
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Del Peso L. Gonzalez-García M. Page C., Herrera R., Nu "Interleukin-3-induced phosphorylation of BAD through th kinase Akt.";
Science 278:587-589(1997).
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MEDLINE-20403302; Pubmed-10949026;
Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B.,
Greenberg M.E.;
Greenberg M.E.;
MI-3-3 proteins and survival kinases cooperate to inactivate BA
BH3 domain phosphorylation.*;
Mol. Cell 6:41-51(2000).
Mol. Cell 6:41-51(2000).
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Mus musculus (Kouse).
Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MCBI_TaxiD=10090;
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06137;
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011.NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last amoutation update)
01-MAR-2002 (Rel. 41 death (BAD) (Bcl-2 binding
6), 18cl-xi/Bol-2 associated death promoter).
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APJ_HUMAN
APJ_MACMU
ACEK_SALTY
ACEK_SALTY
ACEK_SALTY
ADLJ_YEAST
ZO3_MOUSE
THIE_PYRAB
AFBA_YEAREN
SNFA_YEAREN
SNFA_YEAREN
YOJO_NPVAC
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BAD through the protein
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Result No.

Score

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Minimum

DB seq

component

Total number of

Database

Pred. score and is

Sequence: Title: Perfect score:

protein

Scoring table:

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Best Local S
Matches 26
                                                                                                                                                                                                                                                                       TISSUE-OVERY:

MEDILINE-90034386, PubMed-9369453;

HSU S.Y. Kalpla A., Zhu L., Hsuch A.J.W.;

Thterference of BAD (Bcl-xL/Bcl-2-associated death approals in mammallan cells by 14-3-3 isoforms and model. Endocrinol. 11:1859-1867(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAD_RAT 205 AA.

035147; 070256; 093HX1;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
BG12-antagonist of cell death (BAO) (BG1-2 binding
6) (BG1-xL/BG1-2 associated death promotor).
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DOMAIN
MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                             D'Agata V.,
                                                                                                                            D'Agata V., Magro G., To
"Cloning and expression
the rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukharyota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
  TISSUE-Brain;
MEDLINE-21109372;
Hamner S., Arumae
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                        MEDLINE-98194755; PubMed-9535132;
D'Agata V., Magro G., Travali S., Musco
                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L37296; AAA64465.1;
MGD; MGI:1096330; Bad
InterPro, IPR000712; Bel_2.
PROSITE; PS01259; BH3; FALSE_NEG.
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similarity 100.
26; Conservative
                                                                                                              Lett.
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112 113
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  PubMed=11161472;
U., Yu L.-Y., Sun
                                                                  (ISOFORMS ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                  AND MUTAGENESIS
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Pred. No. 8.6
); Mismatches
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Sciurognathi; Muridae;
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Y.-F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                  SER-113
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P11.";
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Lindholm
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Query Match Best Local S Matches 26

th 100.0%; Similarity 100.0%; 26; Conservative 0;

0

Score 138; DB 1; Pred. No. 8.7e-14; Mismatches 0;

Length 205 0; Gaps

0,

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Princtional characterization of two splice variants of rat BAD and Richard interaction with Bcl.w. in sympathetic neurons.';
RL Mol. Cell. Reurosci. 17.97-106(2001).

C. Interaction with Bcl.w. in sympathetic neurons.';
RL Mol. Cell. Reurosci. 17.97-106(2001).

C. Interaction of the second process of Bcl.2 (By cl. and process).

C. Interaction of these proteins with BAX. Can reverse the death repressor activity of Bcl.2 (By similarity). Appears to act as a link between growth factor receptor signaling and the appoint of proteins. Bcl. (I), Bcl.2 and Bcl.w. Also binds protein Sl00A10. The Ser-13.95er-137 phosphorylated form binds 14.3-3 proteins.

C. Interaction locates to the cycopiasm (By similarity).

C. Interaction phosphorylation specific process of the bcl.2 (By similarity).

C. Interaction locates to the cycopiasm (By similarity).

C. Interaction by alternative splicing. They differ only in their compositions of the brain. Testricted to produced by alternative splicing. They differ only in their compositions of the brain. Testricted to produce by alternation death in the brain. Testricted to phosphorylation at Ser-133 in required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic members of the Bcl.2 family.

C. Interaction at Ser-136, a site within the BH3 domain, leading to the release of Bcl.x(L) and the promotion of cell survival.

C. Interaction at Ser-136, a site within the BH3 domain, leading to the release of Bcl.x(L) and the promotion of cell survival.

C. Interaction at Ser-136, a site within the BH3 domain, leading to the release of Bcl.2 (L) and the promotion of cell survival.
            CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: AF003523; AAC53374.1; --
EMBL: AF031227; AAC15100.1; --
EMBL: AF279910; AAF91427.1; --
EMBL: AF279911; AAF91428.1; --
EMBL: AF279911; AAF91428.1; --
INTERFOO, ITENO00712, BG1_2,
PROSITE: PS01259; BH3; FALSE_NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions on its some as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                          MUTAGEN
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205
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148 162
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                                                                                                                         PHOSPHORYLATION (BY CAPK AND PKB) (BY SIMILARITY).

SHALLARITY).

CHARLARITY (BY CAPK AND PKB) (BY SIMILARITY) (BY CAPK AND PKB) (BY SIMILARITY) (BY CAPK AND PKB) (BY SIMILARITY).

ENDEMORPHATION (BY CAPK AND PKB) (BY SIMILARITY).

LEREKASATATORNOSASWIRIIOSWWDRULGKGGSTPSQ.

-> EBLITYSYEFLOVHAIMSCOWPLLWSFOSETHILPTPP PKAMFPLKWFALRAL (IN ISOPONA BETA).

ENDEMORPHATION (BY TENDING ALTERNAL AND SETTING A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternative splicing
                                                                       PROTEINS. NO EFFECT ON HETERODIMERIZATION WITH BCL2 NOR WITH PROTEIN P11.
            PAGGR -> ERRGRK (IN REF. 1).
PAFA71DAE9CF4A81 CRC64;
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BAD_HUMAN

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Q92934; Q14803;
Q1-NOV-1997 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                          "RetLonale for Bcl-xL/Bad peptide complex formation from structure, mutagenesis, and biophysical studies.",

Protein Sci. 9:2528-2534(2000)

- Protein Sci. 9:2528-2534(2000)

- Pronctin Sci. 9:2528-2534(2000)

- Protein Sci. 9:2528-2534(2000)

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Chang S., Weeks S., Fritz L.C., Oltersdorf T.
"Dimerization properties of human BAD.";
J. Biol. Chem. 272:30866-30872(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND DIMERIZATION
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Eukaryota; Metazoa;
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human protein that i
                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of beterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor
DOMAIN: Intract BB3 domain is required by BIK, BID, BAK, BAD AN BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.
                                                                                                                                     SUBCELLULAR LOCATION: Outer mitochondrial membrane. phosphorylation, locates to the cytoplasm.
                                                                                                                                                                                                                                          receptor signaling and the apoptotic pathways. SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bq. x(L), Bcl-2 and Bcl-w. Also binds protein $100A10 (By similarity). The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g H.-G., Rapp U.R., Reed J.C.,
l-2 targets the protein kinase Raf-1 to
                                                                                                        PISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OCT-1997)
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Matayoshi E.D.,
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interacts
                                                                                                            EXPRESSED IN A WIDE VARIETY OF
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Zhang H., Thompson C.
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ID ITH2_M
AC P97279
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D7 15-JUL
D7 10-MAR
DE Inter-
DE Chain
GN HESOCI
OC EUKAY)
OC MASMO
OC MESOCI
OX NCB1-
RP SEQUE
RC TISSU
RX MEDLII

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Best Local
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15-JUL-1998 (Rel. 36, Last sequence update)
11-MAR-2002 (Rel. 41, Last anotation update)
Inter-alpha-trypsin inhibitor heavy chain H2
chain H2) (HC2).
                                                                                                                                                                                                                                                   Mesocricetus auratus
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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Subsequent phosphorylation
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                                                                                                                                                                                                                                                                      Chordata;
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tion on Ser-99 promotes heterodimerizati
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Pred.
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69FD8D27DDEE3241 C
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PHOSPHORYLATION
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Sciurognathi; Muridae;
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Cricetinae;
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\*Moketani T., Suzuki Y., Yamamoto T., Sinohara H.;
\*Moketular cloning and sequencing of cDNAs encoding three precursors of the inter-alpha-trypsin inhibitor in Syrian implications for the evolution of the inter-alpha-trypsin

heavy-chain hamster:

chain

SEQUENCE FROM N.A. TISSUE=Liver;

MEDLINE-97420688; PubMed-9276673;

Mesocricetus

NCB1\_Tax1D=10036;

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                                 RESULT 5
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Best Local
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CARBOHYD
                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
AND SUBUN
ITH2_MOUSE STA
Q61703;
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00092; vwa; 1.
SMART; SM00327; vwa; 1.
PROSITE; PS50234; VWF/
                                                                                                                                                                                                                                                                                                                                                 Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                         Scrine protease
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Yamamoto T., Yamamoto K., Sinohara H.;
"Inter-alpha-trypsin inhibitor and its related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Plasma;
                                                                                                                                                                                                                           BINDING
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                                                                                                                                                                                                                                                                                                                                     SIGNA
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                                                                                                                                    Local
                                                                                                    1 NLWAAQRYGRELRRMSDEFEGSFKGL
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SIMILARITY: BELONGS TO THE ITIH FAMILY.
SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: I ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (HI, H2 OR H3) AND ONE LIGHT CHAIN, BIKUMIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF HI, H2 AND BIKUMIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUMIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUMIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUMIN, PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUMIN, PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUMIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNITS
                                                                              NVWIVELQGMRFLHVPDTFEGHFQGV
                                                                                                                          9; Conservative
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                        STANDARD;
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  Created)
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N-LINKED (GLCNAC...)
CHONDROITIN 4-SULFATE,
(BY SIMILARITY)
V-> Y (IN REF. 2)
E-> I (IN REF. 2)
CA8BF565458E7B2E CRC
                                                                                                                       score 54; DB
pred. No. 2.6;
5; Mismatches
                                                                                                                          5.
                                                                                                                                                                                                                                                                                POTENTIAL.
BY SIMILARITY.
INTER-ALPHA-TRYPSIN 1
H2.
BY SIMILARITY.
VWFA.
                                                                                                                                                                                                                                                         N-LINKED
                        PRT;
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                        946
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(GLCNAC...
(GLCNAC...
                                                                                                                                               DB 1;
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                                                                                                                                   6
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) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                 CHAIN
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EPÓDENCE FROM N. A.

OF STRAIN-CSTEL/GN; TISSUE-Liver;

OK Chan P., Risler J.-L., Raguenez G., Sailer J.-P.;

OK Chan P., Risler J.-L., Raguenez G., Sailer J.-P.;

OK Chan P., Risler J.-L., Raguenez G., Sailer J.-P.;

OK Chan P., Risler J.-L., Raguenez G., Sailer J.-P.;

OK The Industry Chain procurse of the multicopper oxidase protein grow with differential transcription in liver and brain.";

OK BLOCHOM. J. 306:505-512(195)

OK LINCLION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A CHEMEN ANY ACT AS A CARRIER OF HYALURONAN OF HEALTHONIN WHICH ARE COLLUDING PROSESS ON CELL SURFACES IN TISSUES TO REGULATE THE CLOCALIZATION, SYNTHESTS AND DEGRADATION OF HYALURONAN WHICH ARE CLOCALIZATION, SYNTHESTS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
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CARBOHYD
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ITHE?
Mus musculus (Mouse).
Mus musculus (Mouse).
Marvota; Metazoa: Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-slb.ch).
SEQUENCE
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                                                                                                                                                                                                                                                                               SIGNAL
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Pfam; PF00092; vwa; 1.
SMART; SM00327; VWA; 1
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MGD; MGI:96619; Itih2.
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15-JUL-1999 (Rel. 38, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2
                                                        BINDING
                                                                                                                                                                                              PROPER
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                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                    Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: T'ALHAN-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, HIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) OF H3 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (I-ALPHA-I) OF H3 AND BIKUNIN. THE PROTECTIVE PROPERSIES IN BOTH LIVER AND AND HIKUNIN. TISSUE SPECIFICITY: EXERESSED IN BOTH LIVER AND BRAIN. TISSUE SPECIFICITY: EXERESSED IN BOTH LIVER AND BRAIN. PTM. HEAVY CHAINS ARE INTERLIXED MITH BIKUNIN VIA A CHONDROITIN 4-SULPATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY SIMILARITY: BELONGS TO THE TITH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X70392; CAA49842.1; ~.
                                                                                                                                                                                                                                                                                                                                                            protease inhibitor;
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946
                                                                                   703
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      MW.
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                       N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
CHONDROITIN 4-SULFATE,
(BY SIMILARITY).
                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                               POTENTIAL.
BY SIMILARITY
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                                                                                                                                                                                                                                                INTER-ALPHA-TRYPSIN
      40DB6716433ED9DC CRC64;
                                                                                                                                                                                                                                                                                                                                                            Multigene family;
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) (POTENTIAL).
) (POTENTIAL).
                                                            CROSS-LINK
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237

Query Match Best Local S Matches

Similarity 9; Conserv

Conservative

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Mismatches

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RESULT 6
AROG_YEAST
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01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
(EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP
synthetase) (J-deoxy-D-arabino-heptulosonate 7-phosphate synthat
ARO4 OR YBR249C OR YBR1701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aljinovic G., Pohl F.M., Pohl T.M.;
Submitted (AUG-1994) to the EMEL/GENBANK/DDBJ databases.
Submitted (AUG-1994) to the EMEL/GENBANTON OF PHOSPHOENOLPYRUVATE
-I- FUNCTION: STRENGASPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE
-AND D-ERYTHROSE-4-PHOSPHATE (PAP) GIVING RISE TO 3-DEOXY-D-
ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP)
-I- CARALFUL ACTIVITY: 2-dehyylro-3-deoxy-D-arabino-heptonate 7-
phosphate + phosphate - phosphoenolpyruvate + D-erythrose 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dolgnon F., Biteau N., Aigle M., Crouzet M.;
"The complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative dUTPase in a yeast.";
Yeast 9:1131-1137(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthase from Saccharomyces
Gene 113:67-74(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=92225349;
Kuenzler M., Parav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetiales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P32449;
HSSP; P00886; 10R7.
SGD; S0000453; ARO4.
InterPro; IFR001785; DAHP_synth_1; 1.
Pfam; FP00793; DAHP_synth_1; 1.
ProDom; P0005060; DAHP_synth_1; 1.
Aromatic amino acid biosynthesis;
                                                                                                             EMBL; X61107; CAA43419.1; -.
EMBL; L20296; AAA65607.1; -.
EMBL; Z36118; CAA85212.1; -.
PIR; S38185; S38185.
                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictings on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288C:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LINE-92225349; PubMed-114871);
rzler M., Paravicini G. Egli C., Irniger S., Braus G.H.;
oning, primary structure and regulation of the ARO4 gene, encoding
tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate
tyrosine-inhibited 3-deoxy-bvisiae.";
                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF THE BIOSYNTHESIS OF AROMATIC AMINO ACID STARVATION.
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phosphate + H(2)0.
ENZYME REGULATION: INHIBITED BY TYROSINE
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    Lyase; Multigene family.
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synthase).
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AP4_ARACH

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Salanoubat M., Lémcke K., Rieger M., Ansorge M., Unseld M.,
RA Fartmann B., Valle G., Bloceker H., Perez-Alonso M., Obermaler B.,
RA Fartmann B., Valle G., Bloceker H., Perez-Alonso M., Obermaler B.,
RA Delseny M., Boutty M., Grivell L.A., Mache R., Pulgdomenech P.,
RA Meller M., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin M., Ogetter F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin M., Ogetter F.,
RA Schaefer M., Mueller Auer S., Gabel C., Fuchs M., Benes V.,
RA Winche E., Drzonek H., Erile H., Jordan N., Bangert S.,
RA Winche E., Drzonek H., Erile H., Jordan N., Bangert S.,
RA Winche E., Drzonek H., William R., Bardott P., Nyakatura G.,
RA Winche E., Drzonek H., William R., Bardott S., Wakatura G.,
RA Winche E., Drzonek H., William R., Bardott S., Wakatura G.,
RA William R., Kranz H., Voss H., Holland R., Bardott S., Nordsiek G.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T., H., Nordsiek G.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T., H., Nordsiek G.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Banger S., Bascachberta E.,
Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Rodd S., Zaccaria P., Mewes H.-W.,
RA Magyer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
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Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okamoto H., Yano A., Shiraishi H., Okada K., Shimura Y.
"Genetic complementation of a floral homeotic mutation,
with an Arabidopsis thaliana gene homologous to DEFICIE
Antirrhinum majus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92154682: PubMed=1346756;
Jack T., Brockman L.L., Meyerowitz E.M.;
"The homeotic gene APETALA3 of Arabidopsis
box and is expressed in petals and stamens.
Cell 68:683-697(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosk
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Mol. Biol.
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from the equilibrium-neutral model at
genes of Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purugganan M.D., Suddith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                utation, apetala3,
DEFICIENS of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                           Nyakatura
                                             Mewes H.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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RESULT 8
RMUC_PSEAE
ID RMUC_P
AC Q914U3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M86357; AAA32740.1; --
EMBL; D21125; BAA04665.1; --
EMBL; AF115799; AAD51888.1; --
EMBL; AF115800; AAD51889.1; --
EMBL; AF115802; AAD51893.1; --
EMBL; AF115802; AAD51893.1; --
EMBL; AF115804; AAD51903.1; --
EMBL; AF115814; AAD51903.1; --
EMBL; AF115814; AAD51903.1; --
EMBL; AF125814; --
EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFACT T01776;...

TITCH T01776;...

INTCH FOO. JFR002148 J; K-box.

INTCH FOO. JFR002100; MADS-box.

Pfam; PF00149; K-box; 1.

Pfam; PF00119; KR-TF; 1.

PRINTS; PR00404; MADS-DAIN.

SMART; SM00432; MADS; DAX.1; 1

PROSITE; PS00350; MADS_BOX.1; 1

PROSITE; PS00366; MADS_BOX.2; 1
      RMUC_PSEAE
Q914U3;
                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.
Creasy T.H., Haas B., Walti R., Wu D., Peterson J., Van Aken S.,
Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.
Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
Sasmnoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
Kijokawa C., Kohara M., Matsumoto M., Matsumo A., Muraki A.,
Nakayama S., Nakazaki N., Shippo S., Takeuchi C., Wada Y.,
Watanabe A., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>-</del> -
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HSSP; P11746; 1MNM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: EXPRESSED IN PETALS AND STAMENS.
MISCELLANEOUS: MUTATIONS IN APP CAUSE TRANSFORMATION OF PETALS
INTO SEPALS AND STAMINA INTO CARPELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLOWER DEVELOPMENT
                                                                                                                                                   QRLGECUDELDIQELRRLEDEMENTFK 133
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199
232
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3 57
93 165
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                                 STANDARD
                                                                                                                                                                                                                                                                                                                                                                          57 MADS.
165 K-BOX.
199 A -> R (IN REF. 2)
27341 MW; 669070319F9857C3
                                                                                                                                                                                                                                                                            37.0%;
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                                                                                                                                                                                                                                                                            Score 51; [
Pred. No. 1
                              PRT;
                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                 Length 232;
                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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                                                                                                                                                                                                                                     Caps 1;
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P22250;
Ol-AUG-1991 (Rel. 19, C.
Ol-AUG-1991 (Rel. 19, L.
30-MAY-2000 (Rel. 39, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-ATCC 15692 MEDLINE-20437337;
                                                                                                                                                STRAIN-ATCC 1216B;
MEDLINE-91061774; PubMed-1701021;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 NCBI_TaxID-4841;
                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                            Rhizomucor
                                                                                                                                                                                                                                                                                                                                                        RAS3
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DNA recombination; Coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004535; AAG04420.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed-10984043;
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Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrer Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Li Garber R.L., Goltry L., Tolentino E., Westbock-Wadman S., Yu Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K. Li, Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V., Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic pathogen.",

Nature 406.959-964(2000)
Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
"Expression of a gene family in the dimorphic fungus Mucor racen
which exhibits striking similarity to human ras genes.";
Mcl. Cell. Biol. 10:6634-6663(1990).

-i- ENZYME REGULATION. ALTERNATE BETWEEN AN IMACTIVE FORM BOUND
AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EWEL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - FUNCTION: Involved in DNA recombination (By similarity).
- SIMILARITY: BELONGS TO THE RMUC FAMILY.
                                                                                                                                                                                                                                                                                                                                                           racemosus (Mucor circinelloides Fungi; Zygomycota; Zygomycotes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41, Last sequence update)
41, Last annotation update)
protein rmuC homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coiled coil; Complete proteome.

201 COILED COIL (POTENTIAL).
51539 MW; 1E7EA97E82EC5E4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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                                                                                                                                                                                                                                                                                                                                                               f. lusitanicus).
Mucorales; Mucoraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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S., Yuan Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Warrener
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                                    TO GDF
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RESULT 10
6PGL_THEMA
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Best Local
                                                                                                                                                WEDLINE-99287316; PubMed-10360571;
Welson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Elsen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 393:233-239(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institute. There are no rest modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or.send.an.email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003577; Ras.
InterPro; IPR001806; Ras_trnsfrmng
Pfam; PF00071; ras; 1
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00173; RAS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9X0N8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M55177; AAA83379.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 RELRRMSDEFEGSFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
PROSPHO-D-GLUCONATE.

PROSPHATE PATHWAY.

SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.

SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR DEVB OR TM1154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE-EXCHANGE FA
ACTIVATING PROTEIN (GA
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS IN GERMLING AND YEAST.
                                                                                                                 CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone +
                                                                                                                                        PHOSPHOGLUCONATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C36365; C36365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is producen the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermotogales;
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                                                                                                                                                                                                                                                                                                                                                                                              DSM 3109;
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

EFFECTOR REGION (PROBABLE).

FARNESYL (BY SIMILARITY).

OB WM; DBF086466F090F50 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 1;
Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9MT28;
01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Casazza P., Kaiser S., Willmitze "Isolation and characterization from Solanum tubercoum." submitted (AUG-1998) to the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Threonine synthase, chloroplast precursor (EC 4.2.99.2) (TS). Solanum tuberosum (Potato). Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                            Chloroplast;
TRANSIT
                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000457; Glucosamine_iso
Pfam; PF01182; Glucosamine_iso; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; TM1154; -.
                                                                                                                                Threonine biosynthesis; Lyase; Pyridoxal
                                                                                                                                                                                                                                      EMBL; AF082894; AAF74984.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asteridae;
                                                                                                                                                                                                             nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 AAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENTYME REGULATION: Allosterically activated by S-
methionine (SAM) (By similarity).
PATHWAY: Threonine biosynthesis; last step.
SUBUNIT: Homodiner (By similarity)
SUBUNIT: Homodiner (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mitted (AUG-1998) to the EMBL/GenBank/DDBJ databases CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphate.
COFACTOR: Pyridoxal phosphate (By similarity).
ENTYME REGULATION: Allosterically activated by
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8; Conservative
                                                                                                                                                                PS00165;
                                                                                                                                                                                                             IPR001926; B6_enzyme_beta
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220 AA; 25325 MW;
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196
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                                                                                Transit peptide.
   AA;
                                                                                                                                                                                   PALP;
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                                                                                                                                                         DEHYDRATASE_SER_THR;
                                                      519
   57412 MW;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Solanales;
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THREONINE SYNTHASE.

PYRIDOXAL PHOSPHATE (BY SIMILARITY).

114C0979CD231464 CRC64;
                                                                            CHLOROPLAST (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                   phosphate; Allosteric enzyme;
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RA Pohl T., Duestchneft A., Stiekema W., Entlan K. D., Terryn N., Ra Horris B., Ansorge W., Brandt P., Grivall L.A., Rieger M., Weller H., Ansorge W., Brandt P., Grivall L.A., Rieger M., Weller H., Mache R., Mueller M., Richer R., Meller H., Mache R., Mueller M., Richer R., Meller H., Pohler R., Meller H., Mache R., Meller H., Richer R., Meller H., Pohler H., Dehen J., Zimmermann W., Wedler H., Boht R., Weller H., Braun M., Schmidthein T., Robben J., Vandenbussthe F., Ra Langham S. A., McCullagh B., Bilham L., Robben J., Vandenbussthe F., Ra Langham S. A., McCullagh B., Bilham L., Robben J., Vandenbussthe F., Ra Langham S. A., McCullagh B., Bilham L., Robben J., Wenter P., Defoo, E., Ramsperger U., Hilbert H., Braun M., Melternegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Ra Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Ra Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Ra Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Ra Horneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., De Keyser A., Buysshaert C., Gieten J., Villarroel R., De Clercq R., Van Montagu M., Rogers J., Cronin A., Ouall M., McLay K., Mayes R., Ra Pettett A., Rajandaream M.-A., Lyne M., Benes V., Rechmann S., Clark L., Doggett J., Hall S., Kay M., Ennard N., McLay K., Mayes R., Petter H., Schmit M., Grimm M., Loehnert T.-H., Ra Gabel C., Puchs M., Partmann B., Granderath K., Dauner D., Herzl AN, Benes V., Rechmann S., Argiriou A., Vitale D., Liguori R., Pitavandi E., Ra Gabel C., Puchs M., Partman B., Granderath K., Dauner D., Herzl AN, Gabel C., Puchs M., Partman B., Granderath K., Dauner D., Herzl AN, Peter Peter A., Purnelle B., Benti E., Johnson S., Tacon D., Jesse T., Ra Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Peters Peter A., Purnelle B., Benti E., Monfort A., Casacuberta E., Ra Fitchia P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., Ra Peter J., Bentley D., Fulton B., Willer N., Schutz K., Hung E., Schutz K., Hung E., Schutz K., Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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Matches 12
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Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Sparmarcophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mayer K.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CY. Wassilewskija;
MEDLIND-99418329; PubMed-10490396;
Bartlem D., Tamaki Y., Nalto S.;
"Genomic nucleotide sequence of the Arabidopsis threonine synthase •.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20083488; PubMed-10617198;
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Query Match Best Local

Similarity 12; Conserv

Conservative

35.38;

Score 48; DB Pred. No. 11; 6; Mismatches

DВ 11:

Length 526

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EMBL, AB037151; BAA77707,1; -.
EMBL, AL050352; CAB43659,1; -.
EMBL, AL161575; CAB79742.1; -.
EMBL, AL161575; CAB79742.1; -.
EMBL; L41666; AAB04607.1; -.
PDB, 1E53, 02-AUG-01.
InterPro; IPR001926; PALP.
BINDING
CONFLICT
SEQUENCE
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                                PROSITE: PS00165; DENYDRATASE_SER_THR: 1.
Threonine biosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme; Chloroplast; Transit peptide: 9)-structure.
TRANSIT 1 40 CHLOROPLAST.
CHAIN 41 526 THREONINE SYNTHASE.
BINDING 203 203 PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               Curien G., Job D., Douce R., Dumas R.; "Allosteric activation of Arabidopsis threonine synthase S-adenosylmethionine."; Biochemistry 37:13212-13221(1998).
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"Characterization of an Arabidopsis thaliana cDNA encoding an
S-adenosylmethionine-sensitive threonine synthase. Threonine synthase
from higher plants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Crystal structure of threonine synthase from Arabidopsis thaliana."; Protein Sci. 10:638-648(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUMICELLULAR LOCATION: Chloroplast.
-1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
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THREONINE SYNTHASE.

PYRIDOXAL PHOSPHATE.

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043521; 043522;
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16-0CT-2001 (Rel. 40,
16-0CT-2001 (Rel. 40,
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   FMR2_ANTEL
Q16994;
16-OCT-2001
16-OCT-2001
01-MAR-2002
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MEDLINE-98094366; PubMed-9470630;
O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M.,
                                                                                                                               ANTEL
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SEQUENCE
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PROSITE: PS01259; BH3; FALSE_NEG.
PROSITE: PS01259; BH3; FALSE_NEG.
PROSITE: PS01259; Membrane.
POMAIN 148 162 BH3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC ECL-2
PROTEINS INCLUDING WCL-1, ACL-2, ECL-XL, BFL-1, AND BHRF-1. DOES
NOT HETERODIMERIZE WITH PROADPTOTIC PROTEINS SUCH AS BAD, BOK,
BAX OR BAK (BY SIMILARITY).
SUBCELLULAR ICCATION ASSOCIATED WITH INTRACYTOPLASMIC MEMBRANES
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: INDUCES APOPTOSIS. ISOFORM BIML IS
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   (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation updat
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interacting mediator of cell death)
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      update)
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01-MAR-1989 (Rel. 10, Created)
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Anthopleura elegantissima (Sea amemone).
Eukaryota: Metazoa; Cudaria; Anthozoa; Zoantharia; Actiniaria;
Nymantheae; Actiniidae; Anthopleura.
.on; Repeat;
             ANTHO-REAMIDE.
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         ON (G-236 PROVIDE MIDE GROUP)
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or 61-007-1993 (Rel. 27. Last sequence update)
or 16-007-101 (Rel. 40. Last sequence update)
or 16-007-101 (Rel. 4
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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26.122 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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138
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Q919n2 brachydanio
Q10843 mycharterii
Q99e9q arabidopsis
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## ALIGNMENTS

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89 LMAAKKYGOOLRHMSDEFDKGMK 111  T 2 010843 PRELIMINARY; PRT; 223 AA. 0210843 OT-NOV-1998 (TYEMBLYEL) 08, Greated)	Query Match 63.0%; Score 87; DB 13; Length 146; Best Local Similarity 65.2%; Pred. No. 2.8e-05; Best Local Similarity 65.2%; P	SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;	EMBL; AF231017; AAF66962.2;	Cell Death Differ. 7:509-510(2000).	zebrafish.";	"Genes with homology to mammalian apoptosis regulators identified in	Inohara N., Nunez G.;	MEDLINE~20373792; PubMed~10917738;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=7955;	Cypriniformes; Cyprinidae; Danio.	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	rachydanio rerio (Zebrafish) (Zebra danio).	BAD.	BAD.	(TremBLrel. 19,	(TrEMBLrel.	01-OCT-2000 (TrEMBLrel: 15, Created)	•	Q9I9N2 PRELIMINARY; PRT; 146 AA.	F

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Matches
                                     #01. Biol. Bvol. 16:1037-1045(1999).

#M1. Biol. Bvol. 16:1037-1045(1999).

EMBL; AF143380; AAF25590.1:

HSSF; P11746; IMMM.

InterPro: IPR002409 ADSS-box.

Pfam; PF01486; K. box; 1

Pfam; PF00319; SRF-TF; 1

PRINTS: PR00404; AADSS-DOMAIN.

SMART; SM00432; AADSS-DOMAIN.

SMORTER 231 231

SEQUENCE 231 AA; 27176 MM; A67CAEI
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- I SIMILARITY: TO M. PREATUBERCULOSIS IS900.

BMBL, 74075; CAA98415.1.

Tubercullis Re2014;
- ITER 1970: IPRO03316; Transposase_20.

Flam: PR02371; Transposase_20. 1

HypotherLoal protein: Complete proteome.

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09SEGO, 01 MAY-2000 (TERMBLTE). 13, Created)
01-MAY-2000 (TERMBLTE). 13, Last sequence update)
01-JUN-2000 (TERMBLTE). 17, Last annotation update)
APENALAS (FRAMENT).
ARBIOLOGIS JYGLA
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Lawton-Rauh A.L., Buckler B.S. IV. Purugganan M.D.;
"Patterns of molecular evolution among paralogous floral homeotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, viridiplantae: Streptophyta: Embryophyta; Trachoophyta; Spermatophyta; Budicotyledons; core eudicots; Rosidae; Surmatophyta; audicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicacese; Arabidopsis.
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GOLE S.T., BROSCH R., PARKHILL J., GARRIER T., Churcher C., Herris GOLE S.T., BROSCH R., PARKHILL J., GARRIER T., Churcher C., Brosch R., Parkhill J., Brown D., Chillingworth T., Connor R., Baddock K., Basham D., Brown D., Chillingworth T., Connor R., Davids R., Deviln K., Feltwell T., Genles S., Hamin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J., Rutter S., Segor K., Stelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G., Sueston J.E., Sueston J
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Bacteria: Firmicutes: Actinobacteria;
Actinomycetales: Corynebacterineae: My
MCBI_TaxID-1773;
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Pred. No. 5.4;
1; Mismatches
                                                        A67CAE1EEBD8F7AA CRC64;
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PEREQUENCE FROM N.A.

12 SEQUENCE FROM N.A.

13 C STRAIN-CV. GR-3, AND CV. CH1-1;

14 C MEDILINE-90126449; pubMed-9927474;

15 W PURUSHARM N.D., Suddith J.I.;

16 PURUSHARM N.D., Suddith J.I.;

17 SHORECULAR POPULATION SPREETICS OF FLORAL homeotic loci. Development of Arabidopsis thallana.";

18 Genetics 151:839-848(1999).

19 C -1 SUMILARITY: TO THE MADS DOMAIN FAMILY OF THANSCRIPTION

19 EXBEL, AR115033 AND51892.1;

10 RESEL, AR115034 AND51897.1;

10 RESEL, AR115034 AND51897.1;

11 RESEL, AR115034 AND51897.1;

12 RESEL, AR115034 AND51897.1;

13 PIAMI, PRO02105; MADS -BOX.

14 PIAMI, PRO04034; MADS -BOX.

15 PIAMI, PRO04034; MADS -BOX.

17 SHART: SHO0432; MADS -BOX.

18 PROSITE: PS00305; MADS -BOX.

19 PROSITE: PS00306; MADS -BOX.

10 SEQUENCE 232 AA: 27340 MM; 6690703F9E9CFD63 CRC64;
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OL-MAY-2000 (TTEMBLIEL 13, L
OL-DEC-2001 (TTEMBLIEL 13, L
FLORAL HOMBOTIC PROTEIN AP3.
krabidopšis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoltophyta; Eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=7902;
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C995703,
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O1-MAY-2000 (TEEMBLITE1. 13. Created)
O1-MAY-2000 (TEEMBLITE1. 13. Last sequence update)
O1-UNY-2001 (TEEMBLITE1. 17. Last annotation update)
FLORAL HOMEOTIC PROTEIN APS.
APETMIA.3.
APETMIA.3.
ENAMETYCIA, VITIGIPLATE, STREPTOPHYTA; Embryophyta; Tracheophyta;
Epsermatophyta; Magnollophyta; endicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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nilarity 44.4%;
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3; Mismatches
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Last annotation update)
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Best Loo
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STRAIN-CY. KENT:

STRAIN-CY. KENT:

MEDLINE-99126449; PubMed-9927474;

PULIGRAPH N.D., Suddith J.I.;

PMOlecular population genetics of floral homeotic loc
from the equilibrium-neutral model at the APEYALA3 and
genes of Arabidopsis thaliana.";

Genetics 15:1839-848(1999)

-1- SURCELULIAR LOCATION: MUCLEAR (BY SIMILARITY).

-1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRI

EMBL: ARI18805; AAD51894.1;

EMBL: ARI18805. JANM.

EMBL: ARI18805. JANM.
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HSSP, P11746; 1MAM,
InterPro; IPR002407; K-box,
InterPro; IPR002100; MADS-box,
Pfam; PF01486; K-box; 1.
Pfam; PF01486; K-box; 1.
PF18778; PR004040; MADSDOMAIN,
SMART; SW00432; MADS; 1.
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"Molecular population genetics of floral homeofic loci, Departures from the equilibrium restral model at the APSTALA3 and FISTILLATA genes of Arabidopais thaliana,";
Genetics 151:1839-648(1999)
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STRALN=CV. L1-8;
MEDLINE=99126449; PubMed=9927474;
     PROUTE; PROMOĞÓ; MADSDOMAIN.
SMART; SMOG432; MADS; 1.
PROSITE; PSO0350; MADS_BOX_1; 1.
PROSITE; PS50056; MADS_BOX_2; 1.
UNA-binding; Nuclear protein; PC UNA-binding; Nuclear protein; PSCOURNCE 232 AA; 27286 MM; 6
                                                                                                                                                                                                                                           HSSP; P11746; IMNM.
InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box.
InterPro; IPR002100; MADS-box.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS30066; WADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription regulation DNA-binding; Nuclear protein; Transcription CRC64; SEQUENCE 232 AA; 27267 MW; 42A852D697E22A65 CRC64;
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Transcription regulation
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REPAIRETY, CORECALLA,
REPAIRETY, PUBMED-103 FOR THE REPAIRE SET TYPE THE PROPERTY TO PRE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.

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Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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InterPro: FPR002100: MADS-box.
Pfam: PF00148; K-box: 1.
Pfam: PF00319; SRF-TE: 1.
PFALNTS: PR004040: MADSSOMAIN.
PFALNTS: PR00432: MADS: BOX.2: 1
PROSTITE: PS050066; MADS: BOX.2: 1
PROSTITE: PS050066; MADS: BOX.2: 1
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MEDLINE-99126449; PUNNEC-9927474;
PURUSIGNAM M. D., Suddith J. I.
PURUSIGNAM M. D., Suddith J. I.
*MEDLINE-99126449; PUNNEC-9927474;
*MEDLINE-99126449; PUNNEC-9927474;
*MEDLINE-999144440; STRAIN-999146449; PUNNEC-9927449; PUNNEC-9927449; PUNNEC-992749; PU
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MEDLINE-9916449; PubMed-9927474;
PULUGADAR M.D. Suddit, J.I.;
MEDLINE-9916449; PubMed-9927474;
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InterPro: IPR002487; K-box.
InterPro: IPR002100; MAD5-box.
Pfam: PF01486; K-box. I
Pfam: PF01486; K-box.
PFAST: PF00319; SBP-TE: 1.
PFAST: PF00319; SBP-TE: 1.
PFAST: PF00319; MADS: PF0.
PF0STTE: PF003046; MADS: PF0.
PF0STTE: PF0S0066; MADS: PF0.
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Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; KANSDOMAIN.
SMART; SM00432; MADS; 1.
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01-MAY-2000 (TrEMBLrel. 1
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SEROURICE FROM N.A.
STRAIDHCY LISSE;
MEDILIES-99126449;
MEDILIES-9912649;
PULUSGANA M. D. SUNDIELL J.T.
MOLECULAR DEPOLATION OF FLORAL MOMENTAIN AND SUNDIELL MODEL AT THE APPRILAD AND FIVELENA GENERAL STANDARDS.
TOM THE EQUILIBRIUM FRONT OF THE MASS DOMAIN PANTILY OF TRANSCRIPTION FACTORS.
1- STULDARTY: TO THE MASS DOMAIN PANTILY OF TRANSCRIPTION FACTORS.
EMBL. AFLISHIO, AND SERVE.
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STRAIN-CV_LISSE;
MEDLIKR-99126449; Pubmed-9927474;
MEDLIKR-99126449; Pubmed-9927474;
Purugganan M.D., Suddith J.I.;
Purugganan M.D., Suddith J.I.;
From the equilibrium-neutral model at the APETALA3 and PISTILLATA
genes of Arabidopsis thaliana.";
Genetics 151:839-848(1999).
-1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS
EMBL. AF115899. AADS1888.1;
-1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS
EMBL. AF115899. AADS1888.1;
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EMBL. AF115899. AADS18889.1;
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EMBL. AF115899. AADS18889.1;
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EMBL. AF115899. AADS18899.1;
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EMBL. AF115899. AADS18899.1;
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EMBL. AF115899. AADS18899.1;
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EMBL. AF115899.1;
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EMBL. AF115899
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Enkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheo;
Spernatophyta, Magnoliophyta; endicotyledons; core endicots;
Spernatophyta, Magnoliophyta; endicotyledons; core endicots;
NCBI_TaxID-3702;
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PROSITE: PS00066: MADS_BOX_2: 1.
DNA-binding: Nuclear protein: Transcription regulation SEQUENCE 232 AA; 27284 MW; 04FCFC55B73C7729 CRC64;
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II. Brassicales; Brassicaceae; Arabidopsis.
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Pred. No. 11;
3; Mismatches
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Q9SQ15;
Q1-MAY-2000 (
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Q1-DEC-2001 (
09KGW3
                                                                                                                                               PRINTS, PRO0404; MADSDOMAIN.
SMART; SM0413; MADS; 10.
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS0066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription regulation.
SEQUENCE 232 AA: 27300 MW; 5CA05FD44F824DF0 CRC64;
                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridipilantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS50086; MADS_BOX_2;
DNA-binding; Nuclear protein;
SEQUENCE 232 AA; 27314 MW;
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Pfam; PF00319; SRF-TF; 1.
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InterPro; IPR002100; MADS-box.
                                                                                                                                                                                                                                                                                                                   Purugganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic.
from the equilibrium-neutral model at the APETALA3
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-CV. KAS-1;
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InterPro; IPR002487;
InterPro; IPR002100;
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                                                   107 QRVGECLDELDIQELRRLEDEMENTEK 133
                                                                                                      Local Similarity
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PRELIMINARY;
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Pred. No.
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Transcription regulation.
DB8CA1FC835557D6 CRC64;
PRT;
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01-OCT-2000
01-DEC-2001
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037056; 01-JAN-1998 (TYEMBLIFEL 05, Creato
01-JAN-1998 (TYEMBLIFEL 05, LAST:
01-DEC-2001 (TYEMBLEGL 19, LAST:
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                           "Simian immunodeficiency viruses (SIVs) from eastern and southern Africa: detection of a SIVagm variant from a chacma baboon.";
J. Gen. Virol. 79:1809-1814(1998).

EMBL: AF015909: AAC59621.1;
InterPro: IPR000777; GP120.

Pfam: PF00516; GP120. 1.

ALIDS: Coat protein: Glycoprotein.
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MEDLINE-98343740; PubMed-9680146;
van Rensburg E.J., Engelbrecht S., Mwenda J., Laten J.D., Robson B.A.,
Stander T., Chege G.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV) Viruses; Retroid viruses; Retroviridae; Lentivirus
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PROSITE; PS00642; COMPLEX1_75K_2; 1.
PROSITE; PS00643; COMPLEX1_75K_3; 1.
SEQUENCE 904 AA; 98157 MW; C25E8
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EMBL, AF281148, AAF97803.1, -
EMBL, AF281148, AAF978803.1, -
EMBL, AF2811488, AAF978803.1, -
EMBL, AF2811488, AAF978803.1, -
EMBL, AF2811488, AAF978803.1, -
EMBL, AF2811488, AAF978803.1, -
EMBL, AF28114888, -
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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SQKYNLRLRQASCHFQGNWKG
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9; Conserv
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(TremBLrel. 19, Last annotation update)
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94
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Pred. No. 20;
6; Mismatches
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RA MG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

RA Shukla H.D., Lasky S.R., Bailga N.S., Thorsson V., Strogna J.,

RA Shukla H.D., Lasky S.R., Bailga N.S., Thorsson V., Strogna J.,

RA Shukla H.D., Lasky S.R., Bailga N.S., Thorsson V., Strogna J.,

RA Holthauser B., Keller K., Gruz R., Danson M.J., Hough D.W.,

RA Leithauser B., Keller K., Gruz R., Danson M.J., Hough D.W.,

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RA Leithauser B., Keller M., Weller R., Weller B., Weller B., Land B.,

RA Leithauser B., Keller M., P., Angerine C.M., Jung K.-H.,

RA Leithauser B., Keller M., P., Angerine C.M., Jung K.-H.,

RA Leithauser B., Mell M., Weller B., Meller M., Jung K.-H.,

RA Leithauser B., Meller M., P., Angerine C.M., Jung K.-H.,

RA Leithauser B., Meller M., P., Angerine R., Lenason M.J., Hough L.,

RA Leithauser B., Meller M., P., Angerine R., Lenason M.J., Hold H.,

RA Leithauser B., Meller M., Weller B., Meller B.,
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Best Local Similarity 76.9%; Pred. No. 27;
Matches 10; Conservative 1; Mismatches 2; Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
speamIDINE/PUTRESCINE ABC TRANSPORTER.
POTA2 OR YNG1871G.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
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13.104 Million cell updates/sec
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## ALIGNMENTS

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AAB37014 standard; peptide; 27 ð.

AAB37014;

28-FEB-2001 (first entry)

Bc12 polypeptide BH3 domain peptide #14.

RESCULT AAB37014 IN AAB37014 I Cytostatic, neuroprotective; anti-HTV, virucide, cerebroprotective; cardiant; Bel-2 superfamily, Bid domain, cell death agonist, Bed; apoptosis; modulation; b cell lymphoma/leukemia 2; cancer; prostate; melinoma; lymphocytic, eukemia; lung; cens) thyroid; energibrascome; melinoma; lymphocytic, eukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.

Homo sapiens.

WO200059526-A1

12-OCT-2000.

06-APR-2000; 2000WO-US09352

07-APR-1999; 9905-0128202.

(CYJE-) UNIV JEFFERSON THOMAS Wang J, Zhang Z,

Huang 2,

Shan

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WPI; 2000-679325/66

New peptide conjugates for modulating apoptosis or for inhibiting B

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RESULT AAVEAGING AAVEAGING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a poptide conjugate having the formula:

(R. N) repetide where n = 1-10; X = CG-, when the X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH.

CC when the R.X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is 5 COOH or CONIE; and R = 2-18C alkyl or atkoxy, 2-14C alkylenyl containing one two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally compositionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ABB7001-B3705B represent analogues of the peptide portion of the conjugate or tranship to amino acids 72-97 of the BB3 domain of the cell death agonist Bad. The peptide conjugate is cusful for modulating apportusis the cells of a subject or or reversing B cell lymphoma/lenkemia 2 (BCI-2) mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting BCI-2 subject affilicted with a cancer characterized by cancer cells that express BcI-2. The cancer includes prostate, colorectal, gastric, conjugate is also useful for creating a subject affilicted with a cancer characterized by cancer cells that express BcI-2. The cancer includes prostate, colorectal, gastric, only step is also useful for treating a subject affined by renal or thyroid cancers, neuroblastoma, melanoma, or conjugate is also useful for peptide conjugate is also useful for percent and peptide conjugate is necessarily and percent and peptide conjugate is necessarily and percent and peptide conjugate is necessarily and percent and peptide conjugate is a necessarily and percent and peptide conjugate is necessarily and percent and peptide conjugate is a necessarily and percent and percent and percent and percent and percent and pe
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20-AUG-1998;
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cytochrome C.
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98US-0137038
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.5e-15;
s 0;
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AAY84018

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27; Conservative
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Pred. No. 5.9
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Human and murine p15 BID polypeptides with cell death agonist activity are produced by caspase cleavage of BID in cells undergoing FAS or tumour necrosis mediated cell death, useful as modulators of target cell death.

The present sequence represents a human p15 BID polypeptide. p15 BID polypeptides have cell death agonist activity. Cell death mediated by tumour necrosis factor (TNF) and FAS signalling pathways includes the generation of p15 BID, which is translocated to the micochondria where it exerts cell death agonist activity, probably by inducing release of cytochrome C. The p15 BID polypeptides are useful in methods for modulating death of a target cell. Mutants of p15 BID, comprising an inactivating mutation in the BIJ domain, are used in methods for inhibiting death of a target cell. Agents that specifically inhibit caspase cleavage of p22 BID at the p15 Cleavage site are also useful for inhibiting death of a target cell.

Length 135; Indels 0;

0;

tumour necrosis factor; FAS signalling;

Human and murine pl5 BID polypeptides with cell death agonist activity are produced by caspase cleavage of BID in cells undergoing FAS or tumour necrosis mediated cell death, useful as modulators of target cell

The present sequence represents a variant of pl5 sID polypeptide. pl5 polypeptides have cell death aponist activity. Cell death mediated by polypeptides have cell death aponist activity. Cell death sediated by tumour necrosis factor (YNF) and FAS signalling pathways includes the generation of pl5 BID, which is translocated to the mitochondria where it exerts cell death agonist activity, probably by inducing release of

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The invention relates to a method for negative selection assay that comprises introducing a genetic library encoding putative cytotoxic ... agent into a population of target celis, plating the celis on a surface, collecting a subpopulation of the celis that disattach from
                                                                                                                                                            Negative selection of cells for the identification cytotoxic agents -
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33.194
33.194 BID_clone_#1
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'Carres" "This fragment
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The present sequence represents a BH3 interacting domain death agonist (BID) protein given in the present invention. The protein, the DNA encoding it or antisense sequences can be used for preventing or treating a decreased apoptotic state of a cell. The decreased apoptotic state that is treated results from a disease such as cancer, viral infections, lymphoproliferative conditions, arthrills, inflammation and autoimmune diseases. Antibodies against the BTD protein can be used for detecting a BID polypeptide in a cell or population of cell. The nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, BH3 interacting domain death agonist; BID; BCL-2 family; apoptosis; regulation; cell death; inflammation; cancer; arthritis; autolimmune disease; viral infection; lymphoproliferative.
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                                                                                                                               Claim 3; Page 68-69; 118pp; English.
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                                                                                                                                                                            This sequence represents the HIV-1 Tat 1 protein.

The invention relates to a bol homology domain 3 (BH3 domain),
derived from a proapopotot member of the BCL-2 family. The
BH3 polypeptide can be used in a method for promoting apoptosis in a
BH3 polypeptide can be used in a method for promoting apoptosis in a
target cell, especially where the cell is a cancer cell a virus infected
cell or an autoantibody producing cell. The BH3 polypeptide can be used
in therapeutic compositions for treating disease including cencer, other
lymphoproliferative conditions, arthritis, inflammation, and autoimmune
diseases, which may result from the down regulation of cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence and the BID protein can also be used for treating immunodeficiency disease (including AIDS), senescence, neurodegenerations and infertility and insease, ischwemic and reperfusion cell death, infertility and wound healing. Primers derived from the nucleic acid encoding the BID protein can be used for detecting/squantitating the protein and for detecting alterations in the nucleic acid encoding the BID protein.
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                                                                                                                         Sequence
                                                                                                                                                            regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Bcl homology domain 3 polypeptide
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                     Score 137; DB 20;
Pred. No. 8.9e-14;
Mismatches 0;
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This sequence represents a secreted human protein encoded by the clone detailed in the descriptor line. The gene can be used to c fusion proteins by linking to the gene to a human immunoglobulin
                                                                                                                    New isolated human genes and the secreted polypeptides they encode useful for disgnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                 Greene
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1999-070066/06.

Ruben

SM,

Olsen

AAX00641.

Page 288-289; 385pp; English

/ the gene d to generate whulin Fc

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30-MAY-1997
21-MAR-1997
21-MAR-1997
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21-MAR-1997
30-MAY-1997
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                                   Brewer
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Ebner R, Ferrie AM,
Lafleur DW, Moore PA,
, Shi Y, Young P;
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                Florence KA;
N1 J, Olse
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Matches
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The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences AAX07807-W68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the my polypeptides. Pased on which tissues are described for each of the 81 polypucleotides. Specific uses are described are most highly expressed (see AAX00611 for described uses).
                                                                                          Human and murine p15 BID polypeptides with cell death agonist activity are produced by caspase cleavage of BID in cells undergoing PAS or tumour necrosis mediated cell death, useful as modulators of target cell death.
The present sequence represents a human BID polypeptide. The specification describes p15 BID polypeptides which have cell death agonist activity. Cell death mediated by tumour necrosis factor (TNP) and FNS signalling pathways includes the generation of p15 BID, which is translocated to the mitochondria where it exertis cell death agonist activity, probably by inducing release of cytochrome C. The p15 BID
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20-AUG-1998;
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                                                                                                                                                                                                                                                                                                               Domain
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                                                                                                                                                                                                                                                                                                                                                                                    cytochrome
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nes 27; Conser
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                                                                                                                                                                                                                                                                                                                                                                                             cell death agonist; tumour necrosis factor; FAS signalling;
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98US~0137038
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Pred. No. 8.9e-14;
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polypeptides are useful in methods for modulating death of a target cell. Mutants of p15 BLD, comprising an inactivating mutation in the BH3 domain, are used in methods for inhibiting death of a target cell, Agents that specifically inhibit cospase cleavage of p22 BlD at the p15 cleavage site are also useful for inhibiting death of a target
195 AA;
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l Similarity 100 27; Conservative

100.08;

Score 137; DB 21; pred. No. 8.9e-14; Mismatches 0;

Indels Length

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RESULT 9
AAW50255
ID AAW50255 standard; Protein; 200 ⋧

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20-JUL-1998 (first entry)

BH3 interacting domain death agonist protein

Human, BH3 interacting domain death agonist, BHD; BC-2 family; apoptosis, regulation; cell death; inflammation; cancer arthritis; autoimmune disease; viral infection; lymphoproliferative.

sapiens

Misc-difference Misc-difference /note-175 166 /note-Location/Qualifiers "encoded by GT" "encoded by

W-08660860M

12-MAR-1998

09-SEP-1997; 97WO-0S15872

(UNIW ) UNIV WASHINGTON 96US-0706741

WPI: 1998-193540, N-PSDB; AAV22146. 1998-193546/17.

BH3 interacting domain death agonist polypeptide - used for treating decreased apoptotic conditions resulting from inflammation etc.

Claim 4; Page 69; 118pp; English.

The present sequence represents a BH3 interacting domain death agonist BH10) protein given in the present invention. The protein, the DNA encoding it or antisense sequences can be used for preventing or treating a decreased apoptotic state of a cell. The decreased apoptotic state that is treated results from a disease such as cancer, viral interctions, lymphoproliferative conditions, arthritis, inflammation and autoimmune diseases. Antibodies against the BHD protein can be used for detecting a BHD polypeptide in a cell or population of cell. The nucleic acid sequence and the BHD protein can also be used for treating immunodeficiency disease (including AHDs), senescence, neurodegenerative disease, ischaemic and reperfusion cell death, inferturity and the BHD protein can also be used for treating the sequence and the BHD protein can also be used for treating the sequence is chassed (including AHDs), senescence, neurodegenerative disease, ischaemic and reperfusion cell death, inferturity and the BHD protein can be used for treating the sequence of the BHD protein can also be used for treating the BHD protein can also be used for treating the sequence of the BHD protein can also be used for treating the BHD protein can be used for the sequence of the BHD protein can also be used for treating the BHD protein can be used for the sequence of the BHD protein can be used for treating the BHD protein can be used for the sequence of the BHD protein can be used for the sequence of the BHD protein can be used for the sequence of the BHD protein can be used for the sequence of the BHD protein can be used for the sequence of the BHD protein can be used for the sequence of the BHD protein can be used for the sequence of the BHD protein can be used for the sequence of the BHD protein can be used for the sequence of the BHD protein can be used for the BHD protein can be used for the sequence of the BHD protein can be used for the BHD

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  AAB70375 standard;
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                                                                                                                                    The present sequence is the mammalian Bid Bel-2 homology domain 3 (BH3) domain, which was used in a sequence alignment with the same domain of a putative version of the mammalian apoptosis regulator BBC3, which was designated BBC3 PRF2. The BBC3 protein, nucleic acids and antibodies are suitable for use in promoting cell death or for preventing apoptosis in malignant cells and those cause
                                                                                                                                                                                           Disclosure; Fig 4; 47pp; English,
                                                                                                                                                                                                            Novel polynucleatide encoding a BBC3 protein which is useful for modulating apoptosis, especially in the treatment of cancer and autoimmune diseases.
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Mismatches 0;
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and those causing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and for protein.
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                                                                      Gaps '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 12
AAW50273
ID AAW502
                                        뫋
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                                                                                                               Query Match
Best Local:
                                                                        Matches
 AAW50273 standard; peptide;
                                                                                                              Sequence
                                                                                                                              present invention.
                                                                                                                                                                                                                                                                                                                                                                                            28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                                                                                                                                                             (APOP-)
                                                                                                                                                                                                                                                                                                                                                                                                                           15-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200110888-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB70375;
                                       Similarity
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                                                                                                              Ā
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Bed-xW_Bed-? associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; noctropic; antischeemic; vulnerry; cyrostatic; antivital, antiarthritic; antiinflammatory, wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; annear; immunosuppressive; apoptosis inducer; apoptosis inhibitor; annear; ischaemic cell death; reperfusion cell death; arthritis; infertility; ymphoproliferative condition; inflammation; authoritis; infeartility; ymphoproliferative condition; inflammation; authoritis; infeartility;
New mutant Bc1-XL/Bc1-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or Serl13.
                                                                                                                                                                                                                                   WPI; 2001-138734/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BID BH3 consensus peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     APOPTOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US11864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9908-0136783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO:8
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Example 2; Fig 3a; 157pp; English.

The present invention describes an isolated or synthetic polypeptide (I) comprising a less than full lempth amino acid sequence of a mutant (I) comprising a less than full lempth amino acid sequence of a mutant (I) comprising a less than full lempth amino acid sequence of a mutant (I) comprise the contents amino acid substitutions at Serill of a human of the serils of a mutant amino acid substitutions at Serill of a human compression of the seril of a mutant amino acid substitutions at Serill of a mutant (I) has immunostimulant, neuroprotective, and contropic, antivired, antivired, and antiarthritic, antilifiammatory and immunosuppressive activities, and can be used as an apoptosis inducer or inhibitor. Bab polypeptides and drugs of your less that promote cell survival or apoptosis. Other uses include for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds (identified and (mutant) Bab polypeptides are useful in treating climunodeficiency diseases, neurodegenerative diseases, viral infections. (I) imphoproliferative conditions, arthritis, infertility, infammation and caucinamuse diseases. The present sequence represents a Bcl-family member or news that consensus sequence which is used in an example from the

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4 IIRNIARHLAQVGDSMDRSIPPGL 27
                         88.3%;
llarity 100.0%;
Conservative
                        0:
                                 Score 121;
Pred. No.
                          Mismatches
                                  3.2e-
                                            BB
                                          22;
                                         Length 26;
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ARBSULT 13
ARBSTO15
ID ARBSTO
AC ARB
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human: BH3 interacting domain death agonist: BID: BCL-7 family; apoptosis: regulation; cell death; inflammation; concer: arthritis; autolumnume disease; viral infection; lymphoproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 24; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH3 interacting domain death agonist polypeptide - used for treating decreased apoptotic conditions resulting from inflammation etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-193546/17
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Cytostatic; neuroprotective; anti-Hly; virucide; cerebroprotective; cardiant; Bel-2 superfamily; BH3 domain; cell death agonist; BH3; apoptos15 modulation; B cell lymphoma/leukemia 2; cancer; prostate;
                                                                                                                           Bcl2 polypeptide BH3 domain peptide #15.
                                                                                                                                                                                                                                                       AAB37015;
                                                                                                                                                                                                                                                                                                              AAB37015 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OIB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH3 interacting domain death agonist epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW50273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity
22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                   peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.5%; Score 113; DB 19;
100.0%; Pred. No. 6.9e-11;
live 0; Mismatches 0;
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RESULT 1
AAW50264
ID AAW
XX
AC AAW
AC AAW
XX
AC AAW
XX
AC AO
DT 20--
XX
DE Mou
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(CC (R*N)) repetide where a 1-10; X = C-0, when the school of the peptide where to the Kreminus of the peptide, or a side chain of the peptide where to the Kreminus of the peptide. As side chain of the peptide where the functional group of the side chain is the chain of the peptide of the side chain is the peptide or the Kreminus of the peptide chain is the peptide of the side chain is the peptide of the peptide of the peptide of the side chain is the peptide of the peptide o
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Matches 19
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melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
stroke; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 18; Page 18; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide conjugates for modulating apoptosis or for inhibiting ceil lymphoma, leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-APR-1999;
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    Mouse BID BH3 domain peptide
                                                                20-JUL-1998 (first entry)
                                                                                                                                AAW50264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                           AAW50264 standard;
                                                                                                                                                                                                                                                                                                                                              ch 72.3%;
1 Similarity 70.4%;
19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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                                                                                                                                                                                       peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 99; DB
; Pred. No. 1.1e
3; Mismatches
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L
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∠.1e-08;
5;
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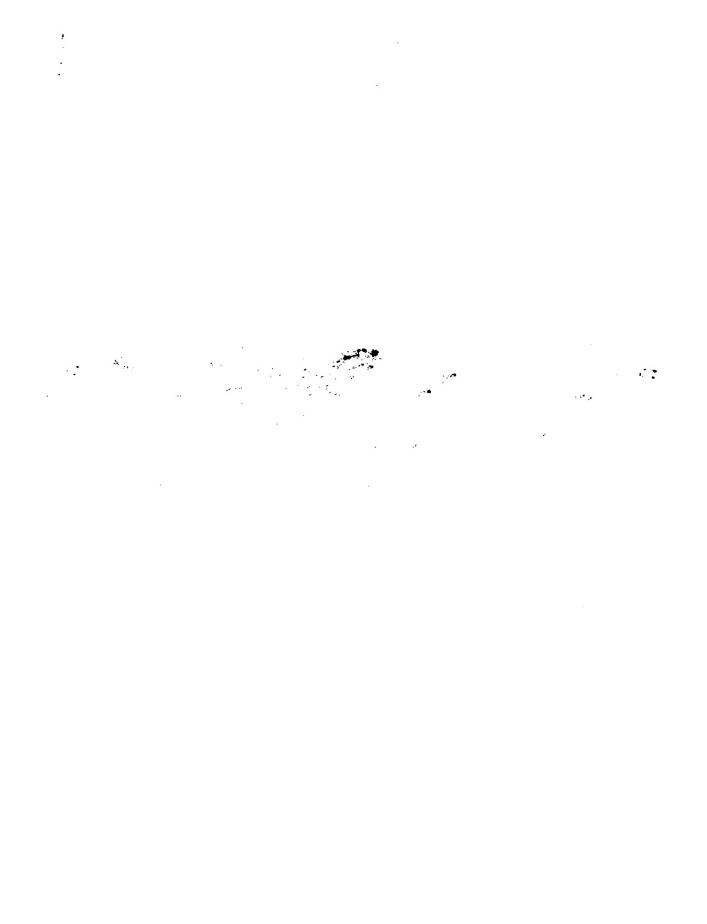
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a BH3 Interacting domain death agonist (BID) HH3 domain peptide given in the present invention. The protectin, the NA encoding it or antisense sequences can be used for preventing or treating a decreased apoptotic state that is treated results from a disease such as cancer, viral infections, lymphoproliferative conditions, arthritis, inflammation and autoimmune diseases. Antibodies against the BID protein can be used for cetecting a BID polypeptide in a cell or population of cell. The nucleic acid sequence and the HID protein can be used for treating immunodeficiancy disease (including AIDS), sensequence, neurodegenerative disease, isoheemic and reperfusion cell deach, infertility and cound-healing. Primers derived from the nucleic acid encoding the BID protein can be used for detecting anticating the protein and for detecting alterations in the nucleic acid encoding the BID protein and a for detecting alterations in the nucleic acid encoding the BID protein.
                                                                                                   Mouse: BH3 interacting domain death agonist; BID: BCL-2 family; apoptosis: regulation; call death; inflammation; cancer: arthritis; autoimmune disease; viral infection; lymphoproliferative.
12-MAR-1998
                                 TV-08650860M
                                                                      Mus sp.
                                                                                                                                                                            Mouse BID truncated protein BID 74-106.
                                                                                                                                                                                                                20-JUL-1998 (first entry)
                                                                                                                                                                                                                                                       AAW50262;
                                                                                                                                                                                                                                                                                       AAW50262 standard; Protein; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BH3 interacting domain death agonist polypeptide - used for treating decreased apoptotic conditions resulting from inflammation etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse: 883 Interacting domain death agonis; BID; BCL-2 family; apoptosis; regulation; cell death; inflammation, cancer; arthritis; autoimmune disease; viral infection; lymphoproliferative.
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                                                                                                                                                                                                                                                                                                                                                                          19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 99; DB 19; 1
Pred. No. 1.3e-08;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH3 interacting domain death agonist polypeptide - used for treating decreased apoptotic conditions resulting from inflammation etc.
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                                                                                                                                                                                      1 QEDIIRNIARHLAQVGDSMDRSIPPGL 27
                                                                                                                                         geeilhniarhlagigdemdhnigptl 32
                                                                                                                                                                                                                                                                          19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             33 AA;
                                                                                                                                                                                                                                                                          Conservative
                          September 20, 2002, 10:35:58
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                                                                                                                                                                                                                                                                                            72.3%;
                                                                                                                                                                                                                                                                      Score 99; DB 19; Pred. No. 1.3e-08; 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                           Length 33;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                      Gaps
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Title: Perfect score: Sequence:

US-09-544-664-14 137

QEDIIRNIARHLAQVGDSMDRSIPPGL

27

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_AA:\*

1: /cgn2\_6/pccdata/2,

2: /cgn2\_6/pcdata/2,

3: /cgn2\_6/pcdata/2,

4: /cgn2\_6/pcdata/2,

5: /cgn2\_6/pcdata/2,

5: /cgn2\_6/pcdata/2,

% Query Match

Length

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SUMMARIES

2222220 2222222 2354 244 2554 2653

Query Match

100.0%;

Score

137;

80 4

Length 140

100.0 100.0

Minimum DB Maximum DB

seq

length:

2000000000

of,

hits satisfying chosen parameters:

231628 seqs, 24425594 residues

Run Š

protein Ģ,

1

protein search, using sw model

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Pred. No. 1s the number of results predicted by chance to score greater than or equal to the score of the result beil and is derived by analysis of the total score distribution
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8:719 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/jaa/54_COMB_pep:*
/cgn2_6/ptodata/2/jaa/58_COMB_pep:*
/cgn2_6/ptodata/2/jaa/68_COMB_pep:*
/cgn2_6/ptodata/2/jaa/68_COMB_pep:*
/cgn2_6/ptodata/2/jaa/PCFUS_COMB_pep:*
/cgn2_6/ptodata/2/jaa/packfilesl.pep:*
231628
Sequence 4 Appli
Sequence 4 Appli
Sequence 3 Appli
Sequence 5 Appli
Sequence 5 Appli
Sequence 3 Appli
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Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-05-136-899-3
Sequence 3. Application US/091368798
Patent No. 652654
Patent No. 652654
RPPLICANT: GROSS, Atta
APPLICANT: KOZEMPEYAT. Stanley J.
APPLICANT: KOZEMPEYAT. Stanley J.
FILE REFERENCE: 60296285Repiacement
CURRENT APPLICATION WOMER: US/09/136.879B
UNDREER OF SEG ID NOS: 7
SOPTWARE: Patentin Ver. 2.0
SED ID NO 3
LENGTH: 135
TYEE: PRT
ORGANISM: Homo sapiens
                                                                                                 RESULT 279-136-199-4

(US-09-136-199-4)

Sequence 4, Application US/09136879B

Fatent No. 626554

GENERAL IMPORMITION:

APPLICANT: GROSS, ARAD

CURRERY APPLICANT: MODULATION OF APPLYOSIS WITH BILL

FILE REFERENCE, 602652858691acement

CURRERY APPLICATION NUMBER: US/09/136.879B

CURRERY PLING DATE: 1198-08-19

SOTWARE: GROSS, 7

SOTWARE: MEGHIN VET. 2.0

SOTWARE: MEGHIN VET. 2.0
                                             ; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-136-879-4
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Best Local S
Matches 27
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l Similarity 100.
27; Conservative
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Pred. No. 1.6
9; Mismatches
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.6e-14;
.s 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 135;
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86, Appl
88, Appl
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45, Appl
45, Appl
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9, Appl
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STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-08-706-7418-4
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 35.197
REFERENCE/POCKET NUMBER: 950
TELECOMMUNICATION INFORMATION:
TELEPHAN: 41.727.518
TELEPHAN: 314.1727.518
INFORMATION FOR SEQ. 10.00.4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0%; Matches 27; Conservative 0;
                                                                                                                                                                                                                                                                                                                                              08-924-695A-4
                                                                                                                                                                                                                                                                                                  equence 4, Application US/08924695A
atent No. 5998583
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                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWAREE PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,741B
PILING DATE: 09-8EP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL 6
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STREET:
ST. LOUL
CITY: ST. LOUL
THE: MISSOURI
USA
                         ADDAM
STREET:
CITY: ST. LOU-
CITY: MISSOURI
USA
COUNTRY: 63105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORNEY/AGENT INFORMATION:
AME: HOLLAND, DONALD R.
EGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4, Application US/087067418
5, 5955593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 100.0%; Score 137; DB 2; l Similarity 100.0%; Pred. No. 2.5e-14; 27; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                              E: HOWELL & HAFERKAMP, L.C.
7733 FORSYTH BLVD., SUITE 1400
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7733 FORSYTH BLVD., SUITE 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KORSMEYER, STANLEY J.
ENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/08/706,741B
                                                                                                                                                                                                                     BH3 INTERACTING DOMAIN DEATH AGONIST
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Mismatches 0;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-136-879-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
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MOLECULE TYPE: protein US-08-924-695A-4
       APPLICANT GROSS, Atan
APPLICANT GROSS, Atan
APPLICANT GROSS, Stanley J.
APPLICANT GROSS, Stanley J.
APPLICANT GROSS, STANLEY GROPTOSIS WITH BID
ITTLE OF INVENTION, WODDILATION OF APOPTOSIS WITH BID
ITTLE PRICE GROSS 
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; EBest Local Similarity 100.0%; EMatches 27; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 137; DB 2; Best Local Similarity 100.0%; Pred No. 2.5e-14; Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 195 amino acids
TYPE: amino acid
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REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 97:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT IN
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                               STRANDEDNESS
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326354
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Pred. No. 2.5e-14;
D; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08924695A Patent No. 5998583 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                APPLICATION NUMBER: U5/08/924,695A FILING DATE: 09-SEP-1997 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: HOLLAND, DONALD R. REGISTRATION NUMBER: 971798 REFERENCE/DOCKET NUMBER: 971798 TELECOMUNICATION INFORMATION: TELEPHONE: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (314) 727-60 INFORMATION FOR SEQ ID NO:
TELEPHONE: (31
TELEFAX: (314)
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KORSMEYER, 1
TITLE OF INVENTION: BH.
NUMBER OF SEQUENCES: BI
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965017
                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/706,741B FILING DATE: 09-SEP-1996
                                                                                                                                                                                                                                                                                                                                                         CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 137; DB 2; 1 Similarity 100.0%; Pred. No. 2.6e-14; 27; Conservative 0: Microscore
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NVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
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(314) 727-6092
PR SEQ ID NO: 5:
  727-6092
ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
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US-08-706-741B-33
; Sequence 33, Application US/08706741B
; Patent No. 5955593
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                                              RESULT 9
US-08-924-695A-33
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; MOLECULE TYPE:
US-08-706-741B-33
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Sequence 33, Application US/08924695A Patent No. 5998583 GENERAL INFORMATION;
                                                                                                                                                                         Matches
                                                                                                                                                                                         Query Match
Best Local :
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Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              TELEFAX: (314) 727-60 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
FILING DATE: 09-SEP
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 7
                                                                                                                                                                       Local Similarity 100.
hes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 QEDITRNIARHLAQVGDSMDRSIPPGL 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                  CENGTH:
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                                                                                                             1 RNIARHLAQVGDSMDRSIPPGL 22
                                                                                                                              6 RNIARHLAQVGDSMDRSIPPGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63146
                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                  29 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KORSMEYER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
Patenth Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                               727-6092
                                                                                                                                                                    82.5%; but
100.0%; Pr
'"" 0;
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100.0%; Pred. No. 2.6e-14;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANLEY J.
H3 INTERACTING DOMAIN DEATH AGONIST
                                                                                                                                                                      Score 113; DB 2; Length 29; Pred. No. 1.7e-11; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              965017
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RESULT 10
US-08-706-741B-55
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; TOPOLOGY: 11
; MOLECULE TYPE:
US-08-924-695A-33
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Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9717
RELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-518
TELEPHONE: (314) 727-5092
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 55, Application US/08706741B Patent No. 5955593
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: HE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patientin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,1
                                                                                    SOFTWARE: Patestin Release #1.0, Version #1.30 CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/706,741B FILING DATE: 09-SEP-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KORSMEYER, SYANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
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TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 7733 FOR:
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
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                                                                                                                                                                                                                                                                                                                         CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                    COUNTRY:
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100.0%; Pr
  965017
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pred. No. 1.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 29;
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US-08-924-695A-55
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US-08-924-695A-55
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                                                                                                                          Matches
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                                                                                                                                                            Query Match
Best Local
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 55:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC COMPATION
COMPUTER: IBM PC COMPATION
COMPUTER: IBM PC COMPATION
COMPUTER: IBM PC COMPATION
COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KORSMEY TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
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TELEPHONE: (314) 727-5188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 7'
CITY: ST.
STATE: MI
                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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ZIP: 63105
                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
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1 QEDIIRNIARHLAQVGDSMDRSIPPGL 27
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5 QEEIIHNIARHLAQIGDEMDHNIQPTL 31
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o. 5998583
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                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KORSMEYER,
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                                                                                                                                                                                                                                                                                                                                            linear
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727-6092

NO: 55:
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                                                                                                                                                    72.3%;
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BH3 INTERACTING DOMAIN DEATH AGONIST
                                                                                                                          3; Mismatches
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                                                                                                                                                    Score 99;
Pred. No.
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Pred. No. 3
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                                                                                                                                                    3e-09;
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                                                                                                                                                                               Length 32;
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                                                                                                                          Indels
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                                                                                                                          0;
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RESULT

US-08-706-741B-53

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US-08-924-695A-53
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                                                                                                                                                                                                                                                                                                                                           Sequence 53, Application US/08924695A Patent No. 5998583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                                     CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/706,741B FILING DATE: 09-SEP-1996 CLASSIFICATION: 514
                APPLICATION NUMBER: FILING DATE: 09-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
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CLASSIFICATION:
                                                                                                                                                                     COUNTRY:
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o. 5955593
                                                                                                                                                       63105
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7733 FORSYTH BLVD., SUITE 1400
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                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
                09-SEP-1997
                                                                                                                                                                                                                                                                                        BH3 INTERACTING DOMAIN DEATH AGONIST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.38;
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                              US/08/924,695A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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1 QEDIIRNIARHLAQVGDSMDRSIPPGL 27 

Query Match Best Local Similarity Matches 19; Conserv

Conservative

72.3%; 70.4%;

Score 99; Pred. No.

4.7e-09;

Length 44; Indels

Mismatches

0;

Gaps

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В
; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-706-741B-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-706-741B-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-924-695A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 35555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (314) 727-60 INFORMATION FOR SEQ ID NO:
                                                                                                     TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KORSMEY TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       APPLICATION NUMBER: US/O FILING DATE: 09-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 19; Conserv
                                            STRANDEDNESS
                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ST.
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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o. 5955593
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                                                                     44 amino acids
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TD NO: 53:
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                                                                                                                                   (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH3 INTERACTING DOMAIN DEATH AGONIST 88
                                                                                                                                                                                                                                                       US/08/706,741B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANLEY J.
                                                                                                                                                                            35,197
                                                                                                       56:
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Pred. No. 3.4e
3; Mismatches
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                                                                                                                                                                965017
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5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 33;
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17 QEEIIHNIARHLAQIGDEMDHNIQPTL 43

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RESULT 15
US-08-924-695A-56
US-08-924-695A-56
; Sequence 56, Application US/08924695A
; Patent No. $998583
; APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST NUMBER OF SOUDENCES 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOMELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA-COUNTRY: E POPPY disk
MEDIUM TYPE: Ploppy disk
MATTON APPLICATION LANGES #1.0, Version #1.30
CURRENT APPLICATION LONALD R.
REGISTRATION UNUMBER: 35.197
REGISTRATION UNUMBER: 35.197
REFERENCE/DOCKET NUMBER: 971798
TELEPOMMUNICATION INFORMATION:
TELEPHAN: (314) 727-5188
TELEPHAN: (314) 727-6932
INFORMATION FOR SEGO ID NO: 56:
Search completed: September 20, 2002, 10:37:20 Job time: 408 sec
                                                                                                                 В
                                                                                                                                                                                                                                                                                                                         US-08-924-695A-56
                                                                                                                                                                                                       Query Match 72.3%;
Best Local Similarity 70.4%;
Matches 19; Conservative 3
                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                           1 QEDIIRNIARHLAQVGDSMDRSIPPGL 27
||:|| ||:|||:|| || :| | |
17 QEEIIHNIARHLAQIGDEMDHNIQPTL 43
                                                                                                                                                                                                       ; Score 99; DB
; Pred. No. 4.7e
3; Mismatches
                                                                                                                                                                                                       DB 2; Length 44;
4.7e-09;
hes 5; Indels
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summeries
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DB seq length: 2000000000
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Query
Match
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1: pir1:*
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      283138 segs, 96089334 residues
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Gapop 10.0 , Gapext 0.5
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137
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEDIIRNIARHLAQVGDSMDRSIPPGL
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      DВ
                                     T6409
T25102
T25102
T25102
T25102
T25205
T692185
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(without alignments)
27.141 Million cell updates/sec
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hypothetical prote
protein-tyrosine k
band 3-r&lated pro
hypothetical prote
pyridoxal phosphat
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DNA-directed RNA p
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kdtB grotein - Syn
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T6J4.7 protein - A
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probable DNA
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                                RESULT 2

T25102

T25102

Rypothetical protein T22C1.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25102
R;McMurray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: 219982
A;Accession: T25102
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;McLession: T25102
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T26103
A;Repianetal source: Chone T22C1
A;Experimental source: chone T22C1
C;Genetics:
A;Gene: CESP:T22C1.2
A;McDposition: 1
A;Introns: 31/3; 88/1; 119/3; 164/1
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Best Local S
Matches 8
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8; Conservative
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T4321586
S25586
S26450
A622450
T501199
D87225
D87225
D87225
D87225
D82735
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Pred. No. 1;
9; Mismatches
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Result No.

Pred. I

298 298 298 298 298 298

Minimum

of

Maximum

Database

Scoring table: Title: Perfect score:

Sequence:

Run OM protein -

DЬ

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A:Molecule type: DNA
A:Residues: 1849 < SIINA
A:Residues: 1849 < SIINA
A:Residues: 1849 < SIINA
A:Cross-resterences: GB:AED003906; GB:AED003849; NID:g9105470; PIDN:AAF83418.1; GSPDB:CN001
A:Experimental source: strain 9a5c
R:Sinpson, A.J.G; Reslanch, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
R:Inpson, A.J.G; Reslanch, F.C.; Arruda, P.; Ah.; Camergo, L.E.A.; Carrero, D.M.; Carrero,
R:Sinpson, A.J.G; Reslanch, P.; Camargo, A.A.; Camergo, L.E.A.; Carrero,
B:Indiana, C.; Blubor, M.R.; Pacincani, A.P.; Ferreira, A.J.S.

as-Neto, E.; Docena, C.; Bluborry, H.; Pracincani, A.P.; Ferreira, A.J.S.

as-Neto, E.; Docena, C.; Bluborry, H.; Pracincani, A.P.; Ferreira, A.J.S.

as-Neto, E.; Docena, C.; Bluborry, H.; Pracincani, A.P.; Ferreira, A.J.S.

as-Neto, E.; Docena, C.; Bluborry, H.; Pracincani, A.P.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kamper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu
chado, M.A.; Madeira, A.M., M.R.; Martino, C.L.; Marques, M.C.; Martins,
B. Authors: Marcins, E.M.F; Matsukuma, A.Y.; Manck, C.F.M.; Miracca, E.C.; Myaki, C.Y.;
F.C.; Nuncs, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli R.Y.; Sanasay
M.; Tsuhako, M.H.; Vallada, H.; Van Sluva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; J
A.Corteste, Rosales, A.J., M.; Van Sluva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; J
A.Corteste, Rosales, A.J., M.; Van Sluva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; J
A.Corteste, Rosales, A.J., M.; Van Sluva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mannosyltransferase xp0608 [imported] - Xylella fastidiose (strain 985c)
C:Species Xylella fastidiose Color 20-Aug-2000 *text_change 20-Aug-2000
C:Accession D82785
R:Anonymous The Xylella fastidiose Consortium of the Organization for Nucleotide Sequent R:Anonymous The Xylella fastidiose Consortium of the Organization for Nucleotide Sequent Nature 405; 151-157, 2000
A:Reference Region sequence of the plant pathogen Xylella fastidiose
A:Reference number: A68515; NUD:20365717
A:Rocession: B62785
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A;Gene: SCOEDB:SCH5.03c
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A. Molecule type; DMA
A. Residues: 1-401 <SEB>
A. Cross-references: EMBL: AL035636; PIDN:CAB38477.1; GSPDB:GN00070; SCOEDB:SCH5.03c
A. Cross-references: EMBL: AL035636; PIDN:CAB38477.1; GSPDB:GN00070; SCOEDB:SCH5.03c
A. Experimental Source: Strain A3(2)
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Matches 10: Conservative
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Local Similarity 25.
12: Conservative
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Pred. No. 3;
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Pred. No. 22;
B: Mismatches
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A;Gene: VC1577
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                                                                                                                                                                                                                             A;Gene: F20P5.5
A;Map position: 1
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                                                                                                                                                                                                                                                                                                                                            A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-416 <STO>
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A; Map position: 1
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3 DIIRNIARHLAQVGDSMDRS 22
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34.3%; 50.0%; 6

Score 47; DB 2; Pred. No. 32; 6; Mismatches

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A.Molecule type: DNA
A.Hoseldues: 1-273 <HEID
A.H
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Matches 9; Conservative
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Similarity 40.9%;
9; Conservative
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9; Mismatches
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Pred. No. 20;
6; Mismatches
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4 IIRNIARHLAQV-GDSMDRSIP 24

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DNA-directed RNA polymerase (EC 2.7.7.6) I second largest chain - fruit fly (Drosophila c;Species: Drosophila melanogaster c;Species: Drosophila melanogaster c;Date: 07-Sep-1990 #text_change 21-Jul-2000 c;Accession: J00354; 807025 c;Revession: J00354; 807025 R;Kontermann, R.; Sitzler, S.; Seifarth, W.; Petersen, G.; Bautz, E.K.F. Nol. Gen. Genet. 219, 373-380, 1989 A;Title: Primary structure and functional aspects of the gene coding for the second-large A;Reference number; J00354; MUID:90158499 A;Accession: J00354.
                                                                                                                                                                                                                                                                                                                                                                                                              A,Experimental Source: Strain 985c

K;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Bar-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.I.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu J.D.; Junqueira, M.A.; Madeira, A.H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, F.A; Marchors: Marrins, E.M.S.; Marchina, A.Y.; Menck, C.F.M.; Miracca, E.C.; Myaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Relmieri, D.A. Rodriques, V.; Rosa, A.C. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, Aluthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tshhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.
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A82856

Conserved hypothetical protein XP0042 (imported) - Xylella fastidiosa (strain C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: FlyBase:FBgn0003278
A;Introns: 30/3; 530/3
C;Superfamily: DNA-directed RNA polymerase 132K polypeptide
C;Steywords: DNA binding; nucleotidyltransferase; nucleus; transcription; zinc finger
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A;Residues; 1-1129 AKON>
A;Cross*references: RMBL:X17298; NID:g8473; PIDN:CAA35185.1; PID:g8474
A;Note: the authors translated the codon CAG for residue 202 as Glu, TCT
A;Note: the authors translated the codon CAG for residue 202 as Glu, TCT
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A;Note: the codon CAG for r
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A;Residues: 1-420 <51H>
A;Cross-references: GB:AE003858; GB:AE003849; NID:g9104799; PIDN:AAF82855.1; GSPDB:GN00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717

A;Note: for a complete list of authors see reference number A59328 below

A;Actession: A82856

A;Status: preliminary
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      hes 8; Conserv
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                                                33.98;
Score 46.5; £
Pred. No. 39;
7; Mismatches
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Pred. No. le+02;
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A:Molecule type: DNA
A:Residues: 1-266 GWHI>
A:Cross-references: GB:AE002060
A:Experimental source: strain R
C:Genetics:
A:Gene: DR2283
A:Map position: 1
C:Superfamily: conserved hypoth
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A. Title: Genome sequence of the radioresistant bacterium Deinococcus A. Reference number: A75250; MJID:20036896
A. Status: preliminary
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VLRGLSY IGDAMSHAVLPGI IARHLAQVGDSMDRSIPPGL Similarity 7; Conser

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27

GB:AE002060; ce: strain R1

GB: AE000513;

NID: g6460082;

PIDN: AAF11829.1;

hypothetical

protein

HI0360

33.6%;

Score 46; DB Pred. No. 28; 7; Mismatches

6;

0

Gaps

0;

Length 268;

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kdtB protein - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sp.10847
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 *sequence_revision 25-Apr-1997 *text_change 20-Jun-2000
C;Accession: S75802
R;Kaneko, T; Sato, S.; Kotani, H; Tanaka, A.; Asamizu, E.; Nakamura, Y.; I
C; Kokumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanable, A.; Yamadd
DNA Res, 3, 109-136, 1996
DNA Res, 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s.
A:Reference number: $7432; MUID:97061201
A:Accession: $75802
A:Status: nucleic acid sequence not shown; transcript tra
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A;Start codon: GTG
C;Superfamily: lipppolysaccharide core biosynthesis
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Matches 7
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128 SIVKEIAKFGGSVDHLVPPSI 148
                                                                                                       7 NIARHLAQVGDSMDRSIPPGL 27
                                                                                                                                                                                                                             h 33.6%;
Similarity 33.3%;
7; Conservative
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Pred. No.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NID:g1001200; PIDN:BAA10537.1; to the EMBL Data Library, June
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Watanabe, A.; Yamada, M.; Yas
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hypothetical protein AT4g10730 [imported] - Arabidopsis thaliana (:Species: Arabidopsis thaliana (mouse-ear cress) C:Dete: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C:Accession: B85112 Union Arabidopsis Genome Sequencing Consortium, The Cold :Rannonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold :Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A:Reference number: A8500; MUID:20083488
A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
A:Molecule (type: DNA
A:Residues: 1-395 <PBT>
A:Cross-references: EMBL;X64131; NID:g1235585; PIDN:CAA45484.1; PID:g46272
C:Superfamily: Reyl-carrier-protein] S-malonyltransferase homology
F;44-327/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
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C;Species: Rhizobium meliloti
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999
C;Accession: S19954
R;Petrovies, G.; Putnoky, P.; Kondorosi A
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A: Molecule type: DNA
A: Residues: 1-329 - KUR>
A: Cross-references: GB:BA000019; PIDN:BAB76817.1; PID:g17134256; GSPDB:GN00179
A: Cross-references: GB:BA000019; PIDN:BAB76817.1; PID:g17134256; GSPDB:GN00179
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A; Description: A fatty acid synthase like gene cluster of Rhizobium meliloti is
A; Reference number: $18953
A; Accession: $18954
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C/Superfamily: stress response protein
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A:Molecule type: mRNA
A;Residues: 1-1237 CCHO
A;Residues: 1-1237 CCHO
A;Cross-references: GB:545791; NID:9256659; PIDN:AAB23488.1; PID:9256660
A;Cross-references: GB:545791; NID:9256659; PIDN:AAB23488.1; PID:9256660
A;Cross-references: CB: Cealand White rabbit, ileal epithelial cells
A;Experimental source: New Zealand White rabbit, ileal epithelial cells
A;Experimental source: New Zealand White rabbit, ileal epithelial cells
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A;Title: CDNA cloning and localization of a band 3-related A;Reference number: A56764; MUID:93035730
A;Accession: A58764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                band 3-related protein, lleum - rabbit
C:species: Oryxtchagus cuniculus (domestic rabbit)
C:Date: 08-Sep-1995 #sequence_revision 08-Sep-1995
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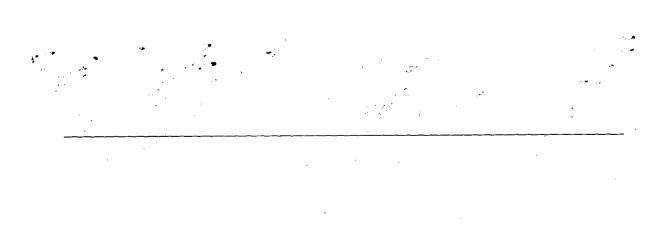
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A; Molecule type: DNA
A; Residues: 1 · 693 < STO
A; Cross - references: GT
C; Genetics:
A; Gene AT4910730
A; Map position: 4
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                                                                                             A; Molecule type: DNA
A; Residues: 1-55 <SHI>
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein
C; Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;1-55/Domain: protein kinase homology (fragment) <KIN>
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(without alignments)
23.237 Million cell updates/sec
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P70444
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8 caenorhabdi
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P55957; (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

16-CCT-2001 (Rel. 40, Last annotation update)

16-CCT-2001 (Rel. 40, Last annotation update)

BH3 interacting domain death agonist (BID).
                                                                                                                                                                          SEQUENCE OF 1-74.
MEDILINE-96159527; PubMed-8593609;
Trotatter J.A., Long K.R., Murrell J.R.,
Gusella J.F., Buckler A.J.;
"An expression-independent catalog of ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SENGUENCE FROM N.A.
MEDILNE-98389636; PubMed-9721221;
FOOLZ T.K., Birren B., Minoshima S.,
Flazi M.A., Mobermid H.D.;
The gene for death agonist BID maps
duplicated in cat eye syndrome chrome
6.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŚEÓUENCE FROM N.A. Pubugue T., Elliston K., Hawkins M., Hillier L., Clark N., Dubugue T., Ie M., Lennon G., Marra M., Holnan M., Hultman M., Kucaba T., Ie M., Lennon G., Marra M., Holnan M., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genes
   MEDINE=99189747; PubMed=10089877; Chou J., Li H., Salvesen G.S., Yuan J., Wag "Solution structure of BID, an intracellular signaling.";
                                                                                                                                                                                                                                                                                                                                     Pojiwara 7. Hirano H. Hishigaki H. Horie M. Kawai A. Kyushiki H. Negata M. Okuno S. Ozaki K. Shimizu F. Shimada Y. Shinomiya H. Suzuki M. Takaichi A. Takeda S Wacandre T. Maekawa H. Nakamura Y. Takahashi E.; Submitted (UN-1996) to the EmBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 51:472-475(1998).
[3]
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MEDLINE-90708762; PubMed-8918887;
Wang K., Yin X.-M., Chao D.T., Milliman C.L., Korsmeyer S.J.;
"BLD: a novel BH3 domain-only death agonist.";
Genes Dev. 10:2859-2859(1956).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                 STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                              Genome Res. 5:214-224(1995)
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                                 PubMed=10089877;
Yuan J., Wagner
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IREL MOUSE
IREL RABIT
IREL RAT
IREL RAT
IREL RAT
IREZ RAT
P100 HCMVA
TERT TETTH
AROC BUCAH
KOLE HUMAN
KOLE HUMAN
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                              amplifier
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P70444;
01-NOV-1997
01-NOV-1997
16-OCT-2001
                                                                          STRUCTURE BY NMR.

MEDLINE-99189748; PubMed=10089878;

MCDOINE-99189748; PubMed=10089878;

MCDOINE-9189748; PubMed=10089878;

MCDOINE-9189748; MILLINAN C.L., KOTSMCYPET S

MCDOINE-9189748; MCDO
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97078762: PubMed=8918887; Wang K., Yin X.-M., Chao D.T., Mi. "BID: a novel BH3 domain-only dea: Genes Dev. 10:2859-2869(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Using by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an cmall to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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PROSITE; PS01259; BH3; 1.
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BL: H23042; -; NOT_ANNOTATED_CDS.
BL: R09650; -; NOT_ANNOTATED_CDS.
BL: R09557; -; NOT_ANNOTATED_CDS.
BL: C17508; -; NOT_ANNOTATED_CDS.
BL: L155493; -; NOT_ANNOTATED_CDS.
B; 281D; 27-JAN-00.
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                                     EFFECT OF
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NOV-1997 (Rel. 35, Last sequence update)
CCT-2001 (Rel. 40, Last annotation update)
interacting domain death agonist (BID).
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FUNCTION: INDUCES ICE-LIKE PROTEASES AND APOPTOSIS. COUNTERS THE PROTECTIVE EFFECT OF BCL-2 (BY SIMILARITY).

SUBURIT: FORMS HETERODINERS EITHER WITH THE PRO-APOPTOTIC PROTEIN BCL-2 (BY SIMILARITY).

BAX OR THE ANTI-APOPTOTIC PROTEIN BCL-2 (BY SIMILARITY).

SUBCELLULAR LOCATION: PREDOMINANTLY CYTOPLASMIC (BY SIMILARITY).

SOMALN: INTACT BH3 DOMAIN IS REQUIRED BY BIK. BLD. BAK. BAD. AND DOMAIN: STREIT BRO-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

BAY THAPTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

APOPTOTIC MEMBERS OF THE BCL-2 PAMILY.

APOPTOTIC MEMBERS OF THE BCL-2 PAMILY.
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27; Conser
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                                     INDUCES CASPASES AND BCL-2.
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Rodentia;
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; B17A07334C1AFBEF CRC64;
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Sciurognathi; Muridae;
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Pred. No. 1.8e-13;
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death agonist.*;
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                                                                                APOPTOSIS, COUNTERS THE PROTECTIVE
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Best Local S
Matches 19
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STRAIN-RD / KW20 / ATCC 51907;
STRAIN-RD / KW20 / ATCC 51907;
MEDILINE-9535053): PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Mirkness E.F.,
Fleischmann R.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
McKenney K., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weldman J.F., Phillps C.A., Spridgs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fittchwan J.L., Fibhrmann J.L., Geophagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
This SWISS-PROT entry is copyright. between the Swiss Institute of Bioi
                                                                                                                                                                                             "Whole-genome random sequencing and assembly of influenzae Rd."; Science 269:406-512(1995).
-i- CATALYTIC ACTIVITY: N-(L-arginino)succinate
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                                                                                                                                                                                                                                                                                                                Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000712; Bc1_2. PROSITE; PS01259; BH3; 1.
                                                                                                                                           arginine.
PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIBURIT: FORMS HETERODIMERS EITHER WITH THE PRO-APOPTOTIC PROTEIN BL. 2.

BAX OR THE ANTI-APOPTOTIC PROTEIN BCL. 2.

SUBCELLULAR LOCATION: PREDOMINANTLY CYTOPLASMIC.

DOMALN: INTACT BH3 DOMALN IS REQUIRED BY BIK, BID, BAK, BAD AND DOMALN: INTACT BH3 DOMALN EACTIVITY AND FOR THEIR INTERACTION BAX FOR THEIR PRO-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QEDIIRNIARHLAQVGDSMDRSIPPGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QEEIIHNIARHLAQIGDEMDHNIQPTL 105
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19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 AA;
                                                                                                                                               THE LAST
                                                                                                               BELONGS TO
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21950 MW;
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                                                                                                               THE
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                                                                                                           ARGININE
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   It is produced informatics and
                                                                                                                                                                                                                                                                                   assembly of Haemophilus
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9.5e-08;
5;
                                                                                                           BIOSYNTHESIS.
FAMILY. ARGIN
                                                                                                               ARGININOSUCCINATE LYASE
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                            through
                         a collaboration
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RP SELURNCE FROM N.A.

RP MEDILINE-97357151; bubmod-9214502;

RA Springer M.S. Cleven G.C. Madden O.J., de Jong W.W., Naddell V.G.,

RA Springer M.S. Cleven G.C. Madden O.J., de Jong W.W., Naddell V.G.,

RA Springer M.S. Cleven G.C. Madden O.J., de Jong W.W., Naddell V.G.,

RA Springer M.S. Cleven G.C. Madden O.J., de Jong W.W., Naddell V.G.,

RA Springer M.S. Cleven G.C. Madden O.J., de Jong W.W., Naddell V.G.,

RA Springer M.S. Cleven G.C. Madden O.J., de Jong W.W., Naddell V.G.,

RE MADDEN M. MARTIN OF CREATE THROUGH THE CATECHOLAMINE

C. INDUCTION OF CONTINUE INTEGRATION OF G.

RECTURE M. MARTIN DELONGS TO PAMILY 1 OF G. PROTEIN COUPLED RECEPTORS.

C. J. SIMELIMIA KOLATION, Integral membrane protein.

C. SIMELIMIA SELONGS TO PAMILY 1 OF G. PROTEIN COUPLED RECEPTORS.

C. J. SIMELIMIA SELONGS TO PAMILY 1 OF G. PROTEIN COUPLED RECEPTORS.

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C. J. SIMELIMIA SELONGS TO PAMILY 1 OF G. PROTEIN COUPLED RECEPTORS.

C. J
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Best Local S
Matches
E EMBL, Y12530; CAM73120.1; ...

R CREED: GCZ_2407; ...

R IncerPro. TERRODOZIÓ; GEGR_Rhodpsn.

R FINCERPRO. TERRODOZIÓ; GEGR_Rhodpsn.

R PROSITE: PS00237; CL. PROTEIN_RECEP_T_2: 1.

R PROSITE: PS00261 - C_PROTEIN_RECEP_T_2: 1.

R GPOCHEÍN COUPLÉS CECEPOCT; TTRANSMENDZARE; Multigene family; PROSPROYELLOS; PALMICACE.

R MACTER POLITICA L'ADOPTOCEIN; PALMICACE.

R MACTER CL. T. POLITICAL L'ADOPTOCEIN; PALMICACE.

R MACTER CL. T. POLITICAL L'ADOPTOCEIN; PALMICACE.

R MACTER CL. T. POLITICAL L'ADOPTOCEIN TALL).

TOMALIN 35 3 1 1 (POTENTIAL).

TOMALIN 36 3 72 EXTRACELLULAR (POTENTIAL).
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O19031;

15-JUL-1998 (Pel. 36, Creeted)

15-JUL-1998 (Pel. 36, Last sequence update)

16-OCT-2001 (Pel. 40, Last annotation update)

16-OCT-2001 (Pel. 40, Last annotation update)

Alpha 28 adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).

DRA2B:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U32763; AAC22470.1; -.
HISBP, P04444; ADS.
TICH. H10811.
InterPro: IPRO00362; Fummarate_lyase.
Pfam, PP00206; lyase_l; L.
Pfam, PP00206; lyase_l; L.
PROSITE; P800163; FUMARATE_LANSES; L.
PROSITE; FUMARATE_LANSES; FUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Talpa europaea (European mole).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Talpidae; Talpa.
NCBI_TaxID=9375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EDIIRNIARHLAQVGDSMDRSIPPG 26
:::||:||| | | ::::||
129 QESVRNLQRHLVQTAENTQQAVMPG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.6%;
Similarity 32.0%;
B; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 57; DB 1;
Pred. No. 0.49;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
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WEDILINS-00158499, PubMed-2485932:

REAL REDILINS-00158499, PubMed-2485932:

REAL REDILINS-00158499, PubMed-2485931:

REAL REDILINS-00158499, PubMed-2485999;

COLLING GENET. 219.377-380(1995).

COLLING
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Best Local s
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Necazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterryota; Neopera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Greated)
01-FEB-1991 (Rel. 17, Last sequence update)
15-UFL-1999 (Rel. 38, Last senotation update)
08N-directed RAN polymerase I 135 kDa polypeptide (EC 2.7.7.6)
(RNA polymerase I subunit 2).
RPI135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SITE
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P20028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397
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CYTOPLASMIC (POTEMTIAL).

6 (POTEMTIAL)

EXTRACELLULAR (POTEMTIAL).

7 (POTEMTIAL).

8 SIMILARITY

ASP/GLUJ-RICH (ACIDIC).

IMPLICATED IN LIGAND BINDING (BY SIMILARITY).

TMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
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Pred. No. 14;
4; Mismatches
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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STARRERERE

B

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MEDILINE-SPACE NO. N.A.

KANDRO T. TORNAGA A. SOLO S. KOLANI H., SAZUKA T., MİYƏJİMƏ N.,

KANDRO T., TORNAGA A., SOLO S., KOLANI H., SAZUKA T., MİYƏJİMƏ N.,

KANDRO T., TORNAGA A., SOLO S., KOLANI H., SAZUKA T., MİYƏJİMƏ N.,

SƏQURICA M., TORNAGA S.,

SYDENONYELI S.,

RET YEYDENONYELI S.,

RET YEYDENONYELI S.,

RET YENCTION: REVERSIBLY TRANSFERS AN ADENYLYL GROUP FROM ATP TO 4'-

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                                                                      ENGL, D64003 BAA10537.1;
HSSP: P23875; 1B6T.
INTERFOR, IPRO01994: Cytldylyltransf.
INTERFOR, IPRO01990: LPS_biosynth.
Pfam: PF01467: Cytldyltransf: 1.
PRINTS: PR01020; LPSBIOSNTHSS.
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PIR, JO0354, 100354,
FIYBase; FEGRO0037278; RPLI35.
Interpro, IFRO01872; RNA_POL_B:
PfSam; PF003652; RNA_POL_B:
PROSITE; PS01165; RNA_POL_B:
PROSITE; PS01165; RNA_POL_B:
RRATERSE; UNLTEST POCEST RNA POLYMETSSE; Transcription: Zinc:
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ZN_FINO 1001 1093
SEQUENCE 1128 AA; 1128 AA; MR: EOA15FF1ECEF1807 CRC64;
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GOAD OR KDTB OR SIX0847.

Synechocystls sp. (Strain PCC 6803).

Synechocystls sp. (Strain PCC 6803).

MCBL/BATD-1148;

MCBL/BATD-1148;
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Pred. No. 42;
6; Mismatches
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PSY763:
16-027-2001 [Rel. 40 Greated]
16-027-2001 [Rel. 40 Last sequence update]
16-027-2001 [Rel. 40 Last sequence update]
16-027-2001 [Rel. 40 Last annotation update)
DNA polymerase sliding clamp B (Proliferating cell nuclear antigen homolog B) (PCNA B).
PCNB OB PCNAB B).
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Archaea; Crenarchaeota; Sulfolobales;
NCBI_TaxID~69656;
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9; Conservative
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33.3%; Pred. No. 7
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MEDLINE-93035730; PubMed-141547;
Chow A., Dobbins J.W., Aronson P.S., Igarashi P.;
"CDNA cloning and localization of a band 3-related protein from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00219; ANION_EXCHANGER_1; 1. PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01231; HCO3TRNSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Am. J. Physiot. 263:G345-G352(
-!- FUNCTION: PLASMA MEMBRANE
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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IPR003020; HC03_cotransp.
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                        Conservative
                                                               STANDARD;
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PALMITATE (BY SIMILARITY),
MW; 2811D11051552BB2 CRC64
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POTENTIAL.
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                                                                        KEL1_YEAST
P38853;
O1-FEB-1995
O1-FEB-1995
16-OCT-2001
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Elqlmeler K., Gas S., Barry C.E. III, Tekkala F., Gordon S.V., Elqlmeler K., Gas S., Barry C.E., III, Tekkala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Decipharing the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh:
STRAIN-CDC 1551 / Oshkosh:
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Foltonay J.F., Nelson W.C., Umayam L.A., Emolaeva M.D., Salzberg KOlonay J.F., Nelson W.C., Umayam L.A., Emolaeva M.D., Salzberg DelCher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03007; UPF0089; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 472 AA; 52597 MW; AC03BDDB4970FCC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: BELONGS TO THE UPF0089 FAMILY.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                      Saccharomyces cerevisiae (Baker's yeast)
                                       Kelch repeats protein KEL1 OR YHR158C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Hypothetical 52.6 kDa protein Rv3087.
RV3087 OR MT3172 OR MTV013.08.
Mycobacterium tuberculosis.
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hes 13; Conser
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AE007134; AAK47508.1; ALT_INIT.
MT3172; -.
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                     Score 45;
Pred. No.
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DPOA_OX
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Best Local Similarity
Thes 8; Conserv
Philips J., Herskowitz I.;

Identification of Kellp, a kelch domain-containing protein involved in cell fusion and morphology in Saccharomyces cerevisiae.";

J. Cell Biol. 143:375-389(1998).

J. Cell Biol. 143:375-389(1998).

PUNCTION: HAS A ROLE IN CELL MORPHOGENESIS AND CELL FUSION AND MIAGONIZE THE PKC1 PATHMAY.

ANTAGONIZE THE PKC1 PATHMAY.

SIMILARITY: COWNAINS 5 KELCH REPEATS.

SIMILARITY: TO YEAST KEL2.
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MEDLINE-94378003; PubMed-8091229;

Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,

Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,

Rucabb T., Hillier L., Jier M., Johnston L., Langston Y.,

Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,

Nhan M., Riftin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,

Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                           _OXYTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/ahnounce/or send an email to license@isb-sib.ch).
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                                       DPOA_OXYTR STANDARD: PRT; 1513 AA.
Q27152;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA polymerase alpha catalytic subunit (BC 2.7.7.7).
Oxytricha trifaliax.
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SEQUENCE
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REPEAT
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REPEAT
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COMPLUYEAST-2DPAGE; P38853;
SGD; S0001201; KEL1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U10397; AAB68991.1; -.
             Eukaryota; Alveolata; Ciliophora; hypotrichs; Stichotrichida;
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Pred. No. 86;
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   G6PD_EMENI
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS, PRO016; DNAPOLB.
SMART; SMO486; POLBC; 1
SMART; SMO486; POLBC; 1
PROSITE; PS00116; DNA_POLYMERASE_B; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
DNA-binding; Nuclear protein.
DNA-binding; Nuclear protein.
SEQUENCE 1513 AA; 173059 MH; 4DF83ZEDCFC4416E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
-1- ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR DIFFERENT REACTIONS OF DNA SYNTHESIS.
-1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA polymerase alpha.":
J. MOL. EVOL. 45:301-310(1997).
-i- FUNCTION: POLYMERASE ALPHA IN A COMPLEX WITH DNA PRIMASE IS A
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Phylogenetic relationships among hypotrichous ciliates determined
with the macronuclear gene encoding the large, catalytic subunit o
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NCBI_TaxID=5946;
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InterPro; IPR002064; DNA_pol_B.
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                                                                                                                                                                                                                                                                                                                                                                   Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
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       van den Broek P., Goosen T., Wennekes B., van den Broek H.;
submitteed (SEP-1996) to the EMBL/GenBenk/DBDL databases.
-i- CATALXTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D
                                                                                          STRAIN-WG096;
                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                 Schaap P.J., Muller Y., Submitted (JAN-1995) to
                                                                                                                                                                                                                                           STRAIN-FGSC 4;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5072;
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ACTIVITY: D-glucose
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Pred. No. 1.1e+02;
   6-phosphate
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(EC 1.1.1.
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1,5-lactone 6-phosphate + NAPPH.

PATHWAY: PIRST STEE IN PENTOSE PHOSPHATE PATHWAY.
SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE PAMILY.

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PPZX_METTE PYZX_M
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O1-APR
D7 O1-APR
D8 P459AA
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R EMBL; X77830; CAA58825.1;

R HSEP; P11411; 1DFG.

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R HSEP; P11411; 1DFG.

R HSEP; P11411; 1DFG.

R FLAM; FP004739; G6PD.

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R FLAM; PR001739; G6PD.

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P25587;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last sequence update)
11-APR-1993 (Rel. 25, Last sequence update)
18 porthetical i6.7 KDa protein (OREII'),
Methanobacterium thermoformicicum.
Plasmid PED.
Archaes; Euryarchaeota; Methanobacteriales; Methanobacteriacese;
Methanobhermobacter.
                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Suropean Bioinformatics Institute of Propean Bioinformatics Institute of Propean Bioinformatics Institution Propean are no restrictions on its use by non-profit institutions as some says as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee\sb-sib.ch).
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STEALN-DSM 3720 / 2-245,
MEDLINE-93126090; PubMed-1336177,
MCOLLING J., Van Eeden F.J.M., Eggen R.I.L., de Vos W.M.;
MCOLLING J., Van Eeden F.J.M., Eggen R.I.L., de Vos W.M.;
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Matches 8
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EMSL: R002571; CAN05592_1; -.

EMSL: R002571; CAN05592_1; -.

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EMSL: R002571; CAN05592_1; -.

EMSL: R002581; FRO.

EMSL: R002582; FRO.

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"Sequence of the Bacillus subtilis genome between xiyA and ykor.";

Submitted (NOV-1977) to the EMBL/GENBARK/DDBAY REDUCTION OF L-GAMMA-
11 FUNCTION OF ACTAIXAES THE NADEH DEPENDENT REDUCTION OF L-GAMMA-
GLITAMYL 5-PHOSPHATE IMTO L-GLITAMATE 5-SENIALDEHYDD AND PAGGENERY. THE PRODUCT SPONTANEOUGH. UNDERGOES CYCLIZATION TO I L-FYRROLLNS-5-CARBOXYLATE.

1- PATRICLY ACTIVITY: L-Glitamate 5-semialdehyde + Phosphate + NADEH.

1- CATALYTIC ACTIVITY: L-Glitamate 5-semialdehyde + Phosphate + NADEH.

1- PATHANY: PROLINE BUSYNTHESIS LATHWAY: SECON STEP.

1- SUBCELUTIAR LOCATION: CYLOPIASMIC (BY SIMILARITY: BELONGS TO THE GAMMA-GLUTAMYL PHOSPHATE REDUCTASE PAMIL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the SWBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no vay modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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p398Zi 03503;

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30-MX-2000 [Rel. 39. Last sequence update)

16-007-2001 [Rel. 30. Last sequence update)

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Ogura M., Kastat-Mukal M., Iraya M., Takio K., Tanaka T.;
"Multiple copies of the prod game enhance degS-dependent extracellular protenses production in Bacillus subtilis.";
J. Bacteriol. 176:5673-5680[1994].
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Bacillus/Staphylococcus group; Bacillus.
NCDI_TaxID-1423;
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RX LIMPSON A.J.G., Relinech F.C., Arruda P., Abreu F.A., Acencio M.,
RS Limpson A.J.G., Relinech F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Balaa G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Balaa G.S., Baptista C.S.,
RA Bueno M.R., Bernecorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R., Colombo C., Costa F.F., Costa M.C.R., Cesta-Necto C.M.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Ferro J.A.,
RA Bueno M.R., Colombo C., Costa F.F., Costa W.C.R., Ferro J.A.,
RA COULLING L.L., Criscian M., Dias-Neto E., Doccens C., E-Poorry H.,
RA Frage J.S., Ferrela A.J.S., Munquelia M., Charles V.C.A., Ferro J.A.,
RA Frage J.S., Ferrela R.J.S., Lalyset F., Costa W.C.R., Kitzlina J.P.,
RA HO P.L., Hobel Sel J.D., Junquelia M.H.S., Gomes S.L., Kitzlina J.P.,
RA KITCHER J.S., Kuramea B.S., Lalyset F., Lambals M.R., Lette L.C.C.,
RA Lemos E. G.H., Limos M.Y., Lopes S.A., Lopes C.R., Machado J.A.,
RA Lemos E. G.H., Limos M.Y., Lopes S.A., Lopes C.R., Machado J.A.,
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RA Lemos E. G. Limos M.Y., Landal C.R., Machado
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Matches 10
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sonctaction update)
16-OCT-2001 (Rel. 40, Last sonctaction update)
16-OCT-2001 (Rel. 40, Last sonctaction update)
16-man-glucamyl phosphate reductase (GPR) (EC 1.2.1,41) (Glutamate-5-
sential debyde dehydrogenase) (Glutamyl-gamma-semialdebyde
dehydrogenase) (GSA dehydrogenase).

Niella fastidiosa.

Niella fastidiosa.

Rocteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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MEDLINE-20365717;
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NCBI_TaxID=2371;
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415
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3; Mismatches
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FERCYCABIGISTORIHAGEWGLPALTSTKYIIKGTGGIR
E -> GCIRLRSRNRHGHNKASCKRTDGASGTDFYKIHH
(IN REF. 1).
BCA4BOD359963D0 CRC64;
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Matches 10
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                                                                                                                                             EMBL, AEO03938; AAR93815.1; ALT_INIT.
Interpro; IPRO00955; GPR.;
PROSITE; PS01123, PROA; 1.
Ox. dooreductuse; Proline biosynthesis; NADP; Complete proteome.
SEDUENCE 415 A3; 4453 MR; 6883A3D26B9454D CRC64;
177 LVQDMARHTMLELLQLSDLIDLVIPRG
                              4 IIRNIARH
                                                               ch 32.1%; l Similarity 37.0%; 10; Conservative
                              LAQVGDSMDRSIPPG
                                                             ; Score 44; DB;
; Pred. No. 40;
7; Mismatches
  203
                              26
                                                                                40;
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                                                                                              Length 415;
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                                                               Indels
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Search completed: September 20, 2002, 11:04:31 Job time: 1628 sec



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Minimum
Maximum
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: sp_arches:*

2: sp_bacteria:*

3: sp_kungi:*

4: sp_human:*

4: sp_human:*

5: sp_invertebrate

5: sp_arches:*

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8: sp_orgen!

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11: sp_rodent:*

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12: sp_virus:*

13: sp_virus:*

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16: sp_bacteriap:

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Gapop 10.0 , Gapext 0.5
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137
1 QEDITRNIARHLAQVGDSMDRSIPPGL
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Copyright (c) 1993 - 2000
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          DB
          1 099K83
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1 09JK60
09JK60
09ALO7
09X2X0
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Compugen Ltd
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Opbra homo sapien
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Opjit6 rattus norv
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Opji60 rattus norv
Opji70 pseudomonas
Opx20 rhodospiri1
Opif14 hordeum vul
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Opif16 drosophila
Opvay7 drosophila
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Matches 27; Conserv
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: BC005884; ARM05864.1; -.

HSSP: P55957; ZBID.

Interpro: IRE000712; Bell_2.

PROSITE; P801259; BHS; 1.

Hypothetical protein.

SEQUENCE 467 AA; 51663 MW; 7D7J2lD47F8E9D4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G9BRX3 PRELIMINARY; PRT; 467 AA.
G9BRX3
01-TUN-2001 (TTEMBLEEL 17, Created)
01-TUN-2001 (TTEMBLEEL 17, Last Sequence update)
01-DN-2001 (TTEMBLEEL 19, Last annotation update)
01-DEC-2001 (TTEMBLEEL 19, Last annotation update)
HYPOTRETICAL 51.7 KDA PROTEIN.
HOMO Sepiens (Human)
EUKARYSOLA: Metazoa; Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Rutheria; Primates: Catarrhini; Hominidae; Homo.
MCBL_TaxID-9606;
  Q99M39 PRELIMINARY; PRT;
Q99M39;
01-JUN-2001 (TremBirel, 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-LUNG CARCINOMA;
                                                                                                                                        351
                                                                                                                                     100.0%; Score 137; DB 4; ilarity 100.0%; Pred. No. 4.5e-12; Conservative 0; Mismatches 0;
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Length 467; indels

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us-09-544-664-14.rspt

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RESULT
O9UK60
ID QS
AC QS
DT 01
DT 01
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Best Local S
Matches 17
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Best Local S
Matches 19
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BMBL 18002031.1; -...
ISSL: BEO02031.1; -...
INCEPTE: PRO00732.9 EL1.2.
PROSTTE: PRO10297. BH3: 1...
EXQUENCE 195 AN. 21951 MW: 5
     Q9JK60
Q9JK60;
Q1-OCT-2000
Q1-OCT-2000
                                                                                                                                                                                                                                                                                                               STRAIM-SPRAGUE-DANLEY.

Chen D., Cao G., Chen J.;

"Clonling of rat apoptotic death agonist (BID) and its different expression in Isohemia and normal rat brain.";

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AF156282; AAF61422.1;

EMSL: AF16282; AAF6142.1;

HSSP: P70444; IDDB.

InterPro, IPR000712; B61.2.

RNSSTE: PS01259; BB1. UNKNOWN_1.

SEQUENCE 196 AA; 22281 MW; C5F6AD3F443C02E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OGULTG: 2000 (TREMBLIEL 15, Created)
01-OCT-2000 (TREMBLIEL 15, Last sequence update)
01-DEC-2001 (TREMBLIEL 15, Last annotation update)
APOPTOTIC DEATH AGONIST BID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9JLT6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BID.
Mus musculus (Mouse).
Eukaryotta: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mommalla: Butheria: Bodentia: Sciurognathi: Muridae: Murinae: Mus.
PCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TEMBLIFE) 17, Last sequence update)
01-DEC-2001 (TEMBLIFE) 19, Last anotation update)
BHJ INTERACTING DOMAIN DEATH AGONIST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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ISSUE-MANMARY TUMOR. WAP-TGF ALPHA MODEL.
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1 Similarity 70.4%;
19; Conservative
  (TrEMBLrel. 15,
                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                67.28;
Created)
Last sequence update)
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Pred. No. 8.5e-06;
4; Mismatches 6;
                                                            PRT;
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No. 7.7e-07;
No. 7.8e-5;
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AC Q9
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                                                                                                                                                                                    Query Match
Best Local S
Matches
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C STRAIN-ATCC 13525.;

A Feng S.F., Rossbach S.;

A Feng S.F., Rossbach S.;

A Locus involved in metal homeostasis in Pseudomonas fluorescens remodes a proton/cation antiporter of the RND family and a two-component system.";

C Submitted (AGG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; ANG07258; ANG093.1; -.

EMBL; ANG07258; ANG093.1; -.

R InterPro; IPR000014; PAS.

R InterPro; IPR000014; PAS.

R InterPro; IPR000014; PAS.

R Pfan; PF00785; PAC; 1.

R SMART; SM00085; PAC; 2.

R SMART; SM00091; PAS: 2.
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Best Local S
Matches 17
Q9X2X0
Q9X2X0;
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NON_TER
SEQUENCE
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Summitted (ARR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL. AF23930; AR71759.1;
HSSP: P7044 LDDB
THEEPFO; TP8007712; BC1_Z
PROSITE: P801259; B31_SUNKNOWN_1.
SEQUENCE 196 AA: 22249 MM; C5F6AD2F5D9B52E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia,
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=294;
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STRAIN-SPRAGUE-DAWLEY;
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BID PROTEIN.
BID.
                                                                                                             308 DVMRDLARHMQQAGDGIE 325
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8; Conservative
                                                                                                                                                                                                                                                                               336
336 AA;
                  PRELIMINARY;
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38039 MW;
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Pred. No. 3.5;
7; Mismatches
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Pred. No. 8.5e-06;
4; Mismatches 6
               PRT;
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                  190
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3.5;
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Query Match
Best Local Similarity 52.0
Watches 13, Conservative
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Proc. Natl. Acad. Sci. U.S.A. 98:373-378(2001).

EMBL: AP305912 PAM.

HSSP. P1393; JPM.

INTERFRO: UPR000719; Euk_pkinase.

INTERFRO: UPR002290; Ser_thr_pkinase.

INTERFRO: UPR00200; SYT_pkinase.

INTERFRO: UPR001245; Myr_pkinase.

R PRAUMS; FR00109; TYKKINASE.

PRAUMS; FR00109; TYKKINASE.
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SMART; SMO0221; STYKC; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYPKC; 1.
PROSITE; PSO0101; PROTEIN_KINASE_ATF; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
ATF-BIRGING; TRANSFELASE,
SEQUENCE 957 AA; 106338 MM; 3CF8ESP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9FPR4;
Q9FPR4;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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01-NOV-1999 (TYEMBLEE). 12, Last sequence update)
01-DEC-2001 (TYEMBLEE). 19, Last annotation update)
HYPOTHETICAL 19.7 KDA PROTEIN.
Rhodospirilim centennum (Rhodosta centenaria).
Bacteria: Proteobacteria: alpha subdivision; Rhodospirillem.
Rhodospirillum.
Rhodospirillum.
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STRAKH-CV. INGRID.
MEDLINE-21065153: Pubmed-11114160;
FEYPE C.A., Tang D. Innes R.W.;
"Negative regulation of defense responses in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
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Science 28: 406-409(1999).
EMBL: AR064527; AAD22393.1;
SEQUENCE 190 AA; 19654 MW; 27F62F131A339580 CRC64:
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STEALIN-ATCC51521;
MEDLINE-99340299; PubMed-10411503;
Jiang I., Swem L.R., Rushing B.G., Devanathan
Baner C.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4513;
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(TrEMBLrel. 16,
(TrEMBLrel. 19,
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                                            37.6%;
                          Score 51.5; D
Pred. No. 52;
2; Mismatches
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Pred. No. 5.2;
3; Mismatches
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09V6N2;
01-MAY-2000
01-MAY-2000
01-JUN-2001
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Eukaryota; Metazoa; Arthropoda; Trachesta; Hexapoda; Insecta;
Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
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Schence 282:2012-2018(1998).
1- SIMILARITY: BELOWGS TO THE GLOBIN FAMILY.
EMBL, 275550; CAN99921.i; "InterPro: IPR000971; Globin.
pfam; pF00042; globin. 1.
pfam; pF00042; globin. 1.
PROSITE; P801033; GLOBIN: 1.
BROSITE; P801033; GLOBIN: 1.
Hene: Oxygen transport; Respiratory protein.
SEQUENCE 183 AA: 21057 MW; 88D04980508NED63 CRC64;
                          SENOURCE FROM N.A.
STRAIN-BERKELEY.

MEDLING-2019000; PubMed-10731132;

MEDLING-2019000; PubMed-10731132;

MEDLING-2019000; PubMed-10731132;

MADAINS M.D., Celniker S.E., Holt R.A., Evans C.A., Godayne J.D.,

Amanatides P.G., Scherer S.E., Li.P.W., Hoskins R.A., Galle R.E.,

Geotige R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.W.,

Sutton G.G., Nortman J.R., Yandeli M.D., Zhang Q., Chen L.X.,

Sutton G.G., Wortman J.R., Yandeli M.D., Zhang Q., Chen E.X.,

Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Man K.H., Doyle C., Barter B.G., Helt G., Nelson C.R., Miklos G.L.G.,

Man K.H., Doyle C., Barter B.G., Helt G., Nelson C.R., Miklos G.L.G.,

Man M.H., Doyle C., Barter B.G., Helt G., Nelson C.R., Miklos G.L.G.,

Man M.H., College M. M., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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Sukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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Abril J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktargglu L., Beasley E.M., Ra Ballew R.M., Basu A., Baxendale J., Bayraktargglu L., Beasley E.M., Ra Ballew R.M., Basu A., Baxendale J., Bayraktargglu L., Beasley E.M., Ra Ballew R.M., Basu A., Baxendale J., Barthakov S., Ra Barris K.Y., Book P.M., Barnan B.P., Bhandari D., Brottler P., Ra Barris K.C., Basam R.A., Bouck J., Brokstein P., Brottler P., Ra Barris K.C., Basam D.A., Batler H., Cadleu E., Center A., Chandra I., Ra de Pablos E., Calley S., Dahlke C., Davanport L.B., Davies P., Ra de Pablos B., Delpir A., Deng Z., Mays A.D., Dew I., Dletz S.M., Dadson K., Doupl L.E., Canter A., Dang R., Mays A.D., Dew I., Dletz S.M., Dadson K., Doupl L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra de Pablos B., Dourle R., Caller R., Davies R., Ra de Pablos B., Dourle R., Caller R., Davies R., Ra de Pablos B., Dourle R., Caller R., Davies R., Ra de Pablos B., Dourle R., Caller R., Davies R., Ra de Pablos B., Dourle R., Caller R., Downes M., Sugar R., Harris M., Glassax K., Ra de Pablos B., Dourle R., Caller R., Downes M., Sugar R., Houck J., Ra de Pablos B., Dourle R., Caller R., Downes M., Sugar R., Houck J., Ra de Pablos B., Dourle R., Caller R., La Ranison J.A., Retchum K.A., Ra Lange R., Caller R., Karpen G., Karyltz S., Kalp D., Laid Z., Lang Y., Lin X., Lange R., Lange Y., Lin X., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R., Lange R
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SEQUENCE FROM N.A.
STRAIN-BERKELEY;
MEDLINE-20196006;
                                                                                                                        NEDLINE-95199263, PubMed-7892196,
Petrante A. W. Jr. Reshnke R. Stanley E.R.;
"Shark a Src hamology 2 ankyrin repeat Lyreshne klasse,
expressed on the apical surfaces of ectodermal epithelia.;
proc. Natl. Acad. Sci. U.S.A. 92:1917-1915(1995).
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
TISSUE-EMBRYO;
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PubMed-10731132
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15. Last sequence update)
19. Last annotation update)
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Pred. No. 29;
2; Mismatches
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RA Ballew R.M., Basu A., Barendale J., Buyraktaroqlu L., Beasley E.M.,

Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Ra Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Ra Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Ra Durbin K.J., Evanqelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

Ra Clodek A., Gong F., Gorrell J.H., Gu Z., Gabart H. W.M., Glasser K.,

Ra Fosler C., Gabrielian A.E., Garg N.S., Gelbart M.M., Glasser K.,

Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Kentison J.A., Ketchum K.A.,

Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Ra Harris N.L., Houston K.A., Howland T.J., Wei M.H., Diegwam C.,

Ra Harris N.L., Harry D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Ra Harris N., Koydra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Ra Harris N., Howland R., Howland T.J., Hernandez J.R., Holek N.,

Ra Harris N., Howland R., Harris M., Harris M.,

Ra Harris N., Howland R., Nanders R., Li J., Li Z., Liang Y., Lin X.,

Ra Harris N., Howland R., Sannders R., Colect J., Sheeler F., Shen H.,

Ra Shue B.C., Siden Kiams I., Shenson M., Stupski M.P., Smith T.,

Ra Shue B.C., Siden Kiams I., Shenson M., Stupski M.P., Smith T.,

Ra Harris N.L., Harris M., Ra Harris M., Walsachach J.,

Ra Harris N.L., Harris M., Ra Harris M., Ra Harris M., Ra Harris M., R
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Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
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Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
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TISSUE SPECIFICITY: CASTBULATION EMBRYOS SHOW EXPRESSION IN
ECTODERWAL CELLS ALONG THE CEPHALIC FURRROW AND VENTRAL MIDLINE
PROCTODERM, STOMODEUM AND THEIR DERLYED STRUCTURES (FOREGUT,
ARTIUM, PHARYEX, ESSPHAGUS AND HINGUIT) CONVINUE TO SHOW
EXPRESSION FROM STAGE 8-9 TO LATE EMBRYOS. OTHER ECTODERWALLY
DERLYED STRUCTURES (FRONTAL SAC, SALIVARY GLAND AND LABIUM) AND
DEVELOPING TRACHEAL SYSTEM ALSO SHOW EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: CYTOPLASMIC. APICAL EXPRESSION IN CEPHALIC FURROW AND TRACHEAL CELLS; LIMITED TO LUMINAL SURFACE AND ABSENT
                                                                      SIMILARITY:
                                                                                                                DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₹. D.,
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P.G., Scherer S.E., I
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                                                                               PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                     EMBRYOS ONLY
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Li P.W., Hoskins R.A., Galle R.F.,
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EMBL; AY051937; AAF3361.1; -.
EMBL; S5982; AAB19099.1; -.
HSSP; P08631; IAD5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: CONTAINS 3 ANK REPEATS: EMBL; U37773; AAA79851.1: -
                                                                                                                                                                                                                                                                  098590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00248; ANK; 3.
SMART; SM00252; SH2; 2.
SMART; SM00252; SH2; 2.
SMART; SM002529; TAVEC; 1.
PROSITE; PS50088; ANK_REPEAT; 3.
PROSITE; PS50017; PROFEIN KINASE_ATP;
PROSITE; PS50011; PROFEIN_KINASE_DOM;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0015295; shark.
InterPro; iPR002110; ANK.
InterPro; iPR000719; suk_pkinase.
InterPro; iPR000980; SH2.
InterPro; iPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00401; SH2DOMAIN. PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00069; pkinase; 1.
Pfam; PF00017; SH2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase; Tyrosine-protein kinase;
                                                                                                ATP SYNTHASE BETA SUBUNIT
                                                                                                                                                                                                                                     098590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
Chloroplast
                            Pleiospermium
                                                                    ATPB
                                                                                                                                                                                                                                                                                                                                                                                                                                       793 RNILLTARHQAKISDFGMSRSLRPG
                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 RNI---ARHLAQVGD-SMDRSIPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00109; PROTEIN_KINASE_TYR; PS50001; SH2; 2.
                                                                                                                                 (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; ank; 3
                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
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                                                                                                (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY

PHOSPHORYLATION (POTENTIAL).

A -> V (IN REF 1).

S -> R (IN REF 1).

L -> F (IN REF 1).

D -> E (IN REF 1).

D -> E (IN REF 1).

C -> S (IN REF 1).

C -> S (IN REF 1).

GT -> RA (IN REF 1).

GT -> RA (IN REF 1).

A -> P (IN REF 1).

A -> P (IN REF 1).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANK 2
ANK 3
SH2 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37CC2C3DA25D3F52
                                                                                                                                                                                                                                                                          485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRFTFNPVSIFHFFRC (IN REF. C3DA25D3F52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
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Best Local Similarity
Matches 10; Conser
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01-NOV-1999 (
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
PUTATIVE DNA POLYMERASE.
SCH5.03C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09x906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
EMBL; AF06680; AAD1173.1; -.
HSSP; P07677; ISKY.
HSSP; P07677; ISKY.
InterPro; IPR003593; AAA.
InterPro; IPR003593; AAA.
InterPro; IPR004100; ATP-synt_ab_N.
InterPro; IPR000793; ATPase_AB_C.
InterPro; IPR000793; ATPase_AB_C.
P1am; PF00005; ATP-synt_ab_1.
P1am; PF00005; ATP-synt_ab_1.
P1am; PF00006; ATP-synt_ab_C; 1.
SHART; SM00082; AAA; 1.
ENART; SM00082; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                         STRAIN-A3(2);
Bentley S.D., Parkhill
                                                                                                                                                                                                  STRAIN-A3(2);
Seeger K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00152; ATPASE_ALPHA_BETA; 1.
ATP synthesis; ATP-binding; CF(1); Chloroplast;
Hydrogen ion transport; Hydrolase; Thylakoid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Phylogenetic relationships of Rutaceae: a cladistic subfamilies using evidence from rbcL and atpB sequenc Am. J. Bot. 86:1191-1199(1999).
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
     SEQUENCE FROM N.A
                                                  Submitted (MAR-1999)
                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                              Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=10449399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eurosids
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 RHLAQ-VGDSMDRSIPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: (BY SIMILARITY).
SUBUNIT: F-TYPE ATFASES HAVE 2 COMPONENTS, CF(1) - THE CATALY
SUBUNIT: F-TYPE ATFASES HAVE 2 COMPONENTS, CF(1) HAS FIV
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIV
SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILION(1).
HAS THREE MAIN SUBUNITS: A. B AND C (BY SIMILARITY).
SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHIAQIIGPVMDVAFPPG
                                                                                                                                                                              J., Harris
(MAR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sapindales;
                                                                                                                                                                                                                                                                                                                        Streptomycineae;
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52091 MW;
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D.;
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                                                     J., I
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12,
                                                                                                                                                                              the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kallunki J.A.;
                                                                         Barrell B.G.,
                                                     Barrell B.G., Rajandream M.A.;
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48.5;
Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6ADF10269485DAF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                           Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401
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                                                                                                                                                                              databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analysis of
ce variation.
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REGULATORY
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                                                                                                            RA Goulinho L.L., CISTOTANI M., Diss-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Marchado M.A., Madeira A.M.B.N., Madeira M.L., Kemper E.L., Kitajima J.P.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,
RA Mono D.H., Nagai M.A., Nascimento A.I.T.O., Netto L.E.S.,
RA Mono D.H., Nagai M.A., Nascimento A.I.T.O., Netto L.E.S.,
RA Mono B.R., Radeira G.A.G., Punnes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Mono B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Queggio R.B., Roberto P.G., Rodrigues V. de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Savasaki H.E.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Savasaki H.E.,
RA de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA de Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Silva A.S., Verjovski -Almeida S., Vettore A.L.,
RA Vallada H., Van Silva M.A., Verjovski -Almeida S., Vettore A.L.,
RA The genome sequence of the plant pathogen Xyiella fastidiosa.",
RE Nature 406:151-159(2000).

DR EMB., ABOJSOG, AARSB3418.1;

RA There From the P.G. Santelli R. Santelli R.J., de Souza A.B.,
RA Charles Sequence of the plant pathogen Xyiella fastidiosa.",
RA There From the P.G. Santelli R.J., de Souza A.B.,
RA Charles Sequence of the plant pathogen Xyiella fastidiosa.",
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"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, ALO35636, CAB38477.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H. Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M.
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01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                 Pfam; PF00534; Glycos_transf_1;
                                                                                                InterPro; IPR001296; Glycos_transf_1
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   proteome.
849 AA;
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401 AA; 42525 MW;
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19,
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Pred. No. 66;
8; Mismatches
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   28FAFACC71C5726C CRC64;
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RESULT 15
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Search completed: September 20, 2002, 11:03:41 Job time: 1658 sec
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Matches 9; Conserv
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(STRAIN-EL TOR N16561 / SEROTYPE 01;
STRAIN-EL TOR N16561 / SEROTYPE 01;
STRAIN-EL TOR N16561 / SEROTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Boddson R.J., Haft D.H., Hickey B.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva W.D., Vamathevan J., Bass S., Oin H., Dragoi I., Seilers P.,
McDonald L., Utterback T., Flelschmann R.D., Nierman W.C., White 0.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M., of both Nirrocorpus of the babolism of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the columns of the col
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN VCL577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
Nature 406:477-483(2000).
EMBL; AE004235; AAF94731.1; -.
TIGR; VC1577; -.
Hypothetical protein; Complete proteome.
SEQUENCE 273 AA; 31087 MW; 9A21040F4DBA773E CRC64;
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NCBI_TaxID-666;
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bcl-x(L)/bcl-2 ass
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Mutant Bcl-XL/Bcl-
Mutant Bcl-XL/Bcl-
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AAG52445	AAG25576	AAG54028	AAG54679	AAG54029	AAG25577	AAG54030	AAG25578	AAG25217	AAG25218	AAG25219	AAB70380	AAB70379	AAB37029	AAY05421	AAB37028	AAY05422	AAR95163	AAB70371	AAY96321	AAW61322	AAW61321	AAW61320	AAW61319		AAG67688	œ	AAB70368	w	57	47	N	03	w
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## ALIGNMENTS

## RESULT AAB37001 AAB37001 standard; peptide; Bcl2 polypeptide BH3 domain peptide #1 28-FEB-2001 (first entry) AAB37001; \_ 26 B

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; Bd3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; apoptosis modulation; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphomytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction. Homo sapiens. Huang (UYJE-) 07-APR-1999; 06-APR-2000; 2000WO-US09352 12-OCT-2000 WO200059526-A1 UNIV JEFFERSON THOMAS Wang ŗ 99US-0128202 Zhang Z, Shan ŝ F. 2

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New peptide conjugates for modulating apoptosis or for inhibiting

WPI; 2000-679325/66

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Best Local
    Huang Z,
                                                                                                                                                         07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic, neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl 2 superfamily; BH3 domain; cell death agonist; BBd; apoptosis modulation; B cell lymphoma/Leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
                                                                            (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                             06-APR-2000; 2000WO-US09352
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Wang J,
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Zhang Z,
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Shan S,
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Sequence

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The invention relates to a peptide conjugate having the formula:

(R X)N-peptide where n = 1-10; X = C-0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = 0 or NH.

CC when the R-X group is attached to the C-terminus of the peptide, or a side chain functional group is cook or CONH2; and R = 2.18C alkyl or alkoxy, 2.14C alkylenyl containing one or converge the bonds, cyclobutyl, cyclopentyl, cyclohaxyl optionally monosubstituted with a 1.5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1.5C straight or branched chain of the peptide portion of the conjugate. The peptides represent examples cof the peptide portion of the conjugate The peptides represent examples cof the peptide portion of the conjugate The peptide conjugate is conjugate is seful for modulating apoptosis in the cells of a subject, or for the seful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (BCl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a conjugate afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, conjugate is also useful for transforma, melanoma, or acute or chronic lymphocytic and non-lymphocytic anakama. The peptide conjugate is useful for second by cancer cells that express Bcl-2; giound the confugate and non-lymphocytic characterized by cancer cells that conjugate is also useful for transformative disorders, acquired conjugate is useful for transformative disorders, acquired conjugate is useful for second conjugate is useful for transformative disorders, acquired conjugate is also useful for transformative disorders, acquired conjugate is useful for transformative disorders, acquired conjugate is useful for transformative disorders, acquired conjugate is use
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h 100.0%; Score 138; DB 21; Similarity 100.0%; Pred. No. 1.4e-14; 26; Conservative 0; Mismatches 0;
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## AAB37003 RESULT w

AAB37003 standard; peptide;

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28-FEB-2001 (first entry)

Bcl2 polypeptide BH3 domain peptide #3

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bc1-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; thelanoma; lymphocytic\_leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction

Homo sapiens.

W0200059526-A1

12-OCT-2000

ACC XXX ACC XX 06-APR-2000; 2000WO-US09352

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The invention relates to a peptide conjugate having the formula:

(R *Nyn *peptide where n * 1-10; X * C-0*, when the R *X group is attached to the N-terminus of the peptide or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X * O OH NH.

CC when the R *X group is attached to the C-terminus of the peptide, or a side chain functional group is COOH or OH; or X * O OH NH.

CC when the R *X group is attached to the C-terminus of the peptide, or a side chain functional group is COOH or OH NH2; and R * 2-18C alkyl or alkyl yor alkowy, 2-14C alkylaryl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclobexyl optionally consulting one or two double bonds, cyclobutyl, cyclopentyl, cyclobexyl optionally composity the did to the standard of the peptide with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ABB7001-B3705B represent examples of the peptide portion of the conjugate of the peptide conjugate is of the peptide portion of the conjugate in the cells of a subject, or for cuseful for modulating apoptosis in the cells of a subject, or for cuseful for modulating apoptosis in the cells of a subject, or for cuseful for modulating apoptosis in the cells of a subject in the cells of a subject afflicted with a cancer characterized by cancer cells that capped to the subject afflicted with a cancer characterized by cancer cells that capped to a subject afflicted with a cancer characterized by cancer cells that cause or chronic lymphocytic and non-lymphocytic leakemia. The apoptide conjugate is also useful for treating disorders and peptide conjugate is also useful for peptide conjugate is also useful for peptide conjugate is also useful for peptide conjugate is also useful for peptide conjugate is also useful for peptide conjugate is also useful for peptide conjugate is also useful for peptide conjugate is also useful for peptide conjugate is also useful for peptide conjugate is also useful for peptide conjugate is also useful for peptide conjugate
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                                                                                                                    Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bc1-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gasttic; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                            Bcl2 polypeptide BH3 domain peptide #56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB37056 standard;
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                                                    Homo sapiens.
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Pred. No. 1.4e-14;
% Mismatches 0;
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The invention relates to a peptide conjugate having the formula:

(R. X)n peptide where n = 1-10; X = C-0, when the X-3 group is attached to the N-terminus of the peptide, or a side chain of the peptide where continued the functional group of the side chain is xH2 or 0; Or NH, continued the functional group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain is xH2 or 0; Or NH, continued the x-3 group is attached to the C-terminus of the peptide, or a side chain side chain is xH2 or 0; Or NH, continued the x-3 group is attached to the C-terminus of the peptide, or a continued the x-3 group is attached to the C-terminus of the peptide, or a continued the x-3 group is attached to the C-terminus of the peptide, or a continued the x-3 group is a tracked chain a 1-5C straight or branched chain and y-3 group, or benzyl. The peptides what 7058 represent axamples continued pounds of the peptide portion of the conjugate or the peptide conjugate is greatly 1 group poptions in the conjugate and y-3 group or benzyl. The peptide corresponding to amino acids 72-97 of the peptide portion of the conjugate is a subject or for a subject. Or for a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject or a subject
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Sequence
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Matches 26
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                                        ch 100.0%; Similarity 100.0%; 26; Conservative
                                        0;
                                       Score 138; DB 21;
Pred. No. 1.4e-14;
Mismatches 0;
27
                                                            Length
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AAB37055 standard; peptide; 28 AA

(first entry)

Bcl2 polypeptide BH3 domain peptide #55

PD XXX

Cyrostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BiH domain, cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; carcer; prostate; molarecta; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic\_leukemia; neurodegenerative disorder; AIDS;

myocardial infarction

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(R * N)n * peptide where n = 1.00; X = C=0, when the R * X group is attached to the N-terninus of the peptide, or a side chain of the peptide where controlled the peptide where the side chain of the peptide where the side chain of the peptide or X = 0 or N; or X = 0 or N; or X = 0 or N; or X = 0 or N; or X = 0 or N; or X = 0 or N; or X = 0 or N; or X = 0 or N; or X = 0 or N; or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 or X = 0 
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uc1.XL/Bc1-2 associated cell death regulator; BAD; mutant: apoptosis;
Immunostimulant; neuroprocective; nootropic; antilicinamic; vulnepary;
cytostatic; antiviral; antivrhitic; autilicinamatory; wound hebiing;
immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;.
                                                                                                                    Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
                                                                                                                                                              02-MAY-2001
                                                                                                                                                                                                            AAB70370;
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26; Conservative
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                                                                                                                                                                                                                                                   protein;
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(APOP-) APOPTOSIS TECHNOLOGY INC.
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                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                       immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autolmmune disease.
                                                                                                                                                          15-FEB-2001
                                                                                                         2000WO-US11864
                                                        99US-0136783
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New mutant Bc1-XL/Bc1-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or Serl13 -WPI; 2001-138734/14. Zhou

Claim 7; Page 148-149; 157pp; English

The present invention describes an isolated or synthetic polypeptide (Compilsing a less than full length amino acid sequence of a mytant (Compilsing a less than full length amino acid sequence of a mytant (Compilsing a less than full length amino acid sequence of a mytant (Compilsing and Contains animo acid substitutions at Seriliof a human factor acid and contains animo acid substitutions at Seriliof a human factor acid animo acid substitutions at Seriliof a human factor acid animo acid sequence acid contains an acid contains an acid contains an acid contains an acid contains an acid contains an acid contains an acid contains an acid contains an acid contains an acid contains an acid contains and acid polynucleotides can be used for activity that promote cell survival or apoptosis other uses include induction or inhibiting apoptosis in a cell. Candidate compounds and drug clanuticide and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, irrail infections of the present sequence represents a specifically claimed shorter murine BAD mutant amino acid sequence from the present contains and acid seq nvention

Sequence 162 Ą

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Query Match
Best Local
                                                                                           Matches
AAR95168 standard; Protein;
                                                  98 nlwaagrygrelrrmsdefegsfkgl 123
                                                                     1 NLWAAQRYGRELRRMSDEFEGSFKGL
                                                                                                   Similarity
                                                                                           Conservative
                                                                                                    100.0%;
 204
                                                                                         0;
                                                                                                    Score 138;
Pred. No.
                                                                        26
                                                                                           Mismatches
                                                                                           1.1e-13;
hes 0;
                                                                                                              DB 22;
                                                                                            Indels
                                                                                                              Length 162;
                                                                                           0
                                                                                           Caps
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0

Вþ Ş

bcl-x(L)/bcl-2 associated death promoter protein. (first entry

06-JAN-1997

Epitope; murine: bcl-x(1)/bcl-2 associated death promoter; Hadi stroke; polypeptide; bcl-x; cell death; regulate; HH1; apoptotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

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This sequence represents the murine bol-x(L)/bol-2 associated death promoter (Bad) geno: Bad is a 2.1 kD protein which interacts with bol-2 and bol-x proteins and regulates cell death. It has homology to the bol-2 related family clustered in the BH and BH2 domain. Bad in spen found to hybridise to bol-x(L) and bol-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of bol-x(L), but is much less effective at countering the death inhibitory activity of bol-x(L), and expression can accelerate apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line expressing bol-x(L), and its also counters the death repressor activity of bol-x(L). Bad competes with Bax for binding to bol-2 or bol-x(L) to form beterodimers. Such agents may be used to identify agents which inhibit its binding to bol-2 or bol-x(L) to form beterodimers. Such agents may be used to treat resurodegenerative diseases, immunodeficiency diseases, ce.g. AIDS, senescence or ischaemia.
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide encoding bcl-x(L)/bcl-2 associated death promotor useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-2 or bcl-x(L) to form beteromultimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-1996
                       Murine BCL-XL/BCL-2 associated cell death regulator
                                                                      07-OCT-1998
                                                                                                                                                             AAW61315 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 1; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-251465/25.
N-PSDB; AAT29479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurodegenerative disease; senescence; ischaemia; neoplasia.
                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                 Similarity 100
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204
                                                                   (first entry)
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38..61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "J
191..192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 138; DB 17;
100.0%; Pred. No. 1.4e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *BH2 conserved amino acids"
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                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                204;
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100
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CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell CC death regulator) proteins, having an amino acid other than Ser at CC position 112 and/or 115, relative to the murine BAD 204 as sequence. The present sequence is the murine BAD protein also described are: (1) CC fragments of mutant BAD protein able to decrease cell viability; (2) CC fision proteins of mutant BAD protein able to decrease cell viability; (2) CC fision proteins of mutant BAD with a heterologous polypeptide that CC or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility. (2) CC inflammation and autoimmune disease. Polypucleotide sequences encoding the following contraints BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD cc mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD cc and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, additional produces of serine phosphorylated and non-certain produced phosphorylated BAD. By usual immunoassays. Mutant BAD proteins have completed by a cativity than wild-type BAD which can become composition of the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family cc substituted cannot bind 14-3-3.
New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 10; 95pp; English
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNIW ) UNIV WASHINGTON
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DB; AAV27833.
204 AA;
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RESULT

AAW61316

ID AAW6

XX

AC AAW6

XX

AC AAW6

XX

AC AAW6

XX

DT 07-C

XX

DE Muta

XX

XX
                                                                                                                                                                                              Matches
                                                                  AAW61316;
                                                                                          AAW61316 standard; Protein; 204 AA
                                                                                                                                                 140 nlwaagrygrelrrmsdefegsfkgl 165
                                                                                                                                                            1 NIWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                               9
                                                                                                                                                                                           Similarity 100
26; Conservative
                                                                                                                                                                                            0;
                                                                                                                                                                                           Score 138; DB 19;
Pred. No. 1.4e-13;
; Mismatches 0;
                                                                                                                                                                                              Indels
                                                                                                                                                                                              0;
                                                                                                                                                                                              Gaps
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밁 δÔ

07-OCT-1998

(first entry)

Murine; mouse; HCL-XL/BCL-2 associated cell death regulator; BAD protein;

Mutant BCL-XL/BCL-2 associated cell death regulator #1.

Query Match Best Local

100.0%;

Length

204;

0

В Ş

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RESULT 10
AAW61317
ID AAW613
XX
AC AAW613
XX
DT 07-OCT
XX
DE Mutant
XX
Murine
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                                                                                                                                                                                                                                                                                                                                                          The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at CC position 112 and/or 136, relative to the mutane BAD 204 as sequence. The position 112 and/or 136, relative to the mutane BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) CC fusion proteins of mutant BAD protein able to decrease cell vability; (2) fusion proteins of mutant BAD protein are used to treat cor prevent diseases associated with aduced approbasis, e.g. cancer. CC viral infection, lymphoproliferation, arthritis, infertility. (2) furiant thon and autoimmune disease. Polynucleotis sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD companies of serims proposed as a such as AIDs, neurodegeneration, and introduced by measuring relative amounts of phosphorylated and non-composure that does not the specified Ser, forming a protein that does not the specified Ser, forming a product that does not the specified Ser, forming a product that does not the specified Ser, forming a product that does not the specified Ser, forming a product that does not the specified Ser, forming a product that does not the specified Ser, forming a product that does not the specified Ser, forming a product that does not the specified Ser, forming a product that does not the specified Ser, forming a product that does not the specified Ser, forming a product that does not the specified Ser, forming a product that does not the specified Ser, forming a p
                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 26
                            Mutant BCL-XL/BCL-2 associated cell death regulator #2
                                                             07-OCT-1998
                                                                                          AAW61317;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mutant BAD polypaptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
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                                                                                                                       AAW61317 standard; Protein;
                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                              WPI; 1998-261422/23
N-PSDB; AAV27834.
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                                                                                                                                                                                                                                                      h 100.0%; Score 138; DB 19; Similarity 100.0%; Pred. No. 1.4e-13; 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                  204 AA;
                                                           (first entry)
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                                                                                                                         204
                                                                                                                                                                                                                                                                                    Length 204;
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                                                                                                                                  RESULT 11
AAW61318
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                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 26
                                                           07-OCT-1998
                                                                                        AAW61318;
                                                                                                                     AAW61318 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for, e.g
viral infection
                                                                                                                                                                                                                                                                                                                                 Sequence
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at C position 112 and/or 156, relative to the murine BAD 204 as sequence. The position 112 and/or 156, relative to the murine BAD 204 as sequence. The position il 12 and/or 156, relative to the murine BAD 204 as sequence. The createst sequence represents a mutant BAD protein. Also described are: (1) for the sequence represents a mutant BAD protein. Also described are: (2) fragments of mutant BAD with a heterologous polypeptide that correspond to the protein are used to treat or prevent diseases associated with reduced applicosis, e.g. cancervital infection, lymphoproliferation, arthritis, infertility.

Confident and autoimmune disease. Polynocleotic sequences encoding mutant BAD proteins can be used similarly by gone therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDs, neurodegeneration, aging or ischaenic cell death. The apoptotic status of cells is aging or ischaenic cell death. The apoptotic status of cells is given by measuring relative amounts of phosphorylated and non-composition of the specified Ser, forming a product that does not the producting activity than wild-type BAD which can become operations in the cytosol, thus promoching cell survival. The mutants with the cytosol, thus promoching cell survival. The mutants with the cytosol, thus promoching cell survival. The mutants with
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N-PSDB; AAV27835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 60; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNIW ) UNIV WASHINGTON
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26; Conservative 0; Mismatches 0;
                                  Length 204;
                       0;
                      Gaps
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(first entry)

204 ξ

Mutant BCL-XL/BCL-2 associated cell death regulator #3.

Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD

protein;

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RESULT 12
AAW58832
ID AAW588:
XX
AC AAW588:
XC AAW588:
XX
DT 23-JUL
XX
DE Murine
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DE Murine
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                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 26
                                Murine BAD protein
                                                                                                                       AAW58832 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 60-61; 95pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for, e.g.
viral infection
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                                                               23-JUL-1998 (first
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DB; AAV27836.
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                                                                                                                                                                                                                                                            100.0%;
Similarity 100.0%;
6; Conservative 0
                                                                                                                                                                                                                                                                                                                                    204 AA;
    Bcl-XL/Bcl-2 associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9605-0733505
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                                                                                                                            204
                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                        Score 138; DB 19;
Pred. No. 1.4e-13;
Mismatches 0;
    cell
  death regulator; 14-3-3;
                                                                                                                                                                                                                                                                                      Length 204;
                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                            0;
RESULT 1
10 AAB70369
AX AAB70369
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Matches 26
                                                                                                                                    Longer murine BAD mutant amino acid sequence SEQ ID
                                                                                                                                                                     02-MAY-2001 (first entry)
                                                                                                                                                                                                                             AAB70369 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-207049/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNIW ) UNIV WASHINGTON.
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                                                                                                                                                                                                                                                                                                     3; Fig 8; 6lpp; English.
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I Similarity 100.0%;
26; Conservative (
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                                                                                                                                                                                                                             protein;
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serine phosphorylation, post-translational modification, apoptosis, signal transduction regulator, phosphosorine phosphatase; senseence; immunodeficiency disease; neurodegenerative disease; infertility; cancer, viral infection; lymphoproliferative condition; arthritis; inflammation; autolumnane diseases.
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Serine-phosphorylated Boi.x-1/pol-2 Associated cell Death regulator polypepiide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases

This sequence represents a novel serine-phosphorylated protein, BAD (BCL-XL/BCL2 associated cell doath regulator). The serine residue is phosporylated in a post-translational modification and allows binding to the 14-3-2 protein which is a signal transduction regulator. Modulators of phosphorylated BAD, which act through inhibition-activation of a phosphoserine phosphatase, are useful for preventing/treating increased/agercased apoptosis in a cell. The increased apoptosis may result from immunodeficiency diseases, sensecence, neurodegenerative disease, isohaemic cell death, reperfusion cell death, infertility and wound-healing. Decreased apoptosis may result from cancer, viral infeaction, hyphoproliterative conditions, arthritis, infertility. Infilammation and autoimmune diseases. Measuring the amount of phosphorylated compared to unphosphorylated BAD polypeptide and/or total BAD in a cell is useful for determining the apoptotic state of a cell.

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Score 138; D
Pred. No. 1.4
D; Mismatches
DB 19;
.4e-13;
ss 0;
               Length
               204;
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NO:2.

Bel-XL/Bel-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; noofropic; mutischaemic; vulnerary; cytostatic; antitivital, antiarthritic; antitivitammentory; wound healing; immunosippressive; apoptosis inducer; apoptosis inhibitor; oncer; immunosippressive; apoptosis inducer; apoptosis inhibitor; oncer; immunosippressive; apoptosis inducer; apoptosis inhibitor; oncer; immunosippressive; apoptosis inhibitor; oncer; immunosippressive; apoptosis inhibitor; oncer; immunosippressive; apoptosis inhibitor; oncer; immunosippressive; apoptosis inhibitor; oncer; immunosippressive; apoptosis inhibitor; oncer; immunosippressive; antiquitality; apoptosis; antiquitality; apoptosis; antiquitality; apoptosis; antiquitality; antiquitality; apoptosis; antiquitality; apoptosis; antiquitality; apoptosis; antiquitality; apoptosis; antiquitality; apoptosis; antiquitality; apoptosis; antiquitality; antiquitality; apoptosis; antiquitality; antiquitality; antiquitality; antiquitality; antiquitality; antiquitality; antiquitality; antiquitality; antiqui

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolated or synthetic polypeptide (I) comprising a less than full length amino acid sequence of a mutant (E) comprising a less than full length amino acid sequence of a mutant (E) contains amino acid substitutions at Serills of a human (E) shows that the sequence of a mutant (E) shows the serills of a mutant (E) has immunostimulant, neuroprotective, concurrent mutant (E) has immunostimulant, neuroprotective, concurrent (E) antischemic, vulnerary, cytostatic, antiviral, and can be used as an apoptosis inducer or inhibitor. Bub polypeptides and comply or inhibiting apoptosis in did munosuppressive activities, and comply or inhibiting apoptosis in a cell. Candidate compounds and drugs (F) activity that promote cell survival or apoptosis. Other uses include thought or inhibiting apoptosis in a cell. Candidate compounds and crustified and (mutant) Bab polypeptides are useful in treating coll describ, reperfusion cell leads, vound healing, camer; viral infections, application of the sequence of the contained to a promote coll contained to many the sequence of the sequence of the present of the present invention of the sequence and sequence from the present coll contained in one of the present of the present of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present invention of the present 
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                                            Mouse: Bad-DTTR: apoptosis; cencer; spinal muscular atrophy; diphtheria toxin receptor binding domain; DTR: neoplass; tuncur; hyper-proliferation; Albehmer a disease; neurodegenerative disorder; translent ischaemic neuronal injury; stroke; spinal cord injury; nuclayers a disease.
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Synthetic.
       Chimeric - Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-138734/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (APOP-) APOPTOSIS TECHNOLOGY INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents the amino acid sequence of Bad-DYTR approals modifying fusion protein comprising and seem sequence fused that short interior dishriberia toxin translocation domain (DYTR), The 1 sequence fused that the functional approals modifying fusion protein is capable of binding a callural approal sequence fused to the carget cell and integrating into or crossing a callural membrane of the carget cell in the papphosis modifying fusion protein comprises at least two domains: the DYR domain, which targets the fusion protein to the carget cell in the Bal-XL domain, which targets the fusion protein to the carget cell and the Bal-XL domain, which modifies an apoptocic response co in the target cell. The fusion protein is useful for modifying complifierative cell or an adjocyte, it is also useful for reducing the fusion protein and though inhibition or enhancement complications through inhibition or enhancement of apportocic cellural response. Including neurodepenerative disorders of apportocic cellural response. Including neurodepenerative disorders and attophy, stroke apsocles and surgulated feel growth as an uncollar and attophy, stroke apsocles and surgulated feel growth as the uncollar callural response.
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel fusion protein for modifying apoptosis in target call and reducing apoptosis after transient ischeamic neuronal injury has two domains which targets protein to a cell and modifies apoptotic response
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N-PSDB; AAS00248.
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(USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-1999;
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                                                                                                                                                                                                                                                                                    161 nlwagrygrelrrmsdefegsfkgl 186
                                                                                                                                                                                                                                                                                                                                    1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                     ich 100.0%; Score 138; DB 22; il Similarity 100.0%; Pred. No. 4.3e-13; 26; Conservative 0; Mismatches 0;
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   for regulating cell death
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                                                                                                                                                     Protein;
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                                                                                                                        Query Match 82.6%; Score 114; DB 18;
Best Local Similarity 91.7%; Pred. No. 6. 1e-10;
Matches 22; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                    The present sequence represents a protein of 166 amino acids. The sequence is disclosed as being a protein called BBC6 which regulates cell death through interaction with BC1-2. The DNA may be used for the production of the recombinant protein, which can be used in unspecified therapeutic or diagnostic procedures, as a molecular weight marker, and to raise antibodies that can be used in unspecified diagnostic or therapeutic applications and to reduce or eliminate the biological activity of the BBC6 protein in vivo.
                                                                                                                                                                                                                                                                                                                                              Claim 1; Column 11-12; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-447980/41.
N-PSDB; AAT91561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CLON-) CLONTECH LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         Isolated BBC6 gene – encodes a protein that regulates cell death through interaction with \mbox{Bcl-2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BBC6 gene; cell death; cell cycle; Bcl2; human.
                                                                                                                                                                                              Sequence
                                                                  166 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 1572
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
   Query Match
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Matches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend Khourie and STREET: 379 Lytton Avenue CITY: Palo Alto CITY: Palo Alto STATE: California COUNTY: Palo Alto STATE: California COUNTY: Palo Alto COUNTY: Palo Alto COUNTY: Palo Alto Computer READABLE FORM:

MEDIOM TYPE: Floppy disk COMPUTER: IBM PC Compatible COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-1002/MS-00S SOFTWARE: Patentin Release $1.0, Version $1 CURRENT APPLICATION NUMBER: US/08/33,565 FILING DATE: 31-OCT-194 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: MAME: SMITH, WILLIam M REGISTRATION NUMBER: 30,223 REGISTRATION NUMBER: 30,23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: KORSME
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and STREET: 379 Lytton Avenue
CITY: Palo Alto
CTAY: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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VENTION: BCL-X/BCl-2 ASSOCIATED CELL DEATH
VENTION: REGULATOR
EQUENCES: 59
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US-08-718-738-18
US-09-721-844-18
US-09-221-844-84-18
US-09-299-843A-40
US-09-359-161-7
US-08-997-362-17
US-08-997-362-17
US-08-997-362-94
US-08-97-362-94
US-08-97-362-94
US-09-9855-99
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Gaps

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US-08-661-479-2
Sequence 1, Application US/08733505A

Patent No. 5856445

GENERAL INFORMATION:
APPLICANT: KORSHEYER, STANLEY J.
TITLE OF INVENTION: SERVINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION: KORSHEYER, Stanley J
TITLE OF INVENTION: Bol-x/Bol-2
TITLE OF INVENTION: REGULATOR
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                       Query Match
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CLASSIFICATION 435

PRIOR APPLICATION DATA:
APPLICATION MUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRESTING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                           140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                     Similarity
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ilarity 100.0%;
Conservative (
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of mouse BAD."
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; MOLECULE TYPE:
US-08-733-505A-1
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Best Local S
Matches 26
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         APPLICATION NUMBER: US/08/733
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5189
TELEPAX: (314) 727-6092
TELEPAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTED:
COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SERINE SUBSTITUTED MITITLE OF INVENTION: BCL.*NL/BCL-2 ASSOCING NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONATD P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ZIP: 631
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COMPUTER: IBM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release. " 1
                                                                                                                                                                                                                                                                                      STATE: MISSOURI
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REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96
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REFERENCE/DOCKET NUMBER:
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SERINE SUBSTITUTED MUTANTS OF
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
60
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965458
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RESULT 5
US-08-733-505A-13
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RESULT
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Patent No. 5856445
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Best Local
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                           Query Match
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (314) 727-6092 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KORSMEYER, STANLEY J.

APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: BELIABLY SUBSTITUTED MUTANTS OF

TITLE OF INVENTION: BELIABLY BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/BELL-ZL/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                      140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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Similarity 100.0%;
26; Conservative (
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7733 FORSYTH BLVD., SUITE 1400
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                                                                                                                                                                                                            Patent No.
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APPLICATION NUMBER: US/G
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CURPUTER REALABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                           APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Acids and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
RAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                   STATE:
                                                                                                                                                              STREET:
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                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                            3, Application US/08717123
5. 5965703
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                                                                                                RY: United States 92122
                                                                                                                               San Diego
California
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amino acid
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                                                                                                                                                              E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
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Pred. No. 4
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Patent No. 5663316
GENERAL INFORMATION:
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Best Local Similarity
Matches 25; Conserv
                                                                 Query Match
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INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                             NAME: Sallwanchik David R
REGISTRATION NUMBER: 31.794
REFERENCE/DOCKET NUMBER: CL
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NOWER: US/08/665,617
APPLICATION NUMBER: US/08/665,617
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REFERENCE/DOCKET NUMBER: PTELECOMMUNICATION INFORMATION:
TELEPHONE: [619] 535-9001
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ATTORNEY/AGENT INFORMATION:
NAME: 5allwanchik, David
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MEDIUM TYPE: Floppy
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LENGTH: 204 amino acid
TYPE: amino acid
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STREET: Gainesville
STATE: Florida
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ADDRESSEE: Saliwanch
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1 NLWAAQRYGRELRRMSDEFEGSFK 24
                                                Local
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                                                Similarity
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2421 N.W. 41st Street, Suite A-1
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                               Score 114: DB 1; Length 166; Pred. No. 1.8e~10; O; Mismatches 2; Indels
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Pred. No. 1
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US-08-717-123-2
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                                                                                                                                                                                                                          Sequence 1,
Patent No.
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Best Local Similarity
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STREET: San Diego
STATE: California
STATE: United States
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COMPUTER: ILM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RAIDAGE #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
LENGTH: 168 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Horne, william A. APPLICANT: Oltersdorf, Tilman TITLE OF INVENTION: Acids and Methods of Use
                                                                                              APPLICANT: Lal, Preeti
APPLICANT: Shab, PULVI
APPLICANT: COLIBY, Neil C.
APPLICANT: COLIBY, Neil C.
TITLE OF INVENTION: PROTIETRATION
                                                                                                                                                                           APPLICANT:
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                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                      103 NLWAAQRYGRELRRMSDEFVDSFK 126
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CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       1 NIWAAQRYGRELRRMSDEFEGSFK 24
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5. 5965703
                                                                                                                                                                                                                            Application US/08985335 6080847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 amino acids
                                                                                                                                                                           Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                            Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (619)
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N: 435
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) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                  82.6%;
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                                                                                                                                                                                                                                                                                                                                                                                  Score 114; DB 2;
Pred. No. 1.8e-10;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 168;
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0;

Length 168; indels

0; Gaps

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RESULT 11
US-08-985-335-7
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NAME B BILLINGS LICY J

REGISTRATION NUMBER: 36,749

RESENENCE/POCKET NUMBER: PF-0

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-655-0555

TELEPHONE: 650-655-0555

TELEPHONE: 650-654-4166

INFORMATION FOR SED ID NO: 1:
SEQUENCE CHRACTERISTICS:
ENGINE LIGHT STORMATION: 166 AMILIO ACIDS

TELEPHONE: 166 AMILIO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application Patent No. 6080847 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.6%;
Best Local Similarity 91.7%;
Matches 22; Conservative
                                                 CONFUTEN READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTEN: IBM Compattible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
PILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
1104 Herewith
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANL...
TOPOLOGY: 11...
IMPEDIATE SOURCE:
LIBRARY: SYNORA/
TONE: 358673
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OPERATING SYSTEM: DOS
SOFTWARE: FRANCES for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/98
FILING DATE: FILED Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                         APPLICANT: COTIEY, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE ATORYCE Pharmaceuticals, Inc.
STREET: 3174 Forter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM
MEDIUM TYPE: Disketi
  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                      STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NLWAAORYGRELRRMSDEFEGSFK 24
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Pred. No. 1.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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US-08-985-335-7
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                                                                     TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 anino acids
TYPE: anino acids
TYPE: anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-410-372-1
                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPOSILBLE
OPERATING SYSTEM, DOS
SOFFWARE: FASTESD FOR WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
APPLICATION NUMBER: US/985,335
APPLICATION MUMBER: 08/985,335
APPLICATION MUMBER: 08/985,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
STRANDEDNESS:
TOPOLOGY: 11ne:
IMMEDIATE SOURCE:
LIBRARY: SYNOR
                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                     NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENCTH:
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0. 6281334
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Incyte Pharmaceuticals, Inc
3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette
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                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No. 1.8e-10;
0; Mismatches 2
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: LENGTH: 168 anino
: TYPE: amino acid
: STRANDEDNESS: sing
: TOPOLOGY: linear
: INMEDIATE SOURCE:
: LINEARY: GenBank
: CLONE: 1683637
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       RESULT 14
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Best Local (
                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 82.6%;
Best Local Similarity 91.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COMPALINE
OPERATING SYSTEM, DOS
SOFTWARE: FEMILISTO for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: COTICY, Well C.
TITLE OF INVENTION: PROTEINS ASSOCIATED W
TITLE OF INVENTION: PROLIFERATION
WITHER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 31/4 Porter Dr.
CITY: DATA AIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE,DOCKET NUMBER: PET-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 NEWAAQRYGREERRMSDEEVDSFK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: CA
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ZIP: 94304
                                                                                                                                               1 NLWAAQRYGRELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 amino acids
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Lal, Preeti
Shah, Purvi
                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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                                                                                                                                                                                                                                      91.78;
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Pred. No. 1.8e
0; Mismatches
                                                                                                                                                                                                                                      Score 114; DB 4;
Pred. No. 1.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF-0421 US
                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; |
| .8e-10;
| es 2;
                                                                                                                                                                                                                                                                  Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 168;
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                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-561-479-10
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: DECOMPACIBLE
COMPUTER: 10 C COMPACIBLE
MEDIUM TYPE: PAPELCOMPUTER: PC-DOS/MS-OOS
SOFWARE: PC-MTON MARER: DOS/MS-OOS
SOFWARE: PC-MTON MARER: DI-MS-MS-OOS
FILTRG DATE: J-CT-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
MARE: SMILLAM M
REGISTRATION WARER: J-MS-OO-
REGISTRATION WARER: J-MS-OO-
TELECOMMUNICATION HTORMANION:
TELECOMMUNICATION HTORMANION:
TELECOMMUNICATION HTORMANION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08661479 Patent No. 5834209
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Him PC COMPAINE:
OPERATING YSYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin melease #1.0, Version #1.25
CURRENT APPLICATION RUMBER: US/08/661,479
APPLICATION RUMBER: US/08/661,479
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES; 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
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TITLE OF INVENTION: BECL-Z/BEL-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: BC1-x/BC1-TITLE OF INVENTION: REGULATOR
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Similarity 100.0%; I
21; Conservative 0;
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                                                                                                                                                                                                                                          SD
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/ENTION: Bc1-x/Bc1-2 ASSOCIATED CELL DEATH
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; Pred. No. 2.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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Length 23

0, Gaps

0;

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FILING DATE: 11-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION NAME: US 08/333,565

APPLICATION NUMBER: US 08/333,565

ATTORNEY/ACENT INFORMATION:

NAME: SAILH, WILLIAM M
REGISTRATION NUMBER: 10.23

REFERENCE/DOCKET NUMBER: 15726A-000700

FELECOMMUNICATION INFORMATION:

TELEPIONE: (415) 326-2400

TELEPIONE: (415) 326-240

TELEPIONE: (415) 326-240

TELEPIONE: (415) 326-240

TELEPAN: (415) 326-240

STENDRATION FOR SED ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-661-479-10
Search completed: September 20, 2002, 10:37:19 Job time: 407 \ \text{sec}
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                                                                                                                                                                                                              Ouery Match 81.9%; Score 113; DB 2; Length 23; Best Local Similarity 100.0%; Pred, No. 2.8e-11; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                  0; Gaps
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Page 7



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Title:
Perfect score:
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C;Species: Mus masculus (house mouse)
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C;Species: Mus masculus (house mouse)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C;Accession: A55671
A;Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot A;Reference number: A55671; MUID:9513651
A;Accession: A55671
A;Status: prellanary; not compared with conceptual translation
A;Malecule type: mRNA
A;Residues: T204 c:AN>
A;Residues: GB:L37296; NID:9639778; PIDN:AAA64455.1; PID:9639779
C;Keywords: becordiners
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## ALIGNMENTS

RESULT

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Inter-alpha-trypein inhibitor heavy chain 2 - golden hamster
C.Decies: Meselicetus auratus golden hamster
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A.M.Cocasion: JC5574; MOID:91694689; DIDN:BAA13939.1; DID:91694690
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A:Experimental : C:Genetics: A:Gene: Rv2014
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c;Speciles: Mycobacterium tuberculosis
c;Date: 17-Jul-1998 sequence_revision 17-Jul-1998 stext_change 22-Oct-1999
c;Accession: D70760
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Raindream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Naturer 393, 537-544, 1998
A;Althore: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitchead, S.; Barrell, B.G.
A;Althe: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:9829587
A;Accession: D70760
A;Status; preliminary; nucleic acid sequence not shown; translation not shown
A;Molocule type: DNA
A;Cossy:references: CB: Z7405; GB:AL123456; NID:93261586; PIDH;CAA98415.1; PID:e1299911;
C;Garelles, A.
2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyoes can
N Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; DAHP synthase;
C Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A. MOLECULE type: mRNA
A. MOLECULE: 1946 CCHAD:
A. CCOSS-TETERENCES: EMBL: X70392; NID:q595633; PIDN:CAA49842.1;
C. Superfamily: Inter-alpha-trypsin inhibitor complex component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inter-alpha-inhibitor H2 chain - mouse C:species Mus masulus (house mouse)
C:species Mus masulus (house mouse)
C:bate: 15-Jul-1995 Requence_revision 01-Sep-1995 Rtext_change 20-Aug-1999
C:Accession: 554354
R:Chan, P: Risler, J.L.; Raguenez, G.; Salier, J.P.
Biochen, J. 306, 505-512, 1995
R:Chan, P: Risler three heavy-chain precursors for the inter-alpha-inhibitor family
A:Reference number; S34333; MUID:95194326
A:Recession: 55454
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Similarity 34.6%;
9; Conservative
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Pred. No. 8.8;
5; Mismatches 1
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Pred. No. 2.8;
1; Mismatches
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C.Accession: S.58185, 946126; 846130, JM0322; 84651
R.DO19001; P.; Bleau; W.; Adjale, M.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet, W.; Crouzet,
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A;Cross:references: SGD:S0000453; MiPS:YBR249c
A;Map position: 2R
C;Function: aldehyde-lyase; carbon-carbon lyase
A;Description: aldehyde-lyase; carbon-carbon lyase
A;Description: aldehyde-lyase; carbon-tarbon lyase
A;Description: aldehyde-lyase; bickinate pathway
C;Superfamilt; phospho-2-dehydro-3-deoxyheptonate aldolase
C;Keywords: aldehyde-lyase; aromatic amino acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCROSS-references: EMBL:M51107

R:KNenchler, M.: Balmelli, T.: Bgli, C.M.: Paravicini, G.: Braus, J. Bacteriol. 175, 5548-5558, 1993

A:Title: Clonding, primary structure, and regulation of the HIS7 g. Reference number: A4851; MUID:93374850

A:Receasion: B48531

A:Status: preliminary

A:Molecule (type: DNA (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) Residues: 352-370 (KU2)-A) 
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Matches 10
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G.H

gene encoding a bifun

of phosphoenolpyruvate and D-erythr

carbon-carbon lyase;

Length 370;

0 Gaps

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су

6 Indels

RESGLY 6
A42095
A42095
Gloral hameotic protein APETALA3 (AP3) - Arabidopsis thaliana
Rioral hameotic protein APETALA3 (AP3) - Arabidopsis thaliana
N:Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: 04-Mar-1993 sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000
C:Accession: A42095; SS5633; T47593
C:Jack, T: Brockman, L.L.: Meyerowitz, E M
Cell 65, 683-667; 1992

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A:Map Position: 3
A:Introns: 63/2; B5/3; 106/2; 139/3; 153/3; 168/3
A:Introns: 71/E18.30
A:Note: 71/E18.30
C:Superfamily: transcription factor squa; serum response factor DNA-binding C:Superfamily: Lranscription regulation
C:Reywords: DNA binding; nucleus; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>
                                                                                                                                                                                                                                                                                                                                                                              RiNg, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, I. Leithauser, B.; Keller, K.; Cruz, R.; Dasson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl. Jung, K.H.; Alam, M.; Ereltas, T. 1970.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2004.

A.Authors: Anoy, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L. A.Fitle: Genome sequence of Halobacterium species NRC-1.

A.Feterence number: A84160; MUID:20504483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spermidine/putrescine ABC transporter [imported] - Halobacterium sp. NRC-1:
C;Species: Halobacterium sp. NRC-1:
C;Species: Halobacterium sp. NRC-1:
C;Species: Darbe-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #text_change 02-Feb-2001
C;Dates 03-8
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A; Residues: 1-222 <BLO>
A; Cross-references: EMBL; AL132971
A; Experimental source: cultivar Columbia; BAC clone T12E18
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A:Molecule Lype: DNA
A:Molecule Lype: DNA
A:Residuss: 1-63 <OKA-
A:Residuss: 1-63 <OKA-
A:Cross:references: GB:D21125
R:Bloceker, H.; Mewes, H.W.; Lencke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes, submitted to the Protein Sequence Database, March 2000
A:Reference number: 724469
A:Accession: 747593
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A;Experimental source: petals, stamens
A;Mote: sequence extracted from NCBI backbone (NCBIN:82520, NCBIP:82521)
R;Okamoto, H.; Yano, A.: Shiralshi, H.; Okada, K.; Shimura, Y.
Plant Mol. Biol. 26, 465-472, 1994
A;Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabic A:Reference number: $52633; MUID:95036018
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A;Molecute type: DNA
A;Molecute: 1-374 <DNA
A;Mostidus: 1-374 <DNA
A;Gross-references: GB:AE004437; NID:g10581314; PIDN:AAG20071.1; GSPDB:GN00138
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A;Gene: potA2
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                                                                                  Local Similarity 76. hes 10; Conservative
       11 ELRRMSDEFEGSF 23
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                                                                                                           36.2%;
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Pred. No. 5.8;
3; Mismatches
                                                                                      Score 50; DB
Pred. No. 13;
1; Mismatches
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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337
A;Recession: B3517
A;Recession: B3517
A;Recession: B3517
A;Recession: B3518
A;Residues: 1-433 cgrox
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C;Genetics:
A;Gene: F1N23.1
A;Map position: 1
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A;Experimental source: strain PAO1
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A; Residues: 1-516 <STO>
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Pred. No. 19;
7; Mismatches
                                                                                                                                                                                                                                                Score 49; DB
Pred. No. 23;
4; Mismatches
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2 7;

Length 516;

8

2; Length 453;

Indels

2:

Gaps

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C:Accession: A96753

R:Theologis. A.; Ecker. J.R.; Falm, C.J.; Federspiel. N.A.; Kaul. S.; White, O.; Alon Chin. C.H.; Chung, M.K.; Conn. L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen. N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti. R.; Marzia R.zzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A.Fitile: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.

A.Rocession. A96753

A. Accession. A96141; MUID:21016719
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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Asp,

Ser)

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transforming protein homolog MRAS3 - Rhizomucor racemosus
C:Species: Rhizomucor racemosus
C:Species: Rhizomucor racemosus
C:Date: 28 + Mar 1991 sequence_revision 28 - Mar 1991 stext_change 19 - Jan - 2001
C:Accession: C36365
R:Casale, M.L.; McConnell, D.G.; Mang, S.Y.; Lee, Y.J.; Linz, J.E.
Mol. Cell. Biol. 10, 6654 - 6663, 1990
A:Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which exhibat Reference number: A36365; MUID:91061774
A:Restorence number: A36365; MUID:91061774
A:Restorence repeliminary
A:Residues: 1 - 206 < CAS>
A:Cross - terrences: GB: MS5177
C:Superfamily: ras transforming protein: translation elongation factor Tu homology
C:Keywords: GFp binding; Muricottde binding; P-loop
F:11-126/Domain: translation elongation factor Tu homology <FTUS
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C;Satces ton: $40376
C;Access ton: $40376
C;Access ton: $40376
C;Access ton: $40376
C;Access ton: $40376
Eur. J. Immunol. 23, 2248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference: $40312; MUID:94080891
A;Accession: $40376
A;Status: preliminary; translation not shown
A;Accession: $40376
A;Gessious: $1-34 <KLED
A;Gross-references: EMBL;X72486; NID:9441440; PIDN:CAA51154.1; PID:9441441
A;Gross-references: EMBL;X72486; NID:9441440; PIDN:CAA51154.1; PID:9441441
C;Superfamily: Immunoglobulin V region: Immunoglobulin homology
C;Keyvords: heterotetramer; Immunoglobulin homology
C;Keyvords: heterotetramer; Immunoglobulin homology
C;Keyvords: heterotetramer; Immunoglobulin homology <IMM>
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Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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A:THIR: Evidence For lateral gene transfer between Archaes and Bacteria from genome A:Reference number: A72200; MUID:99287316
A:Reference number: A72200; MUID:99287316
A:Reference number: A72200; MUID:99287316
A:Reference number: A72200; MUID:99287316
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          A;Molecule type: mRNA
A;Residues: 'L', 3-526 <CUR>
A;Cross-references: EMBL:L41666;
A;Accession: 574307
A;Molecule type: protein
A;Residues: 40-54 <CUI>
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C;Species: Thermotoga maritima (strain MSR8)
C;Species: Il-Jun-1999 stequence_revision 11-Jun-1999 stext_change 21-Jul-2000
C;Date: 11-Jun-1999 stequence_revision 11-Jun-1999 stext_change 21-Jul-2000
C;Accession: F7289
R;MelSon, K, E; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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F:123-126/Region: GTP-binding NKXD motif
F:133-126/Region: GTP-binding SAK/L motif
F:133-125/Region: GTP-binding site: Mg-GTP (Lys, Ser, Thr,
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Pred. No. 14;
2; Mismatches
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Title: Perfect

score:

US-09-544-664-2 138

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protein search, using sw model

Copyright

GenCore (c) 1993

version - 2000

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September 20,

2002, 11:04:28

Scoring table: Sequence:

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Gapext

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No. is the number of results predicted by chance to have a 
greater than or equal to the score of the result being printed, 
s derived by analysis of the total score distribution.
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87 klebsiella
97 komo sapie
86 simian immu
923 caenorhabdl
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923 caenorhabdl
923 caenorhabdl
924 cattus norv
925 secherichia
927 simian immu
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3 homo sapien
4 campylobact
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8 thermotoga
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5 arabidopsis
1 homo sapien
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BAD_MOUSE STANDARD; PRT; 204 AA.

AC 061337;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Bell2-antagonist of cell death (BAD) (Bel-2 binding DE 6) (Bel-xL/Bel-2 associated death promoter).
           "14-3-9 proteins and survival kinases cooperate to inactivate BAD by RT H3 domain phosphorylation.";
RL Mol. Cell 6:41-51(2000).

C: I- PUNCTION: Promotes cell death. Successfully competes for the condition of these proteins with BAX. Can reverse the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the case in the apoptotic pathways.

CC death repressor activity of Bcl-x(L), but not that of Bcl-2 appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

CC is SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein S100All (By Similarity).

CC is SUBUNIT: Forms heterodimers with the anti-apoptotic string.

CC is SUBCELIJIAR LOCATION: Outer microhondrial membrane. Upon phosphorylation, locates to the cytoplasm.

CC is SUBCELIJIAR LOCATION: Outer microhondrial membrane. Upon phosphorylation and serill in response to survival stimul.

CC is DOWANN: Intact BH3 domain is required by BKR, BID, BAX, BAD AND CC is DOWANN: Intact BH3 domain is required by BKR, BID, BAX, BAD AND CC is the survival stimul.

CC is DOWANN: Intact BH3 domain is required by BKR, BID, BAX, BAD AND CC is DOWANN: Intact BH3 domain serill interaction with anti-apoptotic members of the Bcl-2 family.

CC is PROSphorylation at Ser-112 in response to survival stimul.

Subsequent phosphorylation at Ser-155, a site within the BH3 domain, leading the phosphorylation at Ser-155, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotein of cell survival.
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MEDLINE-95136361; Fubhed=7834748;
MEDLINE-95136361; Fubhed=7834748;
Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;
"Bad. a heterodineric partner for Bcl-XL and Bcl-2, displaces Bax and promotes cell (death.")
Cell 80:285-291(1995).
                                                                                                                                                                                                                                                                                                                                                                                                      Datta S.R., Katsov A., Hu L.,
Greenberg M.E.;
"14-3-3 proteins and survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.
MEDILINE-98022383; PubMed-9381178;
Del Peso L., Gonzalez-Garcla M., Page C., Herrera R., Nunez G.;
"Interleukin-3-induced phosphorylation of BAD through the protein kinase akt.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGENESIS OF SERINE RESIDUES,
MEDLINE-20403302; PubMed-10949026;
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Mammalia; Eutheria;
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Mus musculus (Mouse)
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ACEK_SALTY
MDLI_YEAST
ZO3_MOUSE
THIE_PYRAB
THIE_PYRAB
THIE_PYRAB
THIE_PYRAB
SNP4_YEAST
YO30_NPVAC
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THRC\_ARATH
BIM\_HUMAN

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length: 0 length: 2000000000

Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Ser-155

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Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 26; Conservative
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035.17; 070256; 09JHX1;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
BCl2-antagonist of cell death (BAD) (Bel-2 binding component
6) (Bcl-xL/Bcl-2 associated death promoter).
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                                                                                                                                                                       HSU S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;
"Interference of BAD (Bcl.xL/Bcl-2-associated death apoptosis in mammalian cells by 14-3-3 isoforms and Mol. Endocrinol. 11:1858-1867(1997).
                                                                                                                                                                                                                MEDLINE-98034386;
Hsu S.Y., Kaipia /
 MEDLINE-21109372;
Hamner S., Arumae
                                        SEQUENCE FROM N.A.
                                                                                                        D'Agata V., Magro
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                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Rodentia; Sciurognathi;
NCBI_TaxID=10116;
                            TISSUE-Brain
                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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InterPro; IPR000712; Bcl_2
PROSITE; PS01259; BH3; FAL:
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G., Travall S.,
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U., Yu L.-Y., Sun
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A., Zhu L., Hsue
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O PHOSPHORYLATION;
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thi; Muridae; Murinae; Rattus.
 Saarma
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regulator
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Matches 26
                                                                             CONFLICT
SEQUENCE
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-i- FUNCTION: Promotes cell deal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor signaling and the apoptotic pathways.

SUBUNIT: Forms heterodimers with the anti-apoptotic proteins; B

X(I), BCL-2 and BCL-w, Also binds protein $100A10. The Ser-
113/Ser-137 phosphorylated form binds 14-3-3 proteins.

SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
phosphorylation, locates to the cytoplasm (By similarity) bc.
ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;
produced by alternative splicing. They differ only in their C-
terninal regions.

TISSUE SPECIFICITY: Expressed in all tissues tested, including
brain, liver, spleen and heart. In the brain, restricted to
epithelial cemis of the choroid plexus. Isoform alpha is the mc
homears forms.
                                                                                                                                                                                          SIMILARITY: CONTAINS A BCL-3 HOMOLOGY DOMAIN 3 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                       DOMAIN: Intact BH3 domain is required by BHK, BHD, BAK, BAD AND BAX for their pro-apoptootic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

PTM: Phosphorylated on Ser-113 in response to survival stimuli. Subsequent phosphorylation on ser-137 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of ccl survival. Ser-137 is the major site of KMT/PKB phosphorylation, Ser-156 the major site of ART/PKB phosphorylation, Ser-156 the injuriation of protein kinase A (CAPK) phosphorylation (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell. Neurosci. 17:97-106(2001)
FUNCTION: promotes cell death. Successfully competes for binding to Bol-x(L), Bol-2 and Bol-w, thereby affecting of heterodimerization of these proteins with BAX. Can redeath repressor activity of Bol-x(L), but not that of Bol similarity). Appears to act as a link between growth fac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      abundant form.
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WITH 14-3-3 PROTEINS.
5->A: NO HETERODIMERIZATION WITH 1
PROTEINS. NO EFFECT ON HETERODIMER
WITH BCL2 NOR WITH PROTEIN P11.
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4M; 7AFA71DAE9CP4A81 CRC64;
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PHOSPHORYLATION (BY
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LPRPKSAGTATQMRQSASWTRIIQSWWDRNLGKGGSTPSQ
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Score 138; DB 1;
Pred. No. 8.7e-14;
Mismatches 0;
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                                                                                                                                                            "Rationale for Bcl-xL/Bad peptide complex formation from structure, mutagenesis, and biophysical studies.";
Protein Sci. 9:2528-2534(2000).

1- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ottilie S., Diaz J.-L., Horne W., Chang J., Wal
Chang S., Fritz L.C., Oltersdorf T.,
"Dimerization properties of human BAD.";
J. Biol. Chem. 272:30866-30872(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
BCl2-antagonist of cell death (BAD) (BCl-2 binding component
b) (BCl-XL/BCl-2 associated death promoter).
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Q92934; 014803
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Petros A.M., Nette
Mack J., Swift K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Bcl-2 targets the protein kinase Raf-1 to mitochondria."; Cell 87:629-638(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
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                                           SUBCELIJIAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.
TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES
                                                                                                                      receptor signaling and the apoptotic pathways. SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl. x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).
DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AN BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.
                                                                                          similarity)
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                                                                                                         Ser-75/Ser-99 phosphorylated
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interacts with Bcl-2
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EMBL; AF021792; AAB72092.1; --
EMBL; AF031523; AAB89124 1; --
EMBL; BC001901; AAH01901.1; --
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SIMILARITY: CONTAINS 1 BCL-3 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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                                                                                                                                                                                                                                                              Phosphorylation;
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p97279;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Inter-alpha-trypsin inhibitor heavy cl
MRDLINE-97420688; PubMed-9276673;
Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
Precursors of the inter-alpha-trypsin inhibitor in Syrian implications for the evolution of the inter-alpha-trypsin heavy chain family.";
                                                                                                                                                                                                                                                                                  TISSUE-Liver
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mesocricetus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mesocricetus auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chain H2) (HC2).
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; Cricetinae;
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                                                           inhibitor
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RESULT 5
ITH2_MOUSE
ID ITH2_M
AC Q61703
DT 15-JUL
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Best Local
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   ITH2_MOUSE
Q61703;
15-JUL-1998
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CONFLICT
SEQUENCE
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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J. Blochem. 120:145-152(1995)
J. BIOCHEM. 120:145-152(1995)
J. BIOCHEM. 120:145-152(1995)
J. BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
INCLUDING THOSE ON CELL SURFACES IT TISSUES TO REGULATE THE
LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
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"Inter-alpha-trypsin inhibitor and
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(BY SIMILARITY).
V -> Y (IN REF. 2).
E -> I (IN REF. 2).
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Pred. No. 2.6;
5; Mismatches
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GLCNAC...
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Query Match Best Local Matches

Similarity 9; Conser

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15-JUL-1999 (Rel. 38, 1
Inter-alpha-trypsin inl
Chaln HZ).
                                                                                                                                           DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                         CHAIN
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Pfam; PF00092; vwa; 1.
SMART; SM00327; VWA; 1
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Chan P., Risler J.-L., Raguenez G., Salier J.-P.;
"The three heavy-chain precursors for the inter-alpha-inhibitor
family in mouse: new members of the multicopper oxidase protein
with differential transcription in liver and brain.";
      SEQUENCE
                                                               BINDING
                                                                                      CARBOHYD
                                                                                                                    CARBOHYD
                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                       PROPEP
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-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6N; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Mctazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                      Serine protease inhibitor;
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SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
ONE DRIVENIN, INTER-ALPHA-ILKE INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
AND BIKUNIN, INTER-ALPHA-ILKE INHIBITOR (I-ALPHA-I) OF H3 AND BIKUNIN.
TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
THIS SUBSPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
FYM: HEAVY CIAINS ARE INTERLINED MITH BIKUNIN VIA A CHONDROITIN
4-SULPATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE ITIH FAMILY. SIMILARITY: CONTAINS 1 VWFA DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
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PS50234; VWFA; 1.
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                                                                                   N-LINKED
N-LINKED
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BY SIMILAR
CHONDROITÍN 4-SULFATE, CRO (BY SIMILARITY). 

9; 40DB6716433ED9DC CRC64;
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BY SIMILARITY.
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P32449;
01-OCT-1993
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Saccharomycetales;
NCBI_TaxID=4932;
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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30-MAY-2000
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'IR, S181tb; 307.
ISSP, P00086; 1QR7.
ISSP, P000845; ARO4.

InterPro; IPR001785; DAHP_synth_1.

Pfam; PF00793; DAHP_synth_1; 1.

ProDom; PD005060; DAHP_synth_1; 1.

Prolom; PD005060; DAHP_synth_1; 1.

Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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Yeast 9:1131-1137(1993).
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                                                                                                                                                                                                           EMBL; L20296; AAA65607.1;
EMBL; Z36118; CAA85212.1;
PIR; S38185; S38185.
                                                                                                                                                                                                                                                                                                                                               or send an
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jonon F., Biteau N., Aigle M., Crouzet M.;
he complete sequence of a 6794 bp segment located on the
chromosome II of Saccharomyces cerevisiae. Finding of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOEMOLPYRUVATE AND D-ERVTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DECXY-D-ARABIO-HEPTULOSONATE-7-PHOSPHATE (DAMP).

CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nzler M., Paravicini G., Egli C., Irniger S., Braus G.H.; nning, primary structure and regulation of the ARO4 gene, encoding tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate thase from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMAI INDUCTION: BY AMINO ACID STRAVATION, SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
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phosphate + H(2)O.
ENZYME REGULATION: INHIBITED
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113:67-74(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                            and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long
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(Rel. 28, Last sequence up
(Rel. 39, Last annotation
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RA Salanoubat M., Lencke K., Rieger M., Ansorge W., Unseld M.,

RA Fartmann B., Valle G., Bloecker H., Perrez-Alonso M., Obermaler B.,

An Delseny M., Boutry M., Grivell L.A., Mache R., Phigdomenach P.,

An Delseny M., Boutry M., Grivell L.A., Mache R., Phigdomenach P.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Ouetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Ouetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Surin W., Ouetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Surin M., Benes V.,

RA Wincker P., Cattolico L., Weissenbach J., Surin M., Ductier F.,

RA Wincker P., Cattolico L., Weissenbach J., Surin M., Benes V.,

RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,

Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,

RA Navarro P., Collado C., Percz-Percz A., Ottenwelder B., Duchemin D.,

RA Navarro P., Collado C., Percz-Percz A., Ottenwelder B., Duchemin D.,

RA Navarro P., Collado C., Percz-Percz A., Ottett A., Casacuberta E.,

Andel Baan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,

Monfort A., Argirlou A., Flores M., Liguori R., Vitale D.,

Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,

Na Mannhaupt G., Haase D., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
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"The homeotic gene A.PETALA3 of Arabidopsis thaliana encodes a MADS box and is expressed in petals and stamens.";
Cell 68:683-697(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry,
Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P35632; 039003; 12-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence up 16-0CT-2001 (Rel. 40, Last annotation Floral homeotic protein APETALA3.

AP3 OR AT3C54340 OR T1ZE18_30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purugganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
Genetics 151:839-848(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antirrhinum majus.";
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MEDLINE-99126449; PubMed=9927474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LANDSBERG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26:465-472(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.7%;
47.6%;
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No.
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                    Mewes H.-W.,
Jenkins J.,
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RA Creasy T.H. Hass B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Kiyokawa C., Kimura T., Idesawa K., Kawashina K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muzaki A.,
RA Makayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Matanabe A., Yamada M., Yasuda M., Tabata S.,
RY "Sequence and analysis of chromosome 3 of the plant Arabidopsis
Thallana "Sequence and analysis of chromosome 3 of the plant Arabidopsis
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Thallana "RANGCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
FLOWER DEVELOPMENT".
C. -- SIGNINITY" - NOWANGERIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
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FLOWER DEVELOPMENT".
C. -- SIGNINITY" - NOWANGERIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
FLOWER DEVELOPMENT".
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPRO02487; K-box.
InterPro: IPRO02100: MADS-box.
Pfam: PF01486; K-box; 1.
Pfam: PF01319; SRF-TF: 1.
PRINTS: PR00404: MADSOOMAIN.
SMART; SM00432; MADS; 1.
RMUC_PS
Q914U3;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00350; MADS_BOX_1; 1. PROSITE; PS50066; MADS_BOX_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A42095; A42095.
HSSP; P11746; 1MNM.
TRANSFAC; T01776;
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-11 TISSUE SPECIFICITY: EXPRESSED IN PETALS AND STAMENS.
-11 MISCELLANEOUS: AUTOATIONS IN AP3 CAUSE TRANSFORMATION OF PETALS
INTO SEPALS AND STAMINA INTO CARPELS.
-13 SYMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                       107
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AF115799; AAD51888.1;
L; AF115800; AAD51891.1;
L; AF115802; AAD51891.1;
L; AF115804; AAD51893.1;
L; AF115814; AAD51903.1;
L; AF115814; AAD51903.1;
L; AF115814; AAD51903.1;
L; AF115814; AAD51903.1;
L; AL332971; CAB81799.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS
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                                                                                                                                                                                                                                          QRYG-----RELRRMSDEFEGSFK
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                             PSEAE
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Legulati

Lal protein.

3 157

93 159

93 199

27341 MW;
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199
232 AA;
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                             STANDARD
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                                                                                                                                                                                                                                                                                                     Score 51; DB
Pred. No. 1.5;
3; Mismatches
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                             PRT;
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1.5;
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NCBI\_TaxID-4841;

Eukaryota; Rhizomucor RAS3

Fungi;

racemosus (Mucor circinelloides f. lusitanicus).
Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;

Mucor

STRAIN-ATCC 1216B; SEQUENCE FROM N.A.

MEDILINE-91061774; PubMed-1701021; Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.; Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.; Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.; Casale W.L., McConnell D.G. and Fall Interest of the dimorphic fungus Mucor racem which exhibits striking similarity to human ras genes."; Mcl. Cell. Biol. 10:6534-665(1990).

-1- ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE

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RESULT 9 RAS3\_RHIRA

RAS3\_RHIRA

STANDARD; 19, 19, 39,

PRT;

AA

01-AUG-1991 (Rel. 1 01-AUG-1991 (Rel. 1 30-MAY-2000 (Rel. 3 Ras-like protein 3

Last Last Created)

sequence up annotation

update) 205

update

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65 WASERQGREEELRRLASE 82

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9
                                                                                                                          Query Match
Best Local Similarity
Matches 10; Conser
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnegle H.O., Kowalik D.J., Legrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Yuan Y.

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen."
                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                                                                        SEQUENCE
                                                                                                                                                    Pfam; PF02646; DUF195;
DNA recombination; Coil
                                                                                                                                                                                        EMBL; AE004535; AAG04420.1;
InterPro; IPR003798; DUF195.
                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: Involved in DNA recombination (By similarity).-i- SIMILARITY: BELONGS TO THE RMUC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas
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  3 WAAQRYGR--ELRRMSDE
                                                                                                                        453 AA;
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                                    Conservative
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41. Last sequence update)
41. Last annotation update)
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                                                                                                                                                        Coiled
                                                                                                                        51539 MW;
                                                      35.5%;
18
                                                                                                                                                        coil;
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                                                    Score 49; DB
Pred. No. 6.5;
                                                                                                                    il; Complete proteome.
COILED COIL (POTENTIAL).
; le7ea97e82eC5e4b CRC64;
                                      Mismatches
                                                                    1;
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                                                                                                                                                                   STRAIN-MSB8 / DSM 3109;

MEDLINE-99287316; PubMed-10360571;

Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Melson L.B., Clayton R.A., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria fro
                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Last sequence update)
6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
PGL OR DEVB OR TMI154.
Thermotoda marri-1--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                  genome sequence of Thermotoga maritima."; Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09x0NB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M55177; AAA83379.1; -. PIR; C36365; C36365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The Theorem 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 19 and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003577; Ras.
InterPro; IPR001806; Ras_trnsfrmng.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Thermotogales;
                                                                                                                                                                                                                                                                                                                                                                                                                             Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 RELRRMSDEFEGSFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
phospho-D-gluconate.

PATHWAY: SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.

SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GERMLING AND YEAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
ACTIVATING PROTEIN (GAP).
SUBCELLULAR LOCATION: PLASMA MEMBRANE.
DEVELOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS IN
                                                                           CATALYTIC ACTIVITY: 6-phospho-D
                                                                                                                 FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO
                                                                                                 PHOSPHOGLUCONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REIRRMNKEQEGRSKG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P01112; 1PLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00071; ras; 1.
; PR00449; RASTRNSFRMNG.
SM00173; RAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                            Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                           -glucono-l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220
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                                                                           ,5-lactone
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                                                                                                                                                                          and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions on
                                                                           H(2)0
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RESULT
THRC_SO
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Solanum tuberosum (Potato).
Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Srreptophyta; Embryoph
Spermatophyta; Magnollophyta; eudicotyledons; cc
Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9MT28;

O1-MAR-2002 (Rel. 41, Created)

O1-MAR-2002 (Rel. 41, Last sequence update)

O1-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities regulars a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOLTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE00177;
TIGR; TM1154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles reguires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Casazza P., Kaiser S., Willmitzer L., Hoefgen R., Hesse
"Isolation and characterization of a cDNA encoding three
from Solanum tuberosum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000457; Glucosamine_iso.
Pfam; PF01182; Glucosamine_iso; 1.
  SEQUENCE
                            BINDING
                                                CHAIN
                                                                   Chloroplast;
TRANSIT
                                                                                       Threonine biosynthesis; Lyase; Pyridoxal Chloroplast; Transit peptide.
                                                                                                                                    Pfam; PF00291; PALP; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - ! -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Threonine synthase, chloroplast precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                        EMBL; AF082894; AAF74984.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111
                                                                                                                                                                                       nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: Threonine biosynthesis; last step.
SUBUNT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Chloroplast (By similarity).
SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENZYME REGULATION: Allosterically methionine (SAM) (By similarity). PATHWAY: Threonine biosynthesis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphate.
COFACTOR: Pyridoxal phosphate (By similarity)
PROFITATION: Allosterically activated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: 0-phospho-L-homoserine + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _SOLTU
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                                                                                                                                                                                       IPR001926;
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  519
                            196
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  8
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                                                519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteome.
25325 MW;
  57412 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                    B6_enzyme_beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
CHLOROPLAST (BY SIMILARITY).
THREOMINE SYNTHASE.
PYRIDOXAL PHOSPHATE (BY SIMILARITY).
; 114C0979CD231464 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Embryophyta; Tracheophyta;
                                                                                                                   phosphate; Allosteric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,,</u>
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e; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.2.99.2) (TS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by s-adenosyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      threonine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-threonine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthase
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RA Langham S.-A., McCullagh B., Billham L., Robben J.,
RA Van der Schweren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
A Van der Schweren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
A Van der Schweren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Chelen J., Villarroel R., De Clercq R.,
RA Holzer E., Brandt A., Lyne M., Bens Y., Reckmann S.,
RA Clark L., Doggets J., Cronin A., Quall M., Bray Allen S.,
RA Van Montagu M., Rogers J., Cronin A., Quall M., Bray Allen S.,
RA Petett A., Rajandream M.-A., Lyne M., Benes V., Reckmann S.,
RA Petert A., Rajandream M.-A., Lyne M., Benes V., Reckmann S.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller A., Koller R., Echler R.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Hezzl A.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Hezzl A.,
RA Glibbons T., Meber N., Vitale D., Liguori R., Felber R.,
RA Kohabl S., Hiller R., Schmidt W., Bargues M., Terol J., Torres A.,
Perez-Perez A., Purnelle B., Bent E., Johnson S., Teron D., Jesse T.,
RA Perell L., Bedha N., Gooj L., Schutz K., Huang E., Splegel L.,
RA Zaccarla P., Bevan M., Milson R., K., de la Bastide M., Høbermann K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Abbott A., Scott K., Johnson D.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0957B5; 039144;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Threenine synthase, chloroplast precursor (EC
AT4629840 OR F27B13.80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckeert G.,
Pohl T., Duesterhoeft A., Stiekema W., Entlan K.-D., Terryn N.,
Harris B., Ansorge W., Brandt P., Grivell L.A., Rleger M.,
Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Wassilewskija;
MEDLINE-99418329; PubMed=10490396;
Bartlem D., Tamaki Y., Naito S.;
"Genomic nucleotide sequence of the Arabidopsis threonine synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta: Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaless: Arahidanaia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CV. COLUMBIA;
MEDLINE=20083488; PubMed=10617198;
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Reichert B.,
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12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Delseny M., Puigdomenech P., Watson M., Schmidtheini T
t B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft
Hohelsel J., Zimmermann W., Wedler H., Ridley P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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5; Mismatches
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Pred. No.
  Dante M.,
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11;
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  Pepin K.,
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1 NLWAAQRYGRELRRMSD-----EFEGSFKGL

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Query Match Best Local Matches 1

sh 34.8%; Similarity 35.3%; Conservative

Score 48; DB Pred. No. 11; 6; Mismatches

1; L

Length 526

Indels

8; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C., Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A., Chen E., Marra M., Martienssen R., McCombie W.R.;
                                                                                                                                                                                                            EMBL; AB027151; BAA77707.1; -. EMBL; AL050352; CAB43659.1; -. EMBL; AL161575; CAB79742.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Curien G., Job D., Douce R., Dumas "Allosteric activation of Arabidop S-adenosymethionie.",
Biochemistry 37:13212-13221(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Curien G., Dumas R., Ravanel S., Douce R.; "Characterization of an Arabidopsis thallane cDNA encoding an s-adenosylmethioning-sensitive threoning synthase. Threoning synthase from higher plants."; from higher plants."; FEBS Lett. 39:085-90(1996).
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Du H., Ali J., Bergho
                                                                  Chloroplast;
TRANSIT
                                                                                                       Threonine
                                                                                                                      PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
                                                                                                                                                           InterPro; IPR001926; PALP.
                                                                                                                                                                          EMBL; L41666; AAB04607.1; -. PDB; 1E5X; 02-AUG-01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11344332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed-9748328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 402:769-777(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=8706836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            adenosyl-methionine (SAM)
PATHWAY: Threonine biosyn
SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: Pyridoxal phosphate.
ENZYME REGULATION: Allosterically activated
                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)0 - L-threonine
                                                                                 biosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme;
st; Transit peptide; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Threonine biosynthesis; last step.
ΑĀ;
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Berghoff A., Jones K., Dron
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  57776 MW;
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THREONINE SYNTHASE.

PYRIDOXAL PHOSPHATE.

A -> L (IN REF. 3).

B27787A57B882ADO CRC64;
                                                                         CHLOROPLAST
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Cotton M., Joshu C.,
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       FMR2_ANTEL
Q16994;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis; Alternative splicing; Membrane DOMAIN 148 162 BH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF032457; AAC39593.1; EMBL; AF032458; AAC39594.1;
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16-CCT-2001 (Rel. 40, Last annotation update)
BCL2-like protein 11 (BCl2 interacting mediator of cell death).
BCL2L11 OR BIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
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043521; 043522;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last seq
16-0CT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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"Bim: a novel member of the Bcl-2 family that promotes apoptosis.";
BMBO J. 17:384-395(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                               146
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ISOFORM BIMEL.

SUBURIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2

PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BEL-1, AND BHRF-1, DOES

NOT HETERODIMERIZE WITH POAPOPTOTIC PROTEINS SUCH AS BAD, BOX,

BAX OR BAK (BY SIMILARITY)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND CYTOTOXICITY.
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; Bimel (SHOWN HERE) AND Bimel are PRODUCED BY ALTERNATIVE SPLICING.
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                                                                                                                                                                                                                                                                                                           IWIAQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; IPR000712; Bcl_2
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AnthopLeura eLegantissima (Sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae, Actiniidae; Anthopleura.
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J. Biol. Chem. 267:22534-22541(1992)
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"Identification of a novel type of processing sites in the precursor for the sea anemone neuropeptide Antho-RFamide (<Glu-Gly-Arg-Phe-NH2)
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16-CCT-2001 (Rel. 40, Last annotation update)
Antho-Réandde neuropeptides type 1 precursor.
Anthopleura elegantissina (Sea Anemone)
Eukaryota, Metazoa, Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura
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SUBCELLULAR LOCATION: Secreted.
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BRAChydanio rerio (Zebrafish) (Zebra danio).
BRAChydanio rerio (Zebrafish) (Zeraniata; Pertebrata; Buteleostomi; Eukaryota, Metariophysi, Teleostei; Euteleostei, Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBL_TaxID=7955;
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Q919N2:
Q1-OCT-2000
Q1-DEC-2001
Q1-DEC-2001
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Cell Death Differ. 7:509-510(2000).
EMBL; AF231017; AAF66962.2; -.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MUDELINE-20373792; PubMed-10917738; Inobara N., Nunez G.; *Genes *Ath homology to mammalian apoptosis regulators identified in *Genes *Ath homology to mammalian apoptosis regulators.
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                                                                                                            LWAAKKYGQQLRRMSDEFDKGMK 111
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15; Conservative
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RX MEDIJINF98255987; PubMed-9634230;

RX MEDIJINF98255987; PubMed-9634230;

RX COLE S.T., Brosch R., Farkhill J., Garnier T., Churcher C., Harris D.,

RA COLE S.T., Brosch R., Gas S., Barry C.E. III, Tekala F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Badcock K., Basham D., Feltwell T., Gentles S., Hamiln N., Holroyd S.,

RA Hornsby T., Jasels K., Krogh A., McLean J., Moute S., Murpby L.,

RA Hornsby T., Jasels K., Krogh A., McLean J., Moute S., Murpby L.,

RA Hornsby T., Jasels K., Krogh A., McLean J., Moute S., Murpby L.,

RA Hornsby T., Jasels K., Krogh A., McLean J., Moute S., Murpby L.,

RA Hornsby T., Jasels K., Krogh A., McLean J., Moute S.,

RA Hornsby T., Jasels K., Krogh A., McLean J., Moute S.,

RA Badcock K., Basham D., Stall M.A., Rogers J.,

RA Hornsby T., Jasels K., Krogh A., McLean J., Murpby L.,

RA Badcock K., Basham D., Stall M.A., Rogers J.,

RA Hornsby T., Jasels K., Krogh A., McLean J., Murpby L.,

RA RILter S., Seeger K., Skelton S., Squares S., Squares R.,

RA RILter S., Seeger K., Skelton S., Squares S., Squares R.,

RA RILter S., Seeger K., Skelton S., Squares S., Squares R.,

RA RILter S., Seeger K., Skelton S., Squares S., Squares R.,

RA RILter S., Jenong M., Mitchend S., Barrell B.G.;

RA RILter S., Seeger K., Skelton S., Barrell B.G.;

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Mol. Btol. Evol. 16:1037-1045(1999).

EMBL; AF143380; AAF25590.1;

HSSP: p11746; INRM:
InterPro; IPR002407; K-box.
InterPro; IPR002100; MADS-box.
Pfam; PP01486; K-box; 1
Pfam; PP01319; SRP-TF; 1
Pfam; PP00319; SRP-TF; 1
PR187F; PM00404; MADSDOMAIN.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APETALAS (FRAGMENT).
Arabidopsis Jyrata.
Bukaryota; Vifidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnalupphyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-DEC-2001 (TEMBLIEL 19). Last annotation update)
HYPOTHETICAL 24.1 KNA PROTEIN CC39.03C.
RY2014 OR MTCY39.03C.
MYCODOCCETION tuberculosis.
MYCODOCCETIAN tuberculosis.
Bacteria; Firmicules; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriae;
MCBI_TaxID-1773;
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MEDLINE-99404148; PubMed-10474900;
Lawton-Rauh A.L., Buckler E.S. IV, Puri
Patterns of molecular evolution among
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C STRAIN-CV. GR-3, AND CV. CHI-1;
C STRAIN-CV. GR-3, AND CV. CHI-1;
X MEDLINE-99126449; PubMed-9927474;
X MEDLINE-99126469; PubMed-9927474;
Y MOJECULAT POPULATION 9900-ELICS OF FLORALA3 and PISTILLY
T from the equilibrium-neutral model at the APETALA3 and PISTILLY
T genes of Arabidopsis thaliana.";
Genetics 15:1839-848(1999)
C -1- SUBCLIURAN LOCATION. WIGLEAR (BY SIMILARITY).
C -1- SUBCLIURAN LOCATION. WIGLEAR (BY SIMILARITY).
C -1- SUBCLIURAN LOCATION. WIGLEAR (BY SIMILARITY).
R FAILS 15:1839-848(1992).
R EMBL: ARI15789; AAD5187-1; ---
R HSSP: PIJ746; MAD5187-1; ---
R INTERPORT | TROOZEO, MADS-DOX.
R INTERPORT | TROOZEO, MADS-DOX.
R Pfam: PPO1466; MADSDOMMIN.
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Matches 12
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sparmatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosiceurosids II, Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                    095072 PRELIMINARY; PRT; 232 AA.
095072;
011.MAY-2000 (TEMBLEG1 13, Created)
01.MAY-2000 (TEMBLEG1 13, Last sequence update)
01.DEC -001 (TEMBLEG1 19, Last annotation update)
FIGNAL OMBOTIC PROFILE AP3.
APETRALA3
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O998703: O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 17, Last annotation update)
FLORAL HOMEOTIC PROTEIN AP3.
APETALA3.
APETALA3.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnollophyta; endicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Franscription regulation.
SEQUENCE 232 AA; 27340 MW; 6690703F9F9CFD63 CRC64;
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l Similarity 44.4%;
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**C STRAIN-CV. L1-8;

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O9S021: 1, Created)
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-BEC-2001 (TrEMBLrel. 19, Last annotation update)
PLORAL HOMEOPIC PROTEIN AP3.
APBIRLA3.
ARBITIOPSIS thaliana (Mouse-ear cress).
APBIRLA3.
Spermatophyta; Magnoliophyta; embryophyta; Tracheophyta; Embryota; Vrisiciplantae; Streptcphyta; Embryophyta; Rosidae; eurosids II, Brassicales; Brassicaceae; Arabidopsis.
CEL_TaxID-3702;
PROSITE; PS000350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNN-binding; Nuclear protein; Transcription regulation.
SEQUENCE 232 AA; 27286 MW; 66976305888863E3 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 ORLGECLDEUDIQEURRLEDEMENTEK 133
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Q1-MAY-2000 (TrEMBLE-1. 13, C
Q1-MAY-2000 (TrEMBLE-1. 13, L
Q1-UN-2001 (TrEMBLE-1. 17, L
FLORAL HOMEOTIC PROTEIN AP3.
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O1-MAY-2000 (TEMBLES) 13 La
O1-MAY-2000 (TEMBLES) 13 La
O1-DEC-2001 (TEMBLES) 19 LE
FLORAL HOMEOTIC PROFEIN AP3.
APETMLAS.
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InterPro; IFR002180; MANS-box.
InterPro; IFR002180; MANS-box.
Pflam; PF01486; K-box; 1.
Pflam; PF00319; SRP-TF; 1.
PRINTS; PF00404; MANSEDWAIN.
SMART; SM00432; MANS; DX.
PROSITE; PS00350; MANS, BOX. 1.
PROSITE; PS0066; MANS, BOX. 2: 1.
PROSITE; PS0066; MANS, BOX. 2: 1.
DNA-binding; MClear protein; Transcription regulation.
SEQUENCE 232 AA; 27342 MW; BDFDCB59B73F4601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILKES-99126449; Pubmed-9927474;
Purugganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci, Departures
"Molecular population genetics of floral homeotic loci, Departures
from the equilibrium neutral model at the APETALA3 and PISTILLATA
genes of Arabidopsis thaliana.";
Genetics 151:839-848(1999).
-1- SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS
EMBL; AF11586(5 AAD51895.1) -.
HSSP: PI1746; MRM.
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                                                                       APPYALA3.
Arabidopais thaliana (Mouse-ear cress).
Arabidopais thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Core endicots; Rosis
Spermatophyta; Magnoliophyta; eudicotyledons; core endicots; Rosis
eurosids II; Brassicales; Brassicaceae; Arabidopsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
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12; Conservative
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Pred. No. 11;
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OSSQ18:
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WHY-2000 (TrEMBLrel. 13, Last sequence update)
11-UN-2001 (TrEMBLrel. 17, Last annotation update)
11-DRAL, HOMEOTIC PROTEIN AP3.
APETALA3.
Arabidopsis thallana (Mouse-ear cress).
Arabidopsis thallana (Mouse-ear cress).
Arabidopsis thallana (Mouse-ear cress).
Spermatophyta; Hagiolatophyta; Endons; core eudicots; Rosidas;
eurosids II, Brassicales; Brassicaceae, Arabidopsis.
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PURUGGARAN M.D., SUDDITE S. Of FLORAL homeotic loci. Deprive the equilibrium-neutral model at the APETRIA3 and PIST genes of Arabidopsis thaliana.*;
Genetics 15:1839-848 (1999).
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Best Local S
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OSSQ15;
OSSQ15;
OSSQ15;
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O1.MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1.MAY-2001 (TrEMBLrel. 19, Last annotation update)
O1.MC-2001 (TrEMBLrel. 19, Last annotation update)
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Pfam: PF01466; K-box: 1.

Pfam: PF01466; K-box: 1.

Pfam: PF00319; SRF-TF; 1.

PRINTS: PR00404; MADS-MOX_1.

PRINTS: PR00432; MADS: 1.

PR051TF; PS00550; MADS: BOX_2. 1.

PR051TF; PS0066; MADS: BOX_2. 1.

PR051TF; PS0066; MADS: BOX_2. 1.

PR051TF; PS0066; MADS: BOX_2. 1.

PR051TF; PS0066; MADS: BOX_2. 1.

PR051TF; PS0066; MADS: BOX_2. 1.

PR051TF; PS0066; MADS: BOX_2. 1.

PR051TF; PS0066; MADS: BOX_2. 1.

PR051TF; PS0066; MADS: BOX_2. 1.

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APETALA3.

ARENTALA3.

ALTOMODESS thallana (Mouse-ear cress).

ENBATYOLA 'YITIGLJAINTSE, SETEPEOPHYLA: EMBLYOPHYLA:

ENBATYOLA 'YITIGLJAINTSE, SETEPEOPHYLA: EMBLYOPHYLA:

ESPERMALOPHYLA: Magnoliophyla: eudicotyledons; core eu
eurosids II, Brassicales; Brassicacese; Arabidopsis.

CHEF_TEXID-3702;
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InterPro; IPR
    Q9KGW3
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STRAIN-CV. KAS-1;
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udicots; Rosidae;
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J. Gen. virol. 79:1809-1814(1998).
EMEL, APD1599; AAC5991.1;
InterFro; IPR00777; GP120.
Pfam; PF0051; GP120.
Pfam; PF0051; GP120. 1.
AlDS; Coat protein; Glycoprotein.
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037055; 01-CAN-1998 (TrEMBLICE). 05, Created)
01-CAN-1998 (TrEMBLICE). 05, Last sequence update)
01-DEC-2001 (TrEMBLICE). 19, Last annotation update)
01-DEC-2001 (TrEMBLICE). 19, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
ENVELOPE GLYCOPROTEIN (FRAGMENT).
ENV.
CHURSES; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID-11723;
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Bacteria: Proteobacteria: gamma subdivision: Pseudomonadaceae:
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O1-DEC-2001 (TrEMBLrel. 19, Last ann
NADH DENTAROGENASE I SUBUNIT G.
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STRAIN-SIVAMUPPI185;
MEDIINE-98343740; PubMed-9680146;
van Rensburg E.J., Engelbrecht S.,
Stander T., Chege G.K.;
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SEQUENCE
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RESULT 15

Q9HK29

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RY W. D.LINE-20504483; PubMed-11016950;
RN MSDLINE-20504483; PubMed-11016950;
RA Shukla H.D., Lasky S.R., Ballya N.S., Thorsson V., Sbrogna J.,
RA Shukla H.D., Lasky S.R., Ballya N.S., Thorsson V., Sbrogna J.,
RA Shukla H.D., Lasky S.R., Ballya N.S., Thorsson W.J., Hough D.W.,
RA Hell R., Carl R., Danson M.J., Hough D.W.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Lesthauser T.A., Pock R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Isenbarger T.A., Peck R. F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halbacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A., 97:1315-13181(2000),
CC (AEC TRANSPORTERS),
CR EMBL, ACCESSONO, 11;
CR EMBL, ACCESSONO, 11;
CR EMBL, ACCESSONO, 11;
CR EMBL, CRUSSONO, ACC, Transportr.
CR InterPro., IPRO0393; AAA.
DR InterPro., PRO010187; APC, Transportr.
CR Pros., PRO0005; AAC, 17ANSPORTER; 1.
DR SMART; SMO0382; AAA; 1.
CR PROS.TTE, PSO0311, AEC_TRANSPORTER; 1.
CR ATP-blanding; Complete protecome; Transport.
CR ATP-blanding; Complete protecome; Transport.
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O9HNZ9
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O1+ARR-2001 (TIEMBLIEL 15, Created)
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O1-CT-2001 (TIEMBLIEL 18, Last sequence update)
SPERMIDINE/PUTRESCIME ABC TRANSPORTER.
FOTAZ OR VRS18716.
FOTAZ OR VRS18716.
Halobacterium sp. (strain NEC-1).
Archbee; Euryarchaeota; Halobacteriales; Halobacterium
CBL_TAXID=64091;
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score greater than or equal to the score of the result being printed,
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Novel human diagno	Murine Bim-L mutan	Murine Bim-L mutan	Murine Bim-L mutan	Murine Bim-L mutan	Murine Bim-L mutan	Murine Bcl-2 inter	Murine Bcl-2 inter	Arabidopsis thalia	BH3 domain of huma		bc1-x(L)/bc1-2	Bad-DTTR apoptosis	Longer murine BAD	BAD	Mutant BCL-XL/BCL-	BCL-		Murine BCL-XL/BCL-	·	н	Mutant BCL-XL/BCL	BCL-XL,		an		Bcl2 polypeptide	N		Bcl2 polypeptide	bcl-x(L)/bcl-2	Bcl2 polypeptide	Mouse BAD BH3 doma	BAD BH3 domain

## ALIGNMENTS

## BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoproliferative condition; arthritis; autoimmune disease; therapy. 07-OCT-1997; 26-SEP-1997; 02-JUL-1999 (first entry) AAY05421; AAY05421 standard; peptide; 16 WPI; 1999-255058/21 08-APR-1999 W09916787-A1. Homo sapiens Human BAD BH3 domain. Korsmeyer 22-SEP-1998; (UNIW ) UNIV WASHINGTON Н SJ; 97US-0946039 97US-0060133 98WO-US19765 A.

Bcl homology domain 3 polypeptide

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RESULT AAB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 702 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A AB 7029 A
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Best Loc
Matches
The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n = 1-10; x = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or x = 0 or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobretyl, cyclopentyl, cyclobexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; pastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                           New paptide conjugates for modulating apoptosis or for inhibiting ceil lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc alkyl group, or benzyl. The peptides ARBT7001-837058 represent examples cc of the peptide portion of the conjugate. The peptides represent analogues cc of the speptide portion of the conjugate. The peptides represent analogues cc of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BHJ domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2) mediated blockage of capoptosis in cancer cells. It is also useful for Inhibiting Bcl-2 (G function, in particular, the peptide conjugate is useful for treating a subject affilted with a cancer cantracterized by cancer cells that cancer self-2. The cancer includes prostate, colorectal, gastric, con-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or cacute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by concers accurate is also useful for treating disorders characterized conjugate is also useful for treating disorders acquired conjugate is also useful for particular particular increased apoptosis, e.g. neurodegenerative disorders acquired conjugate is also useful for treating disorders acquired conjugate is also useful for treating disorders acquired conjugate is also useful for treating disorders acquired to the minus of the peptide conjugate is also useful for treating disorders acquired conjugate is also useful for treating disorders acquired the peptide conjugate is also useful for treating disorders acquired the conjugate is also useful for treating disorders acquired the conjugate is also useful for treating disorders acquired the conjugate is acquired the conjugate is acquired the conjugate is acquired to the conjugate is acquired the conjugate is acquired to the conjugate is acquired to the conjugate is acquired to the conjugate is acquired to the conjugate is acq
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                                                                                                                                                                                                                                    Novel polymuclectide encoding a BBC3 protein which is useful for modulating apoptosis, especially in the treatment of cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammal; apoptosis; cel
apoptosis inhibition;
                                                                                                                                                                                               Disclosure; Fig 4; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               (CLON-) CLONTECH LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia
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                                                                                                                                                                                                                                                                                                                                                         Yin
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                                                                                                                                                                                                                                                                                                                                                       Chittenden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell death; BBC3;
on; malignant cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homology domain 3 domain.
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Pred. No. 9.3
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apoptosis promotion;
; autoimmune disease.
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).3e-08;
s 0;
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The present sequence is the mammalian Bad Bcl-2 homotopy domain 3 (BH3) domain, which was used in a sequence alignment with the same domain of a putative version of the mammalian apoptosis regulator BBC3, which was designated BBC3-ORF2. The BBC3 protein,

nucleic acids and antibodies are suitable for use in death or for preventing apoptosis in malignant cells

promoting cell and those causing

apoptosis

for preventing ne diseases.

Sequence autoimmune

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RESULT
AAB70371
ID AAB
                                                                               The present invention describes an isolated or synthetic polypeptide (1) comprising a less than full length anino acid sequence of a mutant (CC Ed-Nahol-2 associated ceal death regulator polypeptide (BAD) or its fragment, which contains anino acid substitutions at Serils of a mutant BAD, Serits of a mutant BAD (longer mutant BAD) or Serils of a mutant BAD, shorter mutathe BAD). (1) has immunostimulant, neuroprotective, contexpic, antivital, antification, and demandation and describes and cantenthritic, antificamentory and immunosuppressive activities and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and compounds and device of activity that promote cell survival or apoptosis. Other uses include cinducing or inhibiting apoptosis in a cell. Candidate compounds (contexpined and (mutant) BAD polypeptides are useful in treating cinducing or inhibiting apoptosis in a cell. Candidate compounds (contexpined and (mutant) BAD polypeptides are useful in treating cinducing or inhibiting apoptosis in a cell. Candidate compounds (contexpined and (mutant) BAD polypeptides are useful in treating cinducing or inhibiting apoptosis, are susful in a cell. (candidate compounds of contexpined and (mutant) BAD polypeptides are useful in treating cinducing or inhibiting apoptosis, are thrills, infertility, intal infections, contexpined and contexpined sections, are thrills, infertility, intal infections, and contexpined action and contexpined sections, are thrills, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, infertility, 
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mutant Bc1-XL/Bc1-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Seril8, Seri55 or Seri13 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2hou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bel YM./Bel-2 associated cell death regulator: BAD; matrait; apoptosis; immunostimulant; neuroprotestive; noctopic; antiischeemic; valnacray; cytostatic; antiviral; antistrbritic; antiinflammatory, wound bealing; immunosipicrestive; apoptosis inducer; apoptosis inhibitor; cancer; immunosipicrestive; apoptosis inducer; apoptosis inhibitor; cancer; immunosipicrestive; apoptosis inducer; apoptosis inhibitor; cancer; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative; condition; inflammator; arthritis; infertility; lymphoproliferative; condition; inflammator; arthritis; infertility; lymphoproliferative; condition; inflammator; arthritis; infertility; lymphoproliferative; condition; inflammator; arthritis; infertility; lymphoproliferative; open condition; inflammator; arthritis; infertility; lymphoproliferative; open condition; inflammator; arthritis; infertility; lymphoproliferative; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condition; open condi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-138734/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (APOP-) APOPTOSIS TECHNOLOGY INC
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                                                                present invention
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Pred. No. 1.66
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. 1.6e-07;
ches 0;
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AAW32476
ID AAW3
RESULT
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                                                                          AAW55779;
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Sequence

26

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17-JUL-1998

(first entry)

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Query Match
Best Local S
Matches 16
                                                                                                                                          Query Match
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Matches 16
                                                                                                                                                                                                                                              The present sequence represents a protein of 166 amino acids. The sequence is disclosed as being a protein called mack which regulates cell death through interaction with Bcl-2. The DNA may be used for the production of the recombinant protein, which can be used in unspecified therapeutic or diagnostic procedures, as a molecular weight marker, and to raise antibodies that can be used in unspecified diagnostic or therapeutic applications and to reduce or eliminate the biological activity of the BBC5 protein in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-447980/41
N-PSDB; AAT91561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BBC6 protein for regulating cell death.
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AAW55779
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Column 11-12; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated BBC6 gene \,{}^{\circ} encodes a protein that regulates through interaction with Bcl-2
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grygreirrmsdefvd 121
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                                                                                                                                                           Similarity
  standard;
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Conservative
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llarity 100.0%;
Conservative (
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  Protein;
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Pred. No.
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Pred. No. 1.2e-05;
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1.5e-07;
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                                                                                                                                                                          Length 166;
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                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                cell death
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RESULT AAB13512
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XX Homc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the human Bcl-xL/Bcl-2 associated death promoting polypeptide, Bad, the binding of which to Bcl-xl caults in the induction of programmed cell death, i.e. apoptosis. Bad can be used in screening assays for compounds to treat or prevent diseases characterised by apoptotic cell death, such as neurodegenerative disorders, e.g. Alzbelmer's and Parkinson's disease, amystrophic lateral sclerosis, rettricks pigmentosa and cerebellar degeneration, and myslodysplastic syndromes, e.g. aplastic anaemis and ischemic injury including myocardial infarction, stroke and reperfusion injury. Assays can also be used to obtain apoptosis enhancing compounds to treat or prevent diseases characterised by the loss of apoptotic cell death, such as concers, e.g. systemic lupus erythematosus and immune-mediated observes, e.g. systemic lupus erythematosus and immune-mediated plomerulonephritis and viral infections, e.g., heppewrius, or approach of apoptoric or adenovirus infections. Bad can also be used for prevent or and disease.
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Best Local S
Matches 16
                                                                Human; cell proliferation; APOP-1;
trauma; neurodegenerative disease;
                                                                                                                                 Human cell proliferation protein APOP-1.
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                        Homo sapiens
                                                                                                                                                                                                                                    AAB13512;
                                                                                                                                                                                                                                                                               AAB13512 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IDUN-) IDUN PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                 108 grygrelrmsdefvd 123
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Local Similarity 100.0%;
Local Similarity 100.0%;
ses 16; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene mediating apoptosis - used to develop products for treating neurodegenerative disease, cancers or autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1998-217267/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 AA;
                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                               protein; 168 AA.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                             cancer; inflammation; infection;
ischaemic injury; wasting disease.
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1.2e-06;
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                                                                                                                                                                                                                                                CC The present sequence is the human APOP-1 protein. This protein, which CC shares structural and chemical homology with Bel.2, is involved in cell CC proliferation. Its coding sequence was isolated by screening a symovial tissue cDNA library using a computer search for anino acid sequence CC alignments. The gene and protein can be used in the treatment of various cancers, disorders with associated in the such as Addison's CC cancers, adult respiratory distress syndrome, allergise, anemia, asthwa, cC disease, adult respiratory distress syndrome, allergise, anemia, asthwa, CC atheroscierosis, Crohn's disease, ulcerative collis, diabetes mollitus, caphysema, glomecrulonephritis, gover disease, irritable bowel CC syndrome, lupus crythomatosus, multiple sciencesis, myasthenia gravis, CC myocardial or pericardial inflammation, osteoporosis, rheumatoid compositis, sjogren's syndrome and autolmune thyroiditis, complications of cancer, haemodialysis and extracorporeal circulation, infections, content of sorders with associated apoptosis including AIDs and other traums, disorders with associated apoptosis including AIDs and other the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the con
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Best Local :
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                                                                                                                                                                                                                                            Sequence
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N-PSDB; AAA63332.
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Example 8; Fig 1; 58pp; English.
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                                                                                                                 16;
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                                                                                                                                  Similarity
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ilarity 100.0%;
Conservative 0
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Pred. No. 1.2e-06;
Pred. No. 1.2e-06;
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В
                                                                         Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; noctropic; antiischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
  WO200110888-A1
                                                                                                                                                                                                         Human
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                               Synthetic
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an isolated or synthetic polypeptide (1) comprising a less than full length amino acid sequence of a mutant CC Boll NL/Boll 2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at serils of a human CC BAD, Seril5 of a murine BAD) (1) has immunostimulant, neuroprotective, mootropic, antisischaemic, vulnerary, cytostatic, antiviral, contains an apoptosis inducer or inhibitor. BAD polypeptides and compounds and apoptosis inducer or inhibitor. BAD polypeptides and compounds and apoptosis inducer or inhibitor. BAD polypeptides and compounds and drugs of oplynucleotides can be used for screening candidate compounds and drugs inducting or inhibiting apoptosis in a cell. Candidate compounds compounds and compounds and compounds and compounds and compounds and compounds of inducting or inhibiting apoptosis in a cell. Candidate compounds conditions of inducting or inhibiting apoptosis in a cell. Candidate compounds conditions are useful in treating communodeficiency diseases, neurodegenerative diseases, ischaemic cell death, reperfusion cell death, sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the present sequence represents a specifically contoning the
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Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-138734/14.
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                                            05-JUN-2000; 2000WO-US15449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Bad protein.
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. 1.2e-06;
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Human, cell proliferation; APOP-1, APOP-2, APOP-3, apoptosis; cancer; brain cancer; breast cancer; alzheimer; disease; Parkinson's disease; inflammation; allergy; gout; osteoarthritis; bronchitis.

Amino acid sequence of protein associated with cell proliferation-1.

Modified-site

/note= 16..19

Modified-site

Location/Qualifiers 10..13

Modified-site Modified-site

/note-80..83 /note= 34..36

/note-

"potential casein kinase II phosphorylation site" "potential protein kinase C phosphorylation site" "potential casein kinase II phosphorylation site" "potential casein kinase II phosphorylation site"

Modified-site

28-AUG-2001

US6281334-BI Modified-site Modified-site

/note=

"potential protein kinase C phosphorylation site" "potential cAMP- and cGMP-dependent protein kinase phosphorylation site"

"potential casein kinase II phosphorylation site"

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124..126 /noteHomo sapiens

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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to methods of altering the polypeptide levels in a cell. using proteins selected from S-phase kinase associated proteins a lead 2 (SKPI, SKP2) SKP2-like proteins (SF) and CUL-1 (a member of the cullin/ CDC53 family of proteins). The method is useful for altering the level of p27, cyclin B. Max, Mad, c-Myc, MMW2, P53, Bax, Bad or Bol-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting thmours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG67688 standard; Protein; 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang H, Tsvetkov LM,
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)B; AAC84599.
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Pred. No. 1.2e-06;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; nootropic; antilschaemic; vulnerary; cyrostatic; antilvral; antiarribritic; antilural; antiarribritic; antilural; antiarribritic; antilural; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infection; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a human protein which is associated with cell proliferation, designated APOP-1. The specification also describes APOP-2 and APOP-3. The APOP polypeptides are useful for diagnosing, preventing or treating disorders associated with abnormal cell proliferation and apoptosis. The polypeptides and composition are particularly useful for treating or preventing cancer (e.g. brain or breast cancer), a disorder associated with an increase in apoptosis (e.g. Alzheimer's disease or Parkinson's disease) or inflammation (e.g. allorgies, gout, osteoarthritis or bronchitis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides associated with cell proliferation, useful for preventing or treating cancer (e.g. brain cancer), a disorder associated with an increase in apoptosis (e.g. Alzheimer's disease) inflammation (e.g. gout)
                                Zhou
                                                                                                                                                 28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                     WO200110888-A1
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)B; AAH78430.
                                                                                       APOPTOSIS TECHNOLOGY
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Pred. No.
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. 1.2e-06;
ches 0;
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RESULT 1

AABTOLM 1

AABTOLM 2

XX AABT 2

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Best Local S
Matches 15
                                                                                   (APOP-)
                                                                                                                                              28-MAY-1999;
                                                                                                                                                                                                    30-MAY-2000;
                                                                                                                                                                                                                                                           15-FEB-2001
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                                                                                       APOPTOSIS TECHNOLOGY
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The present invention describes an isolated or synthetic polypeptide (1) comprising a less than full length amano acid sequence of a mutant CC Bcl XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Serila of a human CC BAD, Seril5 of a murine BAD) (or per murine BAD) or Seril3 of a murine CC BAD, Seril5 of a murine BAD) (i) has immnostimulant, neuroprotective, notropic, antischemic, vulnerary, cytostatic, antiviral, controlic, antiinflammatory and immunosuppressive activities, and CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and cut can be used for screening candidate compounds and drugs of oplynucleotides can be used for screening candidate compounds and drugs (activity that promote cell survival or apoptosis. Other uses include inducting or inhibiting apoptosis in a cell. Candidate compounds conducting or inhibiting apoptosis in a cell. Candidate compounds conducting or inhibiting apoptosis in a cell. Candidate compounds conducting or inhibiting apoptosis in a cell. Candidate compounds conducting or inhibiting apoptosis in a cell. Candidate compounds conducting or inhibiting apoptosis in a cell candidate compounds conducting or inhibiting apoptosis in a cell candidate compounds conduction. The prefinsion cell death, reperfusion cell death, wound healing, cancer, viral infections, limphoproliferative conditions, arthritis, infertility, inflammation and cutoimmune diseases. The present sequence represents a BAD BHJ domain constitution in the present sequence represents a BAD BHJ domain constitution in the present sequence represents a BAD BHJ domain constitution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 9; Page 92; 157pp; English
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Similarity
Conservative
       90.48;
        Score 75; [
Pred. No. 2.
Mismatches
        DB 22;
2,6e-06;
              Length
0
Gaps
0
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AAB70380 standard; Peptide; 20

ζ

region related phosphopeptide SEQ ID NO:18.

Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; nootropic; antilistalenic; vulnerary; cyrostatic; antivital; antiarthritic; antivital; antiarthritic; antivital; antivital; antivital; antivital; antivital; antivital; antivital; antivital; antivital; antivital; cancer; thmwwnosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.

2000WO-US11864

99US-0136783

INC

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The present invention describes an isolated or synthetic polypeptide (CC Comprising a less than full length mainto acid sequence of a mutant CC R12/R261-2 associated cell death regulator polypeptide (BAD) or in the control of a mutant CC fragment, which contains amino acid substitutions at serila of a human CC BAD, Seril5 of a murine BAD (longer murine BAD) or Seril3 of a murine CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective, controlled, antischaemic, vulnerary, cytostatic, antiviral, can be used as an apoptesis inducer or inhibitor. BAD plypeptides and complymucleatides can be used for screening candidate compounds and drugs inducting or inhibiting apoptesis in a cell. Candidate compounds and drugs inducting or inhibiting apoptesis in a cell. Candidate compounds and complymunostivity that promote cell survival or apoptesis, other uses include inducting or inhibiting apoptesis in a cell. Candidate compounds compounds and compounds and continuous diseases, neurodegenerative diseases, ischaemic cell death, reperfusion cell death, wound healing, cancer, vital infections, continuous diseases. The present sequence represents a BAD BH3 domain cellone present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 15
                                      Korsmeyer
                                                                                          07-OCT-1997;
26-SEP-1997;
                                                                                                                                  22-SEP-1998;
                                                                                                                                                            08-APR-1999
                                                                                                                                                                                       W09916787-A1
                                                                                                                                                                                                                Mus
                                                                                                                                                                                                                                                   BH3 domain; cell death agonist; bot homology domain; BCL-2 family, apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoproliferative condition;
                                                                                                                                                                                                                                                                                                         Mouse BAD BH3 domain.
                                                                                                                                                                                                                                                                                                                                    02-JUL-1999
                                                                                                                                                                                                                                                                                                                                                             AAY05422;
                                                                                                                                                                                                                                                                                                                                                                                    AAY05422 standard; peptide; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apoptosis,
Serll3 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mutant
useful for
                                                               (UNIW ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                               13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QRYGRELRRMSDEFVD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bcl.*X/RGcl-2 Associated Cell Death Regulator polypeptide, screening for candidate compounds which induce or inhibit comprises amino acid substitutions at Seril8, Seri55 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 92; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                          97US-0946039.
97US-0060133.
                                                                                                                                  98WO-US19765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.48;
                                                                                                                                                                                                                                         disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 75; DB 22;
Pred. No. 2.9e-06;
0; Mismatches 1
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                                                                                                                                                                                                                                       therapy
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The invention relates to a peptide conjugate having the formula:  $(R\cdot X)n$ -peptide where n=1-16; X=C=0, when the  $R\cdot X$  group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X=O or OH, when the  $R\cdot X$  group is attached to the C-terminus of the peptide, or a conside chain of the peptide, where the side chain functional group is OH or

New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (BLI-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer

Claim 18;

Page 18;

74pp;

English.

07-APR-1999; 06-APR-2000;

9905-0128202

2000WO-US09352

(UYJE-) UNIV JEFFERSON THOMAS

WO200059526-A1

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Wang J,

Zhang Z,

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2000-679325/66

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EX SX COO COO COO COO X X X
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the BH3 domain of mouse BAD.
The invention relates to a bcl homology domain 3 (BH3 domain),
The invention relates to a bcl homology domain 3 (BH3 domain),
derived from a proapoptotic member of the BCL-2 family. The
BH3 polypeptide can be used in a method for promoting apoptosis in a
BH3 polypeptide can be used in a method for promoting apoptosis in a
target cell, especially where the cell is a cancer cell a virus infected
cell or an autoautibody producing cell. The BH3 polypeptide can be used
in therapeutic compositions for treating disease including cancer, other
lymphoproliferative conditions, arthritis, inflammation, and autoimmune
diseases, which may result from the down regulation of cell death
                                                       Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardian; Bcl-2 superfamily; BH3 domain; cell death agonist; BH3; apoptosis modulation; B cell Jymphomo/Jeukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; neurodegenerative disorder; AIDS; stokenea; lymphocytic leukemia; neurodegenerative disorder; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bcl homology domain 3 polypeptide
Homo
                                            stroke;
                                                                                                                                                                                              Bcl2 polypeptide BH3
                                                                                                                                                                                                                                          28-FEB-2001
                                                                                                                                                                                                                                                                                                                           AAB37028 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulation.
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                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                              peptide;
                                            infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                domain peptide #28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.0%;
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ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 16
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RESULT
AAR95166
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The sequences given in AAR95155-67 represent epitopes derived from the murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see also AAR95168). Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad has been found
                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                          Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter weeful to treat nepplasia and apoptosis and to identify agents inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell deat cytokine deprivation; Lr-3 dependent cell line; immunodeficiency; AIDS; neurodegenerative disease; senescence; ischaemia; neoplasia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-1994;
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Local Similarity ivv.
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
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                                                                                                                                                                                                               Page 103; 130pp; English
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Mismatches 0;
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Best Local :
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                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                      senescence or ischaemia.
                                                                                                                                                                                        Local Similarity
                                                                                      14:
                                                                                                                                                                                                                                                                  23 AA;
                                                                                                                                                                       Conservative
                September 20, 2002, 10:35:58
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                                                                                                                                                                                     Score 73;
Pred. No.
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7.6e-06;
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time: completed: me: 426 sec

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Perfect score:
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Listing first 45 summaries
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-985-335-7
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US-09-410-372-7
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US-09-410-372-7
US-09-410-372-7
US-08-61-479-10
US-08-733-505A-55
US-08-733-505A-57
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Sequence 1, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 10, Appl
Sequence 50, Appl
Sequence 55, Appl
Sequence 57, Appl
Sequence 57, Appli
Sequence 58, Appl
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Sequence 2, Appli
Sequence 1, Appli
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
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3, Appli
26, Appl
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34, Appl
69, Appl
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Sequence 33, Appl		Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 425, App	Sequence 40, Appl	Sequence 12, Appl	Sequence 110, App	Sequence 10, Appl	Sequence 1, Appli	Sequence 8, Appli				ъ		

ALIGNMENTS

## RESULT 1 ... US-08-665-617-2 ... sequence 2, Application US/08665617 ... Patent No. 5663316 MOLECULE TYPE: protein US-08-665-617-2 GENERAL INFORMATION: TELEPHONE: (352) 375-8100 TELEFAX: (352) 372-5800 INFORMATION FOR SEQ ID NO: 2: APPLICANT: Xudong, Yin TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death NUMBER OF SEQUENCES: 2 COMPRESSORVED TO THE PROPERTY OF THE PROPERTY REGISTRATION NUMBER: 31,794 REFERENCE/DOCKET NUMBER: CL. TELECOMMUNICATION INFORMATION: TELECOMMUNICATION (352) 375-8100 ATTORNEY/AGENT INFORMATION: NAME: Saliwanchik, David REGISTRATION NUMBER: 31,7 COMPUTER: IRM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CORRESPONDENCE ADDRESS: SEQUENCE CHARACTERISTICS: ADDRESSE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA ZIP: 32606 APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 530 TOPOLOGY: STRANDEDNESS: LENGTH: amino acid 166 amino acids linear single US/08/665,617 CL-8

Query Match
Best Local Similarity
watches 16; Conserv:

Conservative

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Mismatches

100.0%;

Score 83; Pred. No.

1.5e-07; DB 1;

Length 166; Indels

0; Gaps

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                                                                                                                                                                                                                                                                                                  Patent No. 6080847
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 APPLICANT: APPLICANT: APPLICANT:
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
TOPOLOCY: lin-
WOLECULE 1
                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                         APPLICANT: Shah, PUTV1
APPLICANT: COTLEY, Neil C.
APPLICANT: COTLEY, Neil C.
ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE,DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                   NUMBER OF SEQUENCES:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Horne, William A. APPLICANT: Oltersdorf, Tilman
                                                                           STREET: 3174 Por
CITY: Palo Alto
                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/UG FILING DATE: 20-SEP-1996
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Local Similarity 100.0%; Pred. No. 1.5e-07;
                                                                                                                   ADDRESSEE:
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                                                                                               3174 Porter Dr
                                                 USA
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States
                                                                                                                                                                                                                                     Lal, Preeti
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                                                                                                                                                                                                                                                                  Hillman, Jennifer L.
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                                                                                                               Incyte Pharmaceuticals, Inc
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) 535-8949
O ID NO: 2:
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Best Local Similarity 100.0%;
Matches 16; Conservative 0
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, Lucy J. 749
REGISTRATION NUMBER: 36,749
REFERBNCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-685-0555
TELEPHAN: 650-845-4166
                                                                                                                                                        COMPUTER REDABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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LIBRARY: SYNORA
CLONE: 358673
                                                                                             APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEI
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOTTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
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FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                 ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08985335
                                                                                                                                                                                                                                                                                                                            3174 Porter Dr.
                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNORAB01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                              Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                            PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                 PF-0421 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0421 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 83;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; I
1.5e-07;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-08-985-335-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-410-372-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
           US-09-410-372-1
                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94.04

ZIP: 94.04

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATABLE
COMPUTER: IBM COMPATABLE
OPERATING SYSTEM: DOS
SOFTWARE: FRASERED FOR WINDOWS VETSION Z.0
CURRENT APPLICATION DATA:
APPLICATION WINDER: US/09/410,372
PETLING DATE:
PRICE APPLICATION NUMBER: 08/965,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09410372 Patent No. 6281334 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
STRAIL.
TOPOLOGY:
LIMMEDIATE SOURCE:
LIBRARY: SYNORAB01
~ ONE: 358673
                                                                                                                TELEFAX: 650-845-4166
INEORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
                                                                                                                                                                                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
ADDRESSEE: Incyte P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 31/-
STREET: 31/-
CITY: Palo Alto
CTATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: COTIEY, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 ORYGRELRRMSDEFVD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                     LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.0%;
Local Similarity 100.0%;
Les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QRYGRELRRMSDEFVD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8: Incyte Pharmaceuticals, Inc
3174 Porter Dr.
                                                        single
linear
RCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 amino acids
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                                                                                                                                                                                                                      PF-0421 US
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Pred. No. 1.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                        US-08-333-565-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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LENGTH: 168 amino acids
TYPE: amino acid
SYRANDEDNESS: single
TOPOLOGY: Linear
IMMEDIATE SORCE:
LIBERRY: GenBank
CLONE: 1683637
US-09-410-572-7
                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J.

REGISTRATION UNBER: 36,749

REFERENCE/DOCKST NUMBER: PP-0

FILECOMUNICATION INFORMATION:

TELEPINE: 650-855-0556

INFORMATION FOR SED ID M0: 7:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application Patent No. 6281334 GENERAL INFORMATION:
Sequence 10, Application US/08333565 Patent No. 5622852 GENERAL INFORMATION:
                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 16; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTES REALABLE FORM.
MEDIUM TYPE: Diskette
COMPUTES: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PRAYED FOR MINDOWS Version 2.
CURRENT APPLICATION UNMER: US/09/410,372
FILING DATE:
PRICE DATE:
PRICE DATE:
PRICE APPLICATION UNMER: 08/965,335
APPLICATION UNMER: 08/965,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: COT-LEY, No.1 C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SQUIENCES: OF CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jennifer L. APPLICANT: Yue, Henry APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 ORYGRELRRMSDEFVD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                        1 QRYGRELRRMSDEFVD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Application US/09410372 6281334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 83; DB 4;
100.0%; Pred. No. 1.5e-07;
Live 0; Mismatches 0;
                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0421 US
                                                                                                                                                                                        Score 83; DB 4;
Pred. No. 1.5e-07;
, Mismatches 0;
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APPORNEY AGENT HEROMATION:

NAME: Seith Hilliam H 223
REGISTRATION UNGERS 30 12726
REFERENCE/COCKET NUMBER: 15726
TELEPONE: (415) 36-2400
TELEFON: (415) 36-242
TELEFON: (415) 36-242
TELEFON: (415) 36-242
TELEFON: (415) 36-242
TELEFON: 105 36-242
TELEFON: 105 36-242
TELEFON: 105 36-242
TELEFON: 30 10 NO: 10:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGT: 23 milno ecid
TERMINENESS: 310916
TOPOLOGY: 110ear
MOLCULE TYPE: peptide
US-08-33-55S-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-661-479-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08661479
Patent NO. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 88.0%; Score 73; DB 1; Length 23; Best Local Similarity 100.0%; Pred. No. 1e-06; Matches 14; Conservative 0; Mismatches 0; Indels
                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: 15M PC COMPATION:
OPERATING SYSTEM: PC-DOS_MS-DOS
SOSTWARE: PAtenth Release 4.0, Version #1.25
CURRENT APPLICATION NUMBER: US_08/661,479
FILING DATE: 11-JUN-1995
FILING DATE: 11-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TIPE: Flappy disk
COMPUTER: 18M PC COMPALINE
OPERATING SYSTEM: NC-005/MS-DOS
OPERATING SYSTEM: NC-005/MS-DOS
SOFTMARE: NC-005/MS-DOS
CURRENT APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
FILING DATE: 31-OCT-1994
TRICKSSLFICATION: 335-0CT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KORSNEYER, Stanley
TITLE OF INVENTION: BC1-X/BC1
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOWNSSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STRIE: California
                                                                                                                                                                                                                                                                     ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: KORSMEYER, STABLEY J.
TITLE OF INVENTION: BCI-X/BCI-2 ASSOCIATED CELL DEATH
ITLE OF INVENTION: REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KORSMEYER, Stanley J. VENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
ON DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15726A-000700
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US 08/333,565

Query Match 88.0%; Score 73; DB 2; Length 59
Best Local Similarity 100.0%; Pred. No. 2:9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels

Length 59;

0;

Gaps

0

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-733-505A-55

Sequence 55.5491 ication US/08733505A
Patent No. 5856445

GENERAL INFORMATION:
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                                                                                                                                                                                          COMPUTER READNALE FORM:

MEDIUM TREE: Ploppy disk
COMPUTER: ITAM FO-DOS/MS-DOS
OPERATING SYSTEM: PO-DOS/MS-DOS
OPERATER SYSTEM: PO-DOS/MS-DOS
OPERATE: PATENTIN RELEASE 41.0, Version #1.30
CURRENT APPLICATION UNBER: US/08/733,505A

FILLING DATE:
APPLICATION: 530
CLASSIFICATION: 530
ATPORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REFERENCE/DOCKET NUMBER: 954.458
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 954.458
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 88.0
Best Local Similarity 100
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ LD NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                              TELEPHONE: (314) 727-5188
TELEPAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KORSMEYER, S
TITLE OF INVENTION: SER
TITLE OF INVENTION: BCI
TITLE OF INVENTION: BCI
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SMITCH, WILLIAM M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI
                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KORSMETER, STANLEY J.

VERTION: SERINE SUBSTITUTED MUTANTS OF

VENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

EQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.0%; Score 73;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
. 1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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US-08-733-505A-57
; Sequence 57, Application US/08733505A
; Patent No. 5856445
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US-08-733-505A-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear ; MOLECULE TYPE: peptide US-08-733-505A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE_DOCKET NUMBER: 9654
TELECOMMUNICATION INCOMMENTION:
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-6092
INFORMATION FOR SED ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dequence 56, Application US/08733505A Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPY disk
MEDIUM TYPE: FIDPY disk
COMPUTER: IBM CP COMPATIBLE
COMPUTER: FIBM CP COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY_ACENT INFORMATION:
NAME: HOLLAND, DONALD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 88.0%; Score 73; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.9e-
Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KORSNEYER, STANLEY J.
TIPLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TIPLE OF INVENTION: BECL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
                                                                                                  APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEVENDENCES.
CORRESPONDENCE. ADDRESS:
3PREST: JOHNELL & HAFERKAMP, L.C.
3PREST: JOHNEL & HAFERKAMP, L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
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CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QRYGRELRMSDEF 14
((((+++++++++)))
46 QRYGRELRMSDEF 59
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                                                            CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                     46 ORYGRELRRMSDEF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QRYGRELRRMSDEF 14
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                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-733-505A-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                        MEDIUM TYPE: Floppy disk
COMPUTES: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
LOTEREW APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
PILING DATE: 530
APTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 95.47
REFERENCE/DOXETY NUMBER: 95.48
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-503
TELEPHONE: CHRACTERISTICS:
SEQUENCE CHRACTERISTICS:
LENGTH: 59 amino acids
TYPE: Arthor Acids
TYPE: Arthor Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 58, Application US/08733505A Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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APPLICATION NUMBER: US/08/733,505A

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.

RECISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 965458

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (314) 727-6092 INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICAMY: KORSMEYER, STAMLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 71
CITY: ST.
STATE: MIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100 hes 14; Conservative
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TOPOLOGY: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 ORYGRELRRMSDEF 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                        TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QRYGRELRRMSDEF 14
                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSOURI
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                        linear
peptide
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                                                                                                                                                                                                                                                                                                                                                                         Release #1.0, Version #1.30
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RESULT 14
US-08-661-479-2
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                                                                                                                                                                                                                                                NAME/KEY: Protein
LOCATION: 1.204
OTHER INFORMATION:
OTHER INFORMATION:
US-08-333-565-2
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                                                                                                                                                                    Matches
      Patent No. 5834209
                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 88.0
Best Local Similarity 100
Matches 14: Conservative
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PLEDETIC Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PMCANEY APPLICATION APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: BC1-x/BC1
TITLE OF INVENTION: REGULATOR
                                                                                                         145 GRYGRELRRMSDEF 158
                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 326-2400
                                                                                                                                                                  Local Similarity 100 hes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 379 Lytton Avenue CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 ORYGRELRRMSDEF 59
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                                                                                                                          1 QRYGRELRRMSDEF 14
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5, 5622852
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linear
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JENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                     88.0%; Score 73; DB 1; Length 204; 100.0%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                              /note= "Deduced amino acid sequence
of mouse BAD."
                                                                                                                                                                      0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5726A-000700
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2.9e-06;
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                                                                                                                                                                    0,
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RESULT 15
US-08-733-505A-1
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                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08733505A Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 88.0
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PCCOSMS DOS
SOTIMARE: PATENTIA Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11.7UN-195
FILING DATE: 11.7UN-195
PAIOR APPLICATION NUMBER: US 08/333,565
PAIOR APPLICATION NUMBER: US 08/333,565
FILING DATE: 31.0CT-194
ATTORNEY/ACENT INFORMATION:
NAME: SILLA MILIAN M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1575A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2402
TELEPAX: (415) 326-2422
TELEPAX: (415) 326-2422
TINFORMATION FOR SEC ID NO: 2:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: BC1-x/BC1
TITLE OF INVENTION: REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                               145 QRYGRELRRMSDEF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                            COUNTRY:
                                                                                               STATE: MI
                                                                                                              ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400 CITY: ST. LOUIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 379 Lytton Avenue CITY: Palo Alto
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                                                           63105
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                                                                                               MISSOURI
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                                                                              USA
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linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KORSMEYER, Stanley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.0%; Score 73; DB 2; I
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of mouse BAD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pattentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND DOMALD R.
REGISTRATION NUMBER: 35,197
REPERENCE/DOCKETS NUMBER: 35,197
REPERENCE/DOCKETS NUMBER: 35,197
REPERENCE/DOCKETS NUMBER: 35,197
REPERENCE: (314) 727-5188
TELEPHONE: (314) 727-5092
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino aclds
TYPE: amino acld
STRANDEDNESS:
TOPOLOGY: 11mear
STRANDEDNESS:
TOPOLOGY: 11mear
OULECULE TYPE: protein
US-08-733-505A-1

Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
MATCHES 14; Conservative 0; Mismatches 0; Indels 0; Gaps

QU 1 ORYGRELRMSDEF 14
Db 145 ORYGRELRMSDEF 158

Search completed: September 20, 2002, 10:37:20

Job time: 408 sec
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein -
                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a sore greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein search, using sw model
                                                                                                                                                                                                                                                                                                                               Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                            4321
                                                                                                                                                                                                                                                                                                                                                                                                                            pre_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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50.6
49.4
49.4
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Gapop 10.0 , Gapext 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-544-664-29
83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                Length
 DВ
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                                                                                  conserved hypothet conserved hypothetical prote probable enzyme [i] hypothetical prote probable enzyme yg gibberellin 2beta hypothetical prote transcription regulation conserved by the specific DNA-probable Fe-5 oxid transcription init
                               hypothetical prote
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probable cationic
            hypothetical prote 
oxidoreductase, so
                                                                                                                                                                                                                  membrane transport
GCR3 protein - yea
hypothetical prote
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hypothetical prote
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                                                                                                                                                                                                                                                                                                          bad protein
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transporter homolo
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H75403
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Best Local Similarity 100.
Matches 14; Conservative
Query Match
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                                                                                                                                                                                                                                                                                                                   1 ORYGRELRRMSDEF 14
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Result No.

Score 45;

DВ

Minimum DB Maximum DB

Database

hypothetical prote	S64604	N	1967	47.0	39	0.
similar to late em	T02712	N	1805	47.0	39	-
two-component hybr	AE2452	Ν	965	47.0	39	w
probable kinesin -	B71405	ب	959	47.0	39	
valine tRNA ligas	SYBSYS	ب	880	47.0	39	_
hypothetical prote	T29772	ы	689	47.0	39	_
acylaminoacyl-pept	F90299	ν	536	47.0	39	•
site-specific DNA-	CTBPRH	ш	503	47.0	39	ω
trigger factor (im	AB0558	N	432	47.0	39	7
	FOXR3D	ب	418	47.0	39	01
sigma 2 protein .	FOXRL2	μ	418		£	01
hypothetical prote	T31738	N	383		39	_
hypothetical prote	T32163	N	380	47.0	39	~
RAD51 protein homo	S42107	ω	365	47.0	υ 9	
protein F12K11.20	D86200	N	360	47.0	39	_
DNA repair procein	E90121	K	331		9	0

## ALIGNMENTS

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C.Accession: H75403
C.Accession: H75403
C.Accession: H75403
C.Accession: H75403
C.Accession: H75403
C.Accession: H75403
J. D. Bodson, R.J
R. White, O.; Elsen, J.A.; Lam, P.; Mickey, E.K.; Peterson, J.D.; Dodson, R.J
M.; Shen, M.; Vänathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 199
A.Tille: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
A.Reference number: A75250; MUID:20036896
A.Accession: H75403
A.Accession: H75403
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-564 -KHIP
A.Cross: references: GB:AE001903; GB:AE000513; NID:96459123; PIDN:AAF10944.1; PID:9645
A.Accession: H75403
C.Genetics:
A.Cross: references: GB:AE001903; GB:AE000513; NID:96459123; PIDN:AAF10944.1; PID:9645
A.Accession: H75403
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A55671
A55671
bad protein - mouse
bad protein - mouse
c;Species: Mar-1995 #sequence_revision D3-Mar-1995 #text_change O5-Nov-1999
c;Pate: O3-Mar-1995 #sequence_revision D3-Mar-1995 #text_change O5-Nov-1999
c;Accession: A55671
R;Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
cell 80, 285-291, 1995
A;Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot
A;Roference number: A55671; MUID:95136361
A;Rocession: A55671
A;Accession: A55671
A;Accession: A55672
A;Cross-references: GB-L37296; NID:9639778; PIDN:AAA64465.1; PID:9639779
C;Keywords: heterodimer
A;Gene: DR1375
A;Map Desition: 1
C;Superfamily: alpha-glucosidase; alpha-amylase core homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycosyl hydrolase, family 13 - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Datte: 03-Dec:1999 #sequence_revision 03-Dec:1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 73; DB 2; I
; Pred. No. 0.00011;
0; Mismatches 0;
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Cobalamin blosynthetic protein CobN PA2944 [imported] - Pseudomonas aeruginosa (strain PC:Species: Fseudomonas aeruginosa) (strain PC:Species: Fseudomonas aeruginosa) (strain PC:Species: Fseudomonas aeruginosa) (strain PC:Species: Fseudomonas aeruginosa) (strain PC:Species: Fseudomonas aeruginosa) (strain PC:Species: Fseudomonas aeruginosa) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: Fseudomonas) (strain PC:Species: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           valine-tRNA ligase (imported) - Staphylococcus aureus (strain N315)
c;Specles: Staphylococcus aureus
c;Date: 10-May-2001 *text_change 22-Oct-2001
c;Date: 10-May-2001 *sequence_revision 10-May-2001 *text_change 22-Oct-2001
c;Accession: E89949
R;Kuroda M, Ohta T; Uchlyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L;
c; Shiba, T; Hattori, M; Godayashi, N; Sawano, T; Inoue, R; Kalto, C; Sekimizu, Lancet 357, 1225-1240, 2001
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
R;Accession: E89949
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type; DMA
A:Residues: 1-876 «KUR»
A:Cross-references: GB:BA000018; PID:gl3701460; PIDN:BAB42754.1; GSPDB:GN00149
A:Experimental source: Strain N315
C:Genetics;
                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                A:Gene: vals
C:Superfamily: valine--trNA ligase
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E89949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: cobM: PA2944
C;Superfamily: Rhodobacter capsulatus magneslum-protoporphyrin O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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Best Local &
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Best Local S
Matches 9
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                                                                                                                           251 GRELPILADEYVD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       615 ESYGPLEDLERLADEFYD 632
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8; Conser
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9; Conservative
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2; Mismatches
                                                                                                                                                                                                                                                                             Score 42; DB
Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB
Pred. No. 47;
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                   membrane transporter - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: O3-bec-1999 #sequence_revision 03-bec-1999 #text_change 18-Feb-2000
C;Accession: T40297
R;Lyne, M: Wood, V:; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Moestl, D.; Due submitted to the EMBL Data Library, May 1998
A;Reference number: Z21919
A;Resizione number: Z21919
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Residows: 1-577 cLYNs
A;Cross-references: EMBL:AL023589; PIDN:CAA19050.1; GSPDB:GN00067; SPDB:SPBC36.02c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein AR4g30490 [imported] - Arabidopsis thaliana c;Species: Arabidopsis thaliana (mouse-ear cress) c;Date: 16-Feb-2001 sequence_revision 16-Feb-2001 stext_change 16-Feb-2001 c;Accession: F8356 sequence_revision 16-Feb-2001 stext_change 16-Feb-2001 c;Accession: F8356 sequence_revision 16-Feb-2001 stext_change 16-Feb-2001 state: 10-Feb-2001 sequence in the column sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488 A;Accession: F85556
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A;Gene: AT4g30490
A;Map position: 4
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F85356
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A; Molecule type: DNA
A; Residues: 1-447 <STO>
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A; Map position:
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A;Molecule type: DNA
A;Residues: 1-191 <KUR>
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 33.3
Matches 11; Conservative
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Pred. No. 18;
2; Mismatches
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Pred. No. 52;
2; Mismatches
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ND3414
hypothetical cytosolic protein BMEI1298 [imported] - Brucella melitensis (strain 16W)
c;Species: Brucella melitensis
c;Species: Ol-Feb-2002 #sequence_revision Ol-Feb-2002 #text_change Ol-Feb-2002
c;Date: Ol-Feb-2002 #sequence_revision Ol-Feb-2002 #text_change Ol-Feb-2002
c;Accession: AD3414
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
; Mazur, M.; Goltsman, E.; Selkov, E.; Bizer, P.H.; Hagius, S.; O'Callaghan, D.; Let
proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella mellit
A;Reference number: AD3252; PMID:11756688
A;Accession: AD3414
                                                                                                                                                                                                                                                                                                                                  A:Cross-references: GB:AE008917; PIDN:AAL52479.1; PID:g17983287;
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    17;
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A;Cross-references: GB:NC\_001268; NID:g7269950; PIDN:CAB79767.1; GSPDB:GN00140

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A:Cross references: EMBL.Z48622; NID:g728663; PIDN:CAA88550.1; PID:g728664; MIPS:YMR125W

R:Lye, G.; Churcher, C.M.

submitted to the EMBL Data Library, May 1995

A:Reference number: S54014

A:Accession: S54094

A:Molecule type: DNA

A:Residues: 'Menkrary, 6-489 <LYE>

A:Residues: 'Menkrary, 6-489 <LYE>

A:Cross-references: EMBL:Z49273; NID:g809577; PIDN:CAA89274.1; PID:g809584; MIPS:YMR125W

C:Genetics:
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A;Title: GGR3 encodes an acidic protein that is
A;Reference number: A44919; MUID:92380925
A;Accession: A44919
A;Molecule type: DNA
A;Residues: 1-858 <UEM>
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C;Date: 30-5ep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Oct-1999
C;Accession: A44919; S53055; S54494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Gene: SPDB:SPBC36.02c
A:Map position: 2
C:Superfamily: benomyl/methotrexate
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hypothetical protein Vng2379h [imported] - Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 #text_change 02-Feb-2001 C;Date: 02-Feb-2001 #text_change 02-Feb-2001 C;Date: 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: F843BB C;Accession: F843BB C;Accession: F843BB C;Accession: F843BB C;Accession: F843BB C;Accession: F843BB C;Accession: Facenation of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of th
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A;Map position: 13R
C;Keywords: DNA binding; nucleus
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A; Reference number: S53055
A; Accession: S53055
A; Molecule type: DNA
A; Residues: 339-858 CBAD>
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A.Note: Sequence extracted from NCB1 Dackbone (NCBIN:112104, NCBIP:112106)
R;Badcook, K.; Churcher, C.
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J. Bacteriol. 174, 5526-5532, 1992
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N.Alternate names: protein YM8564.07; protein YM9553.01; protein YMR125w
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                                                                                                                                          Shukla, H.D.;
Maddocks, D.
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A; Residues: 1-84 <STO>
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A; Residues: 1-113 <KUR>
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Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhre

McAhren,

B.S.

(strain

GSPDB:GN00174

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A:Experimental Source: Strain TIGR4
C;Genetics:
A;Gene: SP0372
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B95043
Conserved hypothetical protein Sp0372 [imported] - Streptococcus pneumoniae conserved hypothetical protein Sp0372 [imported] - Streptococcus pneumoniae cispecies: Streptococcus pneumoniae cispecies: Streptococcus pneumoniae cispecies: Streptococcus pneumoniae
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A;Gene: VNG2379H
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                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-109 < KUR>
A; Cross references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Iltle: Complete Genome Sequence of a virulent isolate of Streptococcus A; Pacference number: A95000; MUID:21357209; PMID:11463916
A;Accession: B95043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 RYGTEASRMEDE 77
1 QRYGRELRRMS----DEFVD 16
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9; Conser
                                                                           Conservative
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MUID:20504483
                                                                           Score 40; DB
Pred. No. 18;
4; Mismatches
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Pred. No.
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 «KAM»
A;Cross-references: GB:AJ248286; GB:AL096836;
A;Experimental source: strain Orsay
C;Genetics;
A;Gene: PAB1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein PABI640 - Pyrococcus abyssi (strain Orsay)
[;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: A75088
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Reseription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome
A;Reference number: A75081
A;Accession: A75081
                   RESULT
F65076
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Best Local Similarity
Tatches 7; Conserve
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C;Genetics:
C;Superfamily: naphthoate synthase: encyl-CoA hydratase homology
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A:Residues: 1-275 <HAY>
A:Cross-reterences: GB:BA000007; PIDN:BAB37212.1; PID:g13363261;
A:Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                    R:HBYBShi, T.: Makino, K.: Ohnishi, M.: Kurokawa, K.: Ishii, K.: Yokoyama, K.: Han, C.G gasawara, N.: Yasunaga, T.; Kuhara, S.: Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and geno A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E91102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable enzyme [Imported] - Escherichia coli (strain 0157:H7, substrain RIMD 0509952)
C:Species: Escherichia coli
C:Decies: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: E91102
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hes 9; Conservative
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  Escherichia coli (strain K-12)
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                                                                                                                                                             3; Mismatches
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Pred. No. 37;
4; Mismatches
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Pred. No. 19;
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Pred. No. 46;
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Search completed: Job time: 481 sec

September

20, 2002,

10:39:09

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A:Title: Genome sequence of enterohemorrhagic Escherichia coli Ol A:Reference number: A65480; MUID:21074935; PMID:11206551 A;Accession: A65948 A;Status: preliminary A;Status: preliminary A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-75 <570>
A:Cross references: GB:AE005174; NID:gl2517451; PIDN:AAG58045.1; A;Experimental source: strain O157:H7, substrain EDL933
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G:Species: Pscherichia coli
G:Batte: 12-Sep-1997 ** **sequence_revision 17-Sep-1997 ** **text_change 08-Oct-1999 **GACCESSION: P55075 ** **sequence Lir, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, G:Batther, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, G:Batther, F.R.; Shao, Y.

A: Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617

A;Reference number: p5075

A;Reference : DBA, Nucleic acid sequence not shown; translation not shown

A;Residues: 1-275-SEAEN

A;Rose, DBA, SEAENDONTE, GB-NDONGE, NID-01780282. DIDN-AACTEGE 1. DIDN-177
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A;Experimental source: Strain K-12, substrain MG1652
C:Superfamily: naphthoate synthase; encyl-Coa hydratase homology
F:40-192/Domain: encyl-Coa hydratase homology <ECH>
                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: ygfG
C; Superfamily: naphthoate synthase; enoyl-CoA hydratase homology
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R;Perna, N.T.: Plunkett III, G.: Burland, V.; Mau, B.; Glasner, iller, L.; Crotbeck, E.J.: Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable enzyme ygfG [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli (species: Escherichia c
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3; Mismatches
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K.; Apoda
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Perfect score:
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Maximum DB seq length: 2000000000
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                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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tabases.  k E.T., Meadows R.P., mpson C.B.,  ion from structure,  competes for the y affecting the level BAX. Can reverse the t that of Bcl-2 (By	oases, Wilson G.,	ndria.";	nidae; Euteleostomi; nidae; Homo. l have homology to mouse databases.	component		099728 homo sapien 049640 mycobacteri 003601 caenorhabdi p38198 saccharomyc 0944216 mycobacteri p44216 halobacteri p44210 bacillus su 097177 drosophila 074806 schizosacch 06496 aquitex aeo 099811 aerobyrum p

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01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
8c12-antagonist of cell death (BAD) (Bc1-2 binding 6) (Bc1-xLBc1-2 associated death promoter).
8AD OR BBC6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatica fristitute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U66879; AAB36516.1; --
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EMBL; AF031523; AAB88124.1; --
EMBL; BC001901; AAH01901.1; --
       Eukaryota; Metazoa; Chordata;
                       Mus musculus (Mouse)
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                                                                                                                                                                                                                                                  1 QRYGRELRRMSDEFVD 16
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TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.

DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND
BAX for their pro-apoptotic activity and for their interaction
with anti-apoptotic members of the Bel-2 family.

PTM: Phosphorylated on Ser-75 in response to survival stimuli.
Subsequent phosphorylation on Ser-99 promotes heterodimerization
with 14-3-3 proteins. This interaction then facilitates the
phosphorylation at Ser-118, a site within the BH3 domain, leading
to the release of Bel-x(l) and the promotion of cell survival.

Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the
major site of FAKT/PKB phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 BCL-3 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity). Appears to act as a link between growth receptor signaling and the apoptotic pathways. SUBUNIT: Forms heterodimers with the anti-apoptotic x(L), Bcl-2 and Bcl-w. Also binds protein S100Al0 (B The Ser 75/Ser 99 phosphorylated form binds 14-3-3 p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            603167;
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                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS01259; BH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000712; Bcl_2
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binding to Bel-X and Bel-W. Thereby affecting the level of heterodimerization of these proteins with BaX. Can reverse the death repressor activity of Bel-X(L), but not that of Bel-2. Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

1. SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bel-X(L), Bel-2 and Bel-W. Also binds protein S100AiD (By similarity). The Ser-112/Ser-136 phosphorylatted form binds 14-3-3 proteins.

1. SUBCELDLAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.

1. DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bel-2 family.

1. PTM: Phosphorylated on Ser-112 in response to survival stimuli. Subsequent phosphorylation of Ser-136 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-155, a site within the BH3 domain, leading to the release of Bel-X(L) and the promotion of cell survival. Ser-136 is the major site of AKT/PKB phosphorylation. Ser-155 the major site of protein kinase A (CAPK) phosphorylation.

1. SIMILARITY: COMMAINS a BEL-3 HOMOLOGY DOMAIN 3 (BH3).
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                                                                                                                                                                                                                                           modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                               Apoptosis;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *14-3-3 proteins and survival kinases cooperate to inactivate BAD BH3 domain phosphorylation.*; BH3 domain phosphorylation. *; Mol. Cell 6:41-51(200), Mol. Cell 6:41-51(200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Datta S.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;
"Interleukin-3-induced phosphorylation of BAD through the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION, AND MUTAGENESIS (MEDLINE-98022383; PubMed-9381178;
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                               MUTAGEN
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E. Zha J., Jockel J., Boise,
a heterodimeric partner for
otes cell death.";
80:285-291(1995).
                                                                                                                                                                                               MGI:1096330;
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TISSUE-Brain;
MEDILRE-93194755; PubMed-9535132;
MEDILRE-93194755; PubMed-9535132;
D'Agata V. Magro G., Travall S., Musco S., Cavallaro S.;
"Cloning and expression of the programmed cell death regulator BAD in the rat brain.";
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 41, Last senotation update)
10.1MAR-2002 (Rel. 41, Last annotation update)
8c12-antegonist of cell death (BAD) (Bc1-2 binding
6) (Bc1-xi/Bc1-2 associated death promoter).
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MEDLINE-9803486; PubMed+9369453;

HSU S.Y., Kaipla A., Zhu L., Hsueh A.J.W.;

HSU S.Y., Kaipla A., Zhu L., Hsueh A.J.W.;

"Interference of BAD (Bcl-xL/Bcl-2-associated death
apoptosis in mammalian cells by 14-3-3 isoforms and
Mol. Endocrinol. 11:1858-1867(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Bukaryota; Metaza; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
RCBI_TaxID=10116;
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                                                                                                                                         brain, live epithelial abundant fo
DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the BC1-2 family.

PfW: Phosphorylated on Ser-II3 in response to survival stimuli. Subsequent phosphorylated on Ser-II3 in response to survival stimuli. Subsequent phosphorylation on Ser-II3 promotes heterodimerization with I4-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-IS6, a size within the BH3 domain, leading to the release of Bc1-x(L) and the promotion of cell survival.
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Matches 14; Conserv
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                                    SPOURNCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND ALTERNATIVE SPLICING.
MEDILINE-9903450; FUNDEd-99305030;
O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M., Cory S., Huang D.C. S.
"Bin: a novel member of the Bcl-2 family that promotes apoptosis.", EMBO J. 17:384-395(1998),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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EMBL: AF031227: AAC11100.1: ...
EMBL: AF279910: AAF91427.1: ...
EMBL: AF279911: AAF91428.1: ...
EMBL: AF279911: AAF91428.1: ...
Interpro: IPB000712. BCL_2.
PROSITE: PS01259: BH3: FALSE_M
                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an small to licenseeisb-sib.ch).
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SIMILARITY: BELONGS TO THE BCL-2 FAMILY
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tion; Alternative splicing.
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EVAMPPLEWPALERLG (IN ISOCOM BETA)
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SIDAGR -> ERGEMEN (IN REF. 1)
Score 73; DB 1; Le
Pred. No. 5.2e-05;
0; Mismatches 0;
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SIMILARITY).
BHOSPHORYLATION (BY CAPK AND PKB) (BY SIMILARITY).
BHOSPHORYLATION (BY CAPK AND PKB) (BY SIMILARITY).
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TICSUE-OVARY.

MEDLINE-98400435; PUDMOd-9731710;

HBU S.Y. ELL. P., HBUM-B A.J.W.;

TOOD BEI-2-related avarian death gene) is containing prospectate Bel-2 protein capa diverse antiapoptotic Bel-2 members.;

Moi. Endocrinol. 12:1437-1440(1959);

Moi. Endocrinol. 12:1437-1440(1959);
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SEQUENCE
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1- DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND CYTOTOXICITY.

1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
                                                 SEQUENCE FROM N.A. (ISOFORM BINL). Chen J. Simon R.P. Chen J. Chen J. Schonlag of rat bimEL and bimL, and schemla and normal rat brain."; and summitted (MAR-1999) to the BMBL/Ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145
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PROTEINS INCLUDING MCL-1, BCL-2, BCL-X, BSL-1, AND BHRF-1, DOES
NOT HETERODIKERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOX,
BAX OR BAX (BY SIMILARITY),
SUBCELIJILAR LOCATION: ASSOCIATED WITH INFRACYTOPLASMIC MEMBRANES.
ALTERNATIVE PRODUCTES 3 ISOCOMENS, BANEL (SHORN HERE), BIML AND
BHMS, ARE PRODUCTED BY ALTERNATIVE SPLICING.
115SUE SPECIFICITY: EXPRESSED IN ANDHER OF B-AND T-LYMPHOID CELL
LINES.
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8; Conservative
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42
196 AA;
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22066 MW;
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                                                     EMBL/GenBank/DDBJ databases
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Pred. No. 6;
2; Mismatches
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MISSING (IN ISOFORM BIMS)
; 531C176E5F1AC9AA CRC64;
                                                                                                          their
                                                                                                                                                                                                                                                                   e) is an ovarian BH3 domain-
capable of dimerization with
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                                                                                                       differential expression
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BMBL, AP05533; AAC23595.1; ...

BMBL, AP055431; AAC23595.1; ...

R BMBL, AP055431; AAC23595.1; ...

R BMBL, AP055431; AAC23595.1; ...

R BMBL, AP055431; AAC23595.1; ...

R BMBL, AP055431; AAC23595.1; ...

R BMBL, AP050712; AD25594.1; ...

R PROSTITE, BS01259; BH3; BALC2-LIKE PROTEIN 11, ISOFORM BDD-L.

R PROSTITE, BS01259; BH3; BALC2-LIKE PROTEIN 11, ISOFORM BDD-L.

R PROSTITE, BS01259; ALCETACLE, BECL2-LIKE PROTEIN 11, ISOFORM BDD-L.

R PROSTITE, BS01259; BCC2-LIKE PROTEIN 11, ISOFORM BDD-S.

PT CHAIN

104 104 POR ISOFORM BDD-S.

PT LOWARD-LC 42 97 MISSING (IN ISOFORM BLML),

PT VARSPLIC 42 197 MISSING (IN ISOFORM BLML),

PT VARSPLIC 42 197 MISSING (IN ISOFORM BLML),

PT VARSPLIC 42 197 MISSING (IN ISOFORM BLML),

PT VARSPLIC 42 197 MISSING (IN ISOFORM BLML),

PT VARSPLIC 42 197 MISSING (IN ISOFORM BLML),

PT VARSPLIC 136 136 P-> D (IN REF. 1; AAC23594).

SO SEDUENCE 196 AA; 22055 MW; BAD2146F9C0B37AD CRC64;
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HT2A_HUMAN STANDARD; PRT; 653 AA.

C 013049; (Rel. 35, Created)

T 01.NOV.1997 (Rel. 35, Last sequence update)

T 01.NOV.1997 (Rel. 35, Last sequence update)

T 01.NOV.1997 (Rel. 41, Last sequence update)

E 10r.fingar protein HT2A (72 kDs Tat-interacting protein HT2A (72 kDs Tat-interacting protein HT2A)

E 20r.fingar protein HT2A (72 kDs Tat-interacting protein HT2A)

E MONTH TAT TATABACA.

C Bukaryota Metazous (Chordata; Craniala; Vertebrata; C Hammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLIANG-95297135; PubMed-7778269;
FIIGELI R.A., Barding L.S., Bogerd H.P., Cullen B.R.;
FIIGELI R.A., Barding L.S., Bogerd H.P., Cullen B.R.;
Tidentification of a novel human zinc finger protein
specifically interacts with the activation domain of
proteins.;
Virology 209-347-357(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the ENURGE property of the ENURGE PROTECTION on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Susage by and for communication entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license(isb-sib.ch).
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8; Conserv
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Pred. No. 6;
2; Mismatches
                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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                                                                                              that
lentiviral
                                                                                                                                                                                                                                                                                      Homo
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                                                                                                 Tat
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MEDIATING

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BIOLOGICAL

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RESULT 7
AROG_CANAL
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Best Local &
Matches &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
ZN_FING
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
10.-CCT-2001 (Rel. 40, Last annotation update)
16.-CCT-2001 (Rel. 40, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
Phospho-2-dehydro-2-keto-3-deoxyheptonate aldolase) (DAHP
synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART: SM00184; RHO; 1.
SMART: SM00184; RHG; 1.
SMART: SM00184; RHG; 1.
PROSITE: PS00119; ZE_RHO; 1.
PROSITE: PS00089; ZE_RHO; 2.
LPROSITE: PS00089; ZE_RHO; 2.
SMART: SMO0189; ZE_RHO; 2.
SMART: SMO0186; ZE_RHO; 2.
SMART: SMO0186; ZE_RHO; 2.
SMART: SMO0186; BOX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                             Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
PARTIAL SEQUENCE FROM N.A. MEDILINE-96207468; PEDMOD-18-96207468; PEDMOD-18-96207468; PEDMOD-86264023;
PAROMATIC annino-acid biosynthesis in Candida albicans: identification of the AROA gene encoding a second DAHP synthase.;
                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 11651 / B792;
SOURA S., Pereira S.A., Livi
Submitted (APR-1996) to the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 QEYGHEERRVQDE 198
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nes 8; Conservative
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SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 1 B BOX-TYPE ZINC FINGER.
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THE ACTIVATION COMMIN OF HIV-1 TAT AND CAN ALSO I
HIV-2 AND EIAV TAT PROTEINS IN VIVO.
SUBCELULIAN LOCATION: NUCLEAR: VIVO.
ILSUE SPECIFICITY: SPLEBU, TRYMUS, PROSTRATE, TE
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6 PC
65 RJ
133 B
71954 MW;
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                                                                                                                                                                                                           L G.P.;
EMBL/GenBank/DDBJ
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RING-TYPE.
B BOX-TYPE.
; 2A803B6B801D7390 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycotina;
Saccharomycetales;
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CLIPTONCTION: STRENGSPECTIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEF)

CC AND D-ERVTHACSE-4-PHOSPHATE (DAHP).

CC AND D-ERVTHACSE-4-PHOSPHATE (DAHP).

CC CI-CARALTYIC (ACTIVITY: 2-dehydro-3-deoxy-b-arabino-heptonate 7-cliptone-deptone-terminal control of the phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - phosphate - p
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HSSP: P00886 1087
InterPro; ZPR001785: DANE Synth_1.
Pfam: PF00793: DANE Synth_1: 1.
Probom: P0005060: DANE Synth_1: 1.
Aromatic amino acid blosynthosis: Lyase: Multigene family.
SEQUENCE 370 AA: 40291 MW: 11E55324CBD785DB CRc64:
                                        Submitted [5]
                                                                   SEQUENCE OF 1-492 FROM STRAIN=S288C / AB972;
Lye G., Churcher C.M., Submitted (MAY-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bemura H., Jigami V.,

"GCR3 encodes an acidic protein that is required

"GCR3 encodes an acidic protein that is required

glycolytic genes in Saccharomyces cerevisiae.";

J. Bacteriol. 174:5526-5532(1992).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-92380925; PubMed-1512188;
MEDLINE-92180925; PubMed-1512188;
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Guo Z., Russo P., She
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RR STRAIN CHARACTERISTICS OF A TRANSCRIPTIONAL ACTIVATOR.

CC -1 SINGLELULAR LOCATION: Nuclear (Probable)

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EMBL: D10550; NOT_ANNOTATED_CDS.
EMBL: L27750; NOT_ANNOTATED_CDS.
EMBL: L27841; NOT_ANNOTATED_CDS.
EMBL: Z46273; CAA89271.1; -
EMBL: Z46273; CAA89271.1; -
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EMBL: Z46273; CAA89270.1; -
EMBL: Z46273; CAA89270.1; -
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Intcrpro; LFR003890; E14G_Cent.
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FL 9
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STRAIN-K12 / MG1655;
MEDLINE-99126617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Kiley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Cregor J. Davis N.M., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGYC_ECOLI STANDARD: PRT; 261 AA. P52045; P76644; 01.0CT-1996 (Rel. 34, Created) 01.0CT-1996 (Rel. 34, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) 17976 OR 32319.
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Bacteria: Proteobacteria: gamma subdivision; Enterobacteriacene; ...
Escherichia.
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      SWISS-PROT entry is copyright.
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ASP/GLU-STECH (ACCIDEC)
ARG/LYS-RICH (BASIC).
D > 1 (IN REF. 3).
A > R (IN REF. 3).
A > R (IN REF. 3).
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Pred. No. 43;
5; Mismatches
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            It is produced through a collaboration
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RS RESPONDED FROM N.A.

RA GARDARDH M.C. CARTAIL N., Webb H., COUREL M., Amorim A.,

RA GARDARDH M.C. CARTAIL N., Webb H., COUREL M., Amorim A.,

RA GARDARDH M.L., CARTAINGON M.;

RA GARDARDH M.L., CARTAINGON M.;

RA GARDARDH M.L., CARTAINGON M.;

RA GARDARDH M.L., CARTAINGON M.;

RELEASES.

CC SUMMILE VARLANT SURFACE GLYCOPROTEIN CONTALING PHOSPHOINOSITOL

CC FROM THE CELL WALL OF T. BRUCEL AFTER CELL LYSIS. IT ALSO CLEAVES

CC SINILAR MEMBRANE ANCHORS ON SOME MAMMALIAN PROTEINS. VSG LIPASE

CC MAY PLAY A ROLE IN PROCESSES SUCH AS PRASTITE DIFFERENTIATION OR

RATIGENIC VARLATION (BY SIMILARITY).

CC CONTAINTING CATLOTTY: VALIANT-SULFACE-91/COPTOLE IN 1.2-didecanoy1-

SUBUNIT, MONOMER (BY SIMILARITY).

CC 1- SUBUNIT, MONOMER (BY SIMILARITY).

CC 1- SUBUNIT, MONOMER (BY SIMILARITY).

CC 1- SUBUNIT, MONOMER (BY SIMILARITY).

CC 1- SUBUNIT, MONOMER (BY SIMILARITY).

CC 1- SUBUNIT, MONOMER (BY SIMILARITY).

CC 1- SUBUNITAL FOR CATALYTIC ACTIVITY.

CC 2- SUBUNITAL FOR CATALYTIC ACTIVITY.
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15-DEC-1998 (Rel. 37, Created)
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IntcrPro; IPR001753; Encyl_CoA_hydrtse.
Pfam; PF00375; ECH: 1.
PROSITE; PS00166; ENCYL_COA_HYDRATASE; 1.
PROSITE; PS00166; ENCYL_COA_HYDRATASE; 1.
Hypothetical protein: Lyase: Complete proteome.
SEQUENCE 261 AA: 29172 MW; B6A8A13EC2C2EBE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U28377; AAA69086.1; ALT_INIT.
EMBL; AE000375; AAC75956.1; ALT_INJ
HSSP; P14604; 2DUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the PMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in many modified and this statement is not removed. Usage by and for commercial entities requires a license appeament (See http://www.lsb-sh.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                              EMBL; AJ000079; CAA03904.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Euglenozoa;
NCBI_TaxID-5693;
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7; Conservative
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Pred. No. 17;
3; Mismatches
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L outstation -
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in no way
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ProDom; PD0416

pF00388; pI-PLC-X; 1.
; PD041675; Varsurfglyc\_PPLC; 1
SM00148; PLCXC; 1.

InterPro; IPR000909; PI\_PLC\_X.
InterPro; IPR003633; Varsurfglyc\_PPLC

PROSITE; PS50007; PIPLC\_X\_DOMAIN; 1

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Matches 8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                XU S-Y., Xiao J.P., Ettwiller I., Holden M., Aliotta J., Poh C.L., Dalton M., Robinson D.P., Petronzio T.R., Moran L., Ganatra M., Ware J., Statko B., Benner J. II;

"Cloning and expression of the Apali, Nspi, Nspil, Saci, Scai, and sapi restriction-modification systems in Escherichia coli.";

Mol. Gen. Genet. 260:226-231(1998).

1- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE OTEGAC, CAUSES SPECIFIC METHYLATION ON C-7 ON BOTH STRANDS, AND PROTECTS THE DNA FROM CLEAVAGE BY THE APALI ENDONUCLEASE.

1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA Cytosine = S-adenosyl-L-homocysteine + DNA 5-methylcytosine.
                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ATCC 12875;
MEDLINE=99077292; PubMed=9862476;
XU.S.-Y., Xiao J.-P., Ettwiller L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Modification methylase ApaLI (EC 2.1.1.73) (Cytosine-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Membrane.
DOMAIN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acetobacter pasteurianus (Acetobacter turbidans).
Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              052702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methyltransferase
                                                                                                                                Transferase; Methyltransferase; Restriction system.
ACT_SITE 81 81 BY SIMILARITY.
SEQUENCE 429 AA; 46547 MW; E011C7D15B33F5F3 CRC64;
                                                                                                                                                                          Pfam: PF00145; DNA_methylase; 2.
PRINTS; PR00105; C5METTRFRASE.
PROSITE; PS00094; C5_MTASE_1; FALSE_NEG.
                                                                                                                                                                                                                                    EMBL; AF044847; AAC97180.1; -. REBASE; 3281; M.Apali.
                                                                                                                                                                                                                        InterPro; IPR001525; C5_DNA_meth.
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129
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                             GRELRRMSDEFVD
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                                                          Conservative
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42736 MW;
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Pred. No.
                                                                       Score 40;
Pred. No.
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; 273CD402B52068C5
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                                                          Mismatches
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                                                                                    Length 429;
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P52323;
01-OCT-1996
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Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Inthigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwin Doughbarty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bomman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B. Smith H.O., Venter J.C.;

"Genomic sequence of a Lyme disease spirochaete, Borrelia burdorferl.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPOD OR BB0712.

Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last annotation update) RNA polymerase sigma factor rpoD (Sigma-70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BORBU
                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan M., Yeh J., Tsai C.,;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND THEM IS RELEASED. THIS IS THE PRIMARY SIGMA-FACTOR OF THIS BACTERIA.

1- SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF
STRAIN-ATCC
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16-OCT-2001
PROSITE; PS00715; SIGMA70_1; 1.
PROSITE; PS00716; SIGMA70_2; 1.
PROSITE; PS00716; SIGMA70_2; DNA-directed RNA polymerase;
DNA-binding; Complete proteome.
DNA-binding; Complete proteome.
DOWAIN 49 432 POLYMERASE CORE BINDING (POTENTIAL).
DOWAIN 49 608 H-T-H MOTIF (BY SIMILARITY).
SEQUENCE 631 AA; 73642 MW; BD565AB7DBF44796 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                        Pfam; PF00140; sigma70; 1.
PRINTS; PR00046; SIGMA70FCT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature
                                                                                                                                                                                                                                                                           Interpro; IPR000943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hesis (1994),
                                                                                                                                                                                                                                                                                                  AE001171; AAC67061.1; -. U68006; AAC45100.1; -. P00579; 1SIG. BB0712; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         U17591; AAC44104.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390:580-586(1997).
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(Rel. 37, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89-631 FROM N.A.
35210 / B31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165-614 FROM N.A.
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                                                                                                                                                                                                                                                                    Sigma_70
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Score Pred. 3; Mis

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RA51_SCHPO STAN
P36601;
01-JUN-1994 (Rel. 16-OCT-2001 (Rel. 14-01)
                     Ol-JUN-1994 (Rel. 29, Created)
Ol-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA repair protein rhp51 (RAD51 homolog).
RHP51 OR RAD51 OR SPAC644.14C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-WSB8 / DSW 3109;
MEDLINE-99287316; PubMed-10360571;
MEDLINE-99287316; PubMed-10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Melson K.E., Clayton R.A., Gill S.R., Helson W.C., Ketchum H.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Beldelberg J., Sutton G.G., Flelschmann R.D., Elsen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 39:323-329(1999)

1- FUNCTION: HYDBOLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
PHOSPHOGLUCONATE.
   Sch1zosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROF entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last seq
16-CCT-2001 (Rel. 40, Last seq
6-phosphogluconolactonase (EC
PGL OR DEVB OR TM1154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000457; Glucosamine_iso.
Pfam; PF01182; Glucosamine_iso; 1.
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Bacteria; Thermotogales; Thermotoga.

NCBI_TaxID=2336;
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PATHWAY: SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.
SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBRAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
6; Conserv
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220 AA; 25325 MW;
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                                                                                                                                                                                                                STANDARD;
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   pombe
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(Fission yeast)
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annotation update)
(EC 3.1.1.31) (6PGL).
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Pred. No.
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Matches 7
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PIR; $34713; $34713;

PIR; $42107; $42107;

PIR; $37672; $37672;

PIR; $36159; $36159.
                                                                                                                                                                                                                       DNA damage; DNA repair; ATP-binding; DNA recombing damage; DNA repair; ATP-binding; DNA recombing the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the 
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SMART; SM00278; HhH1; 1.
PROSITE; PS50162; RECA_2; 1.
PROSITE; PS50163; RECA_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z22691; CAA80399.1; --
EMBL; D13805; BAA02963.1; --
EMBL; D24756; CAA80879.1; --
EMBL; Z24756; CAA80878.1; A:
EMBL; AL355012; CAB90141.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyne M.H., Rajandream M.A., Barrell B.G., Brown S., Harl
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
-1-FUNCTION: REQUIRED BOTH FOR RECOMBINATION AND FOR TI
DNA, DAMAGE CAUSED BY X-BAYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muris D.F.R., Vreeken K., Carr A.M., Broughton B.C., Lehmann Lohman P.H.M., Pastink A.; "Cloning the RAD51 homologue of Schizosaccharomyces pombe."; Nucleic Acids Res. 21:4586-4591(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000445; HHH.
InterPro; IPR003583; HHH_1
InterPro; IPR001553; RecA.
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"Cloning of human, mouse and fission
homologous to RAD51 and recA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93364417; PubMed=8358431; Shinohara A., Ogawa H., Matsuda Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
   269
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MEDLINE-94051565; PubMed-8233794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces
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REMRTLQRLADEE
                                                 RYGRELRRMSDEF
                                                                                                   Similarity 7; Conser
                                                                                                   Conservative
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28
                                                 14
                                                                                                                      47.0%;
53.8%;
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                                                                                                4
                                                                                                                      Score 39;
Pred. No.
                                                                                                   Mismatches
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n yeast recombination
                                                                                                                                                                                                                                                                                                        DNA recombination
                                                                                                                      DВ
37;
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                                                                                                                                                                                                                             AND 4).
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MEDILINE-89243203; PubMed-2718385;
Wiener J.R., McLaughlin T., Joklik W.K.;
"The sequences of the $2 genome segments of reovirus serotype 3 and
of the dsRMA-negative mutant ts447.";
Virology 170:340-341(1989).
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01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
Sigma 2 protein (Core protein).
S2.
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VARIANT
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EMBL: J02327: -: NOT_ANNOTATED_CDS.
PIR: A31475; FOXT3D.
InterPro; FPR004317; Sigma_1_2.
Pfam: PF03084; Sigma_1_2; 1.
Coemposets
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-83117734; PubMed-6961439;
MEDLINE-83117734; PubMed-6961439;
Cashdollar L.W., Esparza J., Hudson G.R., Chmelo R.A., Lee P.W.K.,
Joklik W.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reovirus (type 3 / strain Dearing).
Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
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H -> V (IN REF. 2).
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Pred. No. 42;
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## ALIGNMENTS

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BA Whitco C. Strong J. Hiddelberg J. F., Bickey E.K., Peterson J.D.,

BA Dodson R.J., Haft D.H., GALINDER, J. Nelson N.C., Richnicon D.L.,

BA Dodson R.J., Haft D.H., GALINDER, Nelson N.C., Richnicon D.L.,

BA Dodson R.J., Haft D.H., GALINDER, Nelson H.G., Richnicon L.,

BA Dodson R.J., Lam P., McDonald L., UtterBack T., Zalzewski C.,

BA Whethewan J.J., Lam P., McDonald L., UtterBack T., Zalzewski C.,

BA Mekarova K.S., Aratund L., Dally M.J., MILLON K.M., Fleischmann R.D.,

BA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,

BA Frasar C.M.;

Tolonome sequence of the radioresistant bacterium Delnococcus

BR Tradiodurans R1.",

Tradiodurans R1.",

Tradiodurans R1.577(1999).

BR Science 286.1571.1577(1999).

BR Science 286.1571.1577(1999).

BR STERRI, NED011831, NATD94.Am.,

BR TICR, PR13132, 1UOK.

BR TICR, PR13132, 1UOK.

BR TICR, PR13178,000.61; Alpha_amylase.

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Interpre, 1PR004111, tetR_C.
Pfam, PP00440, tetR.
Pfam, PP02909, tetR.
PRINTS: PP004655; HTH/EFR.
PRINTS: PP00455; HTH/EFR.
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HEDLING-2112565; Pubmed-11225601; Amanda Y., Nihira T.;

HEDLING-212565; Pubmed-11225601; Amanda Y., Nihira T.;

*Identification of the varR gene as a transcriptional regulator of 
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01-UNY-2001 (TERBELFEL 17, Last annotation undate)
01-YOU-2001 (TERBELFEL 17, Last annotation undate)
01X750.

Delinococcus radiodurans.

Bacteria: Thermus/Delinococcus group; Delinococcales; Delinococcus.
MCBI_TaxID-1299:
[1]
                                                                                                                               DNA-binding; Transcription regulation.
SEQUENCE 247 AA; 27328 MW; B6326F43374598AB CRC64;
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Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:
Actinomycetales: Streptomycineae; Streptomycetaceae; Streptomyces
RDI_TexID-1961;
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Query Match

53.0%;

Score 44;

DB 2;

Length 247

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RE SÉDUBNCE FROM N.A.

RES SÉDUBNCE FROM N.A.

RES SÉRAINANCE 115892 / FAO1:

RES MEDLINE-200477377; PubMed-10084043;

RA HICKEY M.J., BEINKMAD F.S.L., Hufingale W.O., Kowalik D.J., Lagrou W. RA HICKEY M.J., BEINKMAD F.S.L., Hufingale W.O., Kowalik D.J., Lagrou W. RA Garber E.L., Collet S.N., Folget K.R., Kas A., Landby K., Lian R.M., RA BRODY, L.L., Collet S.N., Folget K.R., Kas A., Landby K., Lian R.M., RA BRODY, L.L., Sepande H. Hibinody R.E. W., W. B.

RE SELECT J., Sepande H. Hibinody R.E. W. S., Dalsen I.V., RA BRILOT J., Sepande H. Hibinody R.E. W., W. S., Dalsen I.V., RA BRILOT J., Sepande H. Hibinody R.E. W., W. S., Dalsen I.V., RA BRILOT J., Sepande H. Hibinody R.E. W., W. S., Dalsen I.V., RA BRILOT J., Sepande H. Hibinody R.E. W., W. S., Dalsen I.V., RA BRILOT J., Sepande H. Hibinody R.E. W., W. S., Dalsen I.V., RA BRILOT J., Sepande H. H. Hibinody R.E. W., W. S., Dalsen I.V., RA BRILOT J., Sepande H. H. Hibinody R.E. W., W. S., Dalsen I.V., RA BRILOT J., Sepande H. H. HIBINOGY J., Sepande H. H. HIBINOGY J., Sepande H. H. HIBINOGY J., Sepande H. H. HIBINOGY J., Sepande H. H. HIBINOGY J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPANDE J., SEPAND
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OSHIZO3.

OL MAR-2001 (TERMBLIFE! 16, Created)

OL MAR-2001 (TERMBLIFE! 16, Last sequence update)

OL-CCT-2001 (TERMBLIFE! 18, Last annotation update)

COBALAMIN BIOSYMPHETIC PROTEIN COBN.

COBALAMIN BIOSYMPHETIC PROTEIN COBN.
SEQUENCE FROM N.A.
STRAIM-FRIEDLIN:
STRAIM-FRIEDLIN:
Nedler H., Wedler E., Ducsterhoeft A., Ivens A C
Quall H., Rejandream N.A., Barrell B.G., Togethoeft A., Ivens A C
Summitted (JUN-2009) to the EMBL/Genbank/DDBJ databases
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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pred. No. 1.1e+02;
4; Mismatches 3; Indels
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01-MAY-2000 (Trem
01-MAY-2000 (Trem
01-JUN-2001 (Trem
CG15612 PROTEIN.
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EMBL; AL359781; CAB95305.1; -...

InterPro: IPR000169; Thiolprot_act_site.

PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
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01-DEC-2001 (TREMBLIRE). 16, Last sequence update)
01-DEC-2001 (TREMBLIRE). 19, Last annotation update)
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                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                        CG15612
                                                                                                                                                                   Q9V7Y6
                                                                                                                                                                                                                                                                                                                                                                                        Frohlich M.W., Estabrook G.F.;
"Wilkinson Support Calculated with Exact Probabilities: An Example Using Floricaula/LEAPY Amino Acid Sequences that Compares Three Hypotheses Involving Gene Gain/Loss in Seed Plants.";
Mol. Biol. Evol. 17:1914-1925(2000).
EMBLI, AF2806055; AGA42695.1;
EMBLI, AF2806055; AGA42695.1;
InterPro, IPRO02910; FLO_LEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Polytrichaceae; Atrichum,
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SEQUENCE FROM N.A
                                                                         Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                       NCBI_TaxID=7227;
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nes 9; Conserv
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8; Conserv
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1 (TrEMBLrel.
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Pred. No. 8.3e+02;
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Pred. No.
                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                     A978F91BD8C912CA CRC64;
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54;
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RESULT
Q983UA
ID Q1
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RA Beleson K.Y., Benos P.V., Berman B.P., Bhandarl D., Boshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Chodek A., Cong F., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Chodek A., Gong F., Gorrell J.H., Gu J., Guan P., Harris M.,
RA Chodek A., Gong F., Gorrell J.H., Gu J., Guan P., Harris M.,
RA Chodek A., Gong F., Gorrell J.H., Gu J., Guan P., Harris M.,
RA Chodek A., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Melson D.R., Melson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Melson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Ra Melson D.R., Melson S., Stapleton M., Stupski M.P., Smith T.,
Ra Spiar E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spiar E., Spradling A.C., Turner R., Venter E., Mang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Moyon S. J., Shon W., Zhou X., Zhu X., Smith H.O.,
RA Milliams S.M., Moyon S. J., Shon W., Zhou X., Zhu X., Smith H.O.,
RA When S. J., Shon W., Jakon J., Shon W., Jakon J., Shon W., Jakon J., Shon W., Jakon J., Shon W., Jakon J., Shon W., Jakon J., Shon W., Jakon J., Shon W., Ja
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Best Local
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Adbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballow R.M., Bashawani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballow R.M., Bashawani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballow R.M., Bashawani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                           Rhizobium loti (Mesorhizobium loti)
Bacteria; Proteobacteria; alpha sub
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, C)
01-OCT-2001 (TrEMBLrel. 18, L;
01-OCT-2001 (TrEMBLrel. 18, L;
01-OCT-2001 (TrEMBLRel. 18, L;
                                                                                                                                                                                                                 Q983J4;
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00621; RhoGEF; 1.
SMART; SM00233; PH; 1.
SMART; SM00325; RhoGEF; 1.
SEQUENCE 415 AA; 49479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The genome sequence of Drose Science 287:2185-2195(2000).
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                                                                                                                     MLR8303.
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8; Conser
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                                                                       alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                Created)
Last sequence update)
Last annotation updat
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Pred. No.
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68;
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CG15612

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Best Local S
Matches
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Best Local Similarity 43.
Matches 7; Conservative
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Haigler B.E., Suen W.C., Spain J.C.;
"Purification and sequence analysis of 4-me:
"purification and sequence analysis of 4-me:
"oxygenase from Burkholderia sp. strain DNT."
J. Bacteriol. 178:6019-6024(1996).

EMBL; U68411; ANC44479.1:
EMBL; U684411; ANC44479.1:
Interpro; IPR002038; Moxy-FAD_binding.
Interpro; IPR002038; Moxy-FAD_binding.
Interpro; IPR003042; Rng_mnoxygenase.
Pfan; PF01360; MONOCOXYGNASE.
PRINTS; PR00402; RNGMNOXGNASE.
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P71029;
01-FEB-1997
01-FEB-1997
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome structure of the nitrogen-fixing symbiotic bacterium Resorhizobium loti.";
DNA Res. 7:331-338(2000);
EMBL: APO03013; BAB53887.1; -
Dlaxygenase; Complete proteome.
SEQUENCE 457 AA; 51046 MW; 6A20B69E9A2B2BD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sase watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot Takeuchi C., Yamada M., Tabata S.;
              Q960B3;
01-DEC-2001
01-DEC-2001
01-DEC-2001
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SEQUENCE
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STRAIN-MAFF303099;
STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4-METHYL-5-NITROCATECHOL OXYGENASE
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-DNT
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    SD09786P.
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7; Conser
              1 (TrEMBLrel.
1 (TrEMBLrel.
1 (TrEMBLrel.
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(TremBLrel. 02, Last sequence update)
(TremBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                548 AA;
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                                                              PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (strain RASC)
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19,
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Pred. No.
               Last sequence update)
Last annotation update)
                                       Created)
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75;
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DNT.";
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RESULT
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Best Local
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PÉAM; PF00643; Zf.B_box; 1.

PÉAM; PF00097; Zf.GHC4; 1.

PÉAM; PS00097; Zf.GHC4; 1.

SMART; SM00136; BBOX; 1.

SMART; SM00136; RBOX; 1.

SMART; SM00184; RING; 1.

SMART; SM00189; CYTOCHROME_C; UNKNOWN_1.

PROSITE; PS00028; ZINC_FINGER_C3HC4; 1.

PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.

DNA-binding; Metal-binding; Zinc; Zinc-finge SEQUENCE 653 AA; 71988 MM; D83B1595CA837
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EMBL. AVOS2140; AAK83564 l; *.

EMBL. AVOS2140; AAK83564 l; *.

SEQUENCE 592 AA; 69459 MW; CC5FD772459F2A83 CRC64:
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Q9NQP8;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-DCC-2001 (TrEMBLrel. 19, Last annotation update)
BA67K19_2 (ZINC-FINGER PROTEIN HT2A (72 KDA TAT-INTERACTING PROTEIN))
(TAT-INTERACTIVE PROTEIN, 72-KD).
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ORYGRELRRMSDEFV
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                                                                                                               zīnc; Zinc-finger.
w; D83B1595CA8378FD CRC64;
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Pred. No.
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1e+02;
                              DB 4;
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                           Length 653;
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Query Match Best Local Similarity

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1.1e+02;

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099TJ8; 01-JUN-2001 (TEMBLTel. 17, CI
1 01-JUN-2001 (TEMBLTel. 17, LI
1 01-DEC-2001 (TEMBLTel. 19, L
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VALINE-TRAA LIGASE.
VALS OR SAV1663
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Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
Matsumaru H., Maruyama A., Murakami H., Hosyama A., Mizutani-Ui Y.,
Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus."; 1225-1240(2001).
EMBL, AP003134; BAB42754.1; -.
HSSP, P96142; IGAX.
                                                                                                                                                        Staphylococcus aureus (strain Mu50).
Bacitria; Firmicutes; Bacillus/Clostridium gro
Bacitlus/Staphylococcus group; Staphylococcus
NCBI_TaxID-158878;
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InterPro: IPRO01412; tRNA-synt_1.
InterPro: IPRO01412; tRNA-synt_1e.
InterPro: IPRO02301; tRNA-synt_1e.
InterPro: IPRO02303; tRNA-synt_1p.
Pfam: PF00133; tRNA-synt_1p.
PRINTS; PR00986; TRNASYNTHVAL.
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Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
NCBI_TaxID=158879;
   MEDILINE-21311952; PubMed-11418146; Wirdama I., Baba T., Yuzawa H., Kuroda M., Otka T., Uchiyama I., Baba T., Yuzawa H., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O.,
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                                                                                               SEQUENCE FROM N.A.
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SEQUENCE 876 AA; 101723 MW;
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8; Conserv
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Bacillus/Clostridium group;
us group; Staphylococcus.
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Pred. No. 1.5e
3; Mismatches
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1.5e+02;
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Submitted (APR-2000) to th
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SMART; SM00478; ENDO3c; 1.
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Mol. Microbiol. 21:77-96(1996).
EMBL; AL353870; CAB89025.1; -.
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Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekinizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus aureus.;
Lancet 357:1225-1240(2001).
EMBL, AP003363; BAB57825.1; -.
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Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 17, Last annotation update)
HTPOTHETICAL 23.8 KDA PROTEIN.
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e EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 50.8 KDA PROTEIN.
ATG330490.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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EU Arabidopsis sequencing project;

EU Arabidopsis sequencing project;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; ALI61577; CAB79767.1; -.

Hypothetical protein.

SEQUENCE 447 AA; 50837 MM; CB24C84F167CE3AF CRC64;
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Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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84 RELQRLYDELVD 95
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26-SEP-1997;
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## ALIGNMENTS

AAY05423 standard; peptide; 16 AA .

02-JUL-1999 (first entry)

BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoproliferative condition; arthritis; autoimmune disease; therapy.

970S-0946039. 970S-0060133. 98WO-US19765

(UNIW ) UNIV WASHINGTON

Bcl homology domain 3 polypeptide

# x 55555555555555

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Matches 16
The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n = 1-10; x = C-O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COON or CONH2; and R = 2-18C alkyl or alkoxy, 2-18C alkylenyl containing one or two double bonds, cyclobusyl, cyclopentyl, cyclohexyl opstionally monosubstituted with a 1-5C straight or branched chain alkyl group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the BH3 domain of human BAK.
The invention relates to a bcl homology domain 3 (BH3 domain),
derived from a proapopictic member of the BCL-2 family. The
BH3 polypeptide can be used in a method for promoting apoptosis in a
target cell. especially where the cell is a cancer cell a virus infected
cell or an autoantibody producing cell. The BH3 polypeptide can be used
in therapeutic compositions for treating disease including cancer; other
lymphoproliferative conditions, arthritis, inflammation, and autoimmune
diseases, which may result from the down regulation of cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic, neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bel-1 superfamily; BB domain; cell death agonist; Bed; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric, non-small lung; tensi; thyroid; neuroblastoms; melinoms; lymphocytic_leukemia; neurodegenerative disorder; AIDS;
                                                                                                                                                                      Claim 18;
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                                                                                                                                                                                                                                                                                                                                           phenyl optionally monosubstituted with a 1-5C straight or branched chain ally group, or benzyl. The peptides AAB37001-37058 represent examples cof the peptides portion of the conjugate. The peptides represent analogues cof the gall domain of the conjugate are present analogues. The BBL-2 superfamily polypeptide corresponding to amino acids 72-97 of the BBJ domain of the cell death agonist BBL. The peptide conjugate is useful for modulating apoptosis in the cells of a subject or for reversing B cell lymphomal/leukemia 2 (BCL-2)-mediated blockage of capoptosis in cancer cells. It is also useful for inhibiting Bcl-2 apoptosis in particular, the peptide conjugate is useful for treating a subject afflicted with a cancer conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, con-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic laukemia. The peptide conjugate is also useful for treating disorders characterized by cancer acquired conjugate is also useful for treating disorders characterized conjugate is also useful for treating disorders characterized by cancer acquired conjugate is also useful for treating disorders characterized by cancer acquired conjugate is also useful for treating disorders characterized by cancer acquired conjugate is also useful for treating disorders characterized by cancer acquired conjugate is also useful for treating disorders characterized by cancer acquired conjugate is also useful for provider acquired to the conjugate is also useful for treating disorders acquired conjugate is also useful for treating disorders acquired to the conjugate is also useful for treating disorders acquired to the conjugate is also useful for treating disorders acquired to the conjugate is acquired to the conjugate is acquired to the conjugate is acquired to the conjugate is acquired to the conjugate is acquired to the conjugate is acq
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RESULT AAB71977 AAB71977 AAB71977 standard; w peptide; 16 ⋛

Bak BH3 peptide 11-MAY-2001 (first

Bak; BH3 domain; antiapoptotic; cytostatic; antimycin; neoplasia; cancer apoptosis;

WO200114365-A1 Mammalia.

18-AUG-2000; 2000WO-US22891

20-AUG-1999; 99US-0149968

Hockenbery DM, HUTCHINSON CANCER RES CENT FRED Simon JA, Tzung

WPI; 2001-244291/25

protein, antimycin useful derivatives that bind to antiapoptotic Bcl-2 for modulating the apoptotic state of a cell family

Example 6; Page 41; 60pp; English.

The present sequence was used in an example illustrating an invention relating to an antimycin derivative which modulates apoptosis by binding to a Bc1-2 family protesin and preferentially induces apoptosis in a cell which over expresses the Bc1-2 family protesin. The antimycin derivative is used in treating an apoptosis associated disease and for inducing apoptosis. It is also useful for treating empaphasis and drug resistance. The present sequence binds to the hydrophobic poket of Bc1-2. A competitive binding assay was used to determine if the site of antimycin A3 interaction the hydrophobic pocket

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The invention relates to a peptide conjugate having the formula:

(R*X)n*peptide where n = 1-10; X = C=0, when the R*X group is attached to the N*terminus of the peptide, or a side chain of the peptide where c the functional group of the side chain is NH2 or 0H; or X = 0 or NH.

CC when the R*X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain is NH2 or 0H; or X = 0 or NH.

CC or two double bonds, cyclobutyl cyclopentyl cyclobexyl optionally components and the peptide with a 1-5C straight or branched chain akyl group, or benzyl. The peptides ANB37001-B37058 represent examples of the peptide pertion of the conjugate The peptides can analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the Billy domain of the coll death agonist Had. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of subject affilted with a cancer characterized by cancer cells that conspess Bcl-2. The cancer includes prostate, colorectal, gastric, consmall lung, renal or thyroid cancers, beuroblastcma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bel-2) function, especially useful for trasting neurodegenerative disorders, stroke, or cancer
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Pred. No. 1.2e-07
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                                                                                                                                                                                                                                                                                                                                                                                         Seguence
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16; Conserv
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100.0%; pr
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The present sequence is the mammalian Bak BCI-2 homology domain 3 (BH3) domain, which was used in a sequence alignment with the same domain of a putative version of the mammalian apportosis regulator BBC3, which was designated BBC3-ORF2. The BBC3 protein, nucleic acids and antibodies are suitable for use in promoting cell death or for preventing apoptosis in mallynant cells and those caus autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polymucleotide encoding a BBC3 protein which is useful for modulating apoptosis, especially in the treatment of cancer and autoimmune diseases \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conjugate is also useful for treating disorders characterized by increased approasts e.g. neurodesgenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammal; apoptosis; cell death; BBC3; apoptosis promotion; apoptosis inhibition; malignant cell; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 4; 47pp; English.
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Pred. No. 1.3
0; Mismatches
Score 80; DB 21;
Pred. No. 2.1e-07;
y Mismatches 0;
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RESULT
AAB37004
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                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apoptosis,
Serll3 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (APOP-) APOPTOSIS TECHNOLOGY INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-138734/14.
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nes 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC1-XL/PG1-2 Associated Cell Death Regulator polypeptide screening for candidate compounds which induce or inhibit comprises amino acid substitutions at Seril8, SeriS5 or
                                                                                                                                                                                                                                                                                                                                                                                                          26
                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                              Score 80; DB 22; I
Pred. No. 2.1e-07;
Pred. No. 2.1e-07;
                                                                                                                                                                                                                                                                                                        Length 26;
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The invention relates to a peptide conjugate having the formula:

(R * N)n * Peptide where n = 1.10; X = C=0, when the R * X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = 0 or NH, CC when the R * X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is group is trached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or two double bonds, cyclobuty1, cyclopenty1, cyclopenty1, cyclobexy1 containing one or two double bonds, cyclobuty1, cyclopenty1, cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobexy1 cyclobe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (Bel-1) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; neuroprotective; enti-NIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; BBd; apoptosis modulation; B cell lymphome/Leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; hupphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; Page 17; 74pp; English.
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27
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The term GD domain refers to a protein domain first identified in Bak and shown to be essential for the interaction of Bak with Bcl.x(L) and for Bak's cell killing function; and to peptides and/or molecules capable of minicking its structure and/or function. The present sequence represents a GD domain corresponding to amino acid residues 67-94 of Bak. An antibody raised against a GD domain may be used to screen a CDNA expression library for clones comprising cDNA inserts encoding immunocrossreactive proteins. Truncated GD domain peptides have been shown to maintain the protein binding and cell killing function exhibited by wild type Bak. These molecules may induce apoptosis in tumour cell. These peptides act independently of p53 status. Bak or GD domain mimetics that inhibit Bcl-2 may be selectively toxic to certain timustres.
                                            AAW79535;
                                                                                       AAW79535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 52; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide(s) comprising GD domains - have similar activities to wild type Bak, and cause cellular apoptosis for treatment of viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chittenden TD,
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  11-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 infected cells.
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                                                                                                                                                                                                                                           GQVGRQLAIIGDDINR 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumours, e.g. follicular lymphoma, which depend on high levels for their continued growth and survival. GD domain mimetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT42428
                                                                                       standard; Protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region for Bak amino acid residues 67-94.
                                                                                                                                                                                                                                                                                                                                                                                                    28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           follicular lymphoma; tumour; p53; antibody
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used for combatting viral infections by causing apoptosis
  (first entry)
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                                                                                                                                                                                                                                                                                                             Score 80; I
Pred. No. 2
                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                             JB 17;
2.2e-07;
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                                                                                                                                                                                                                                                                                                                               Length 28;
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80
                                                        Matches
                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                         This is the amino acid sequence of Bak-delta2-TM, a truncated polypeptide comprising amino acids 71-187 of Bak (see AAW79534). A nucleotide sequence encoding Bak-delta2-TM was obtained from CDNA by PCR and cloned as an in-frame fusion to the GAL4-DNA binding domain in vector pAS2-1. The construct was used in a two-hybrid screen of human heart cDNA for the identification of clones encoding Bak binding proteins. The invention relates to a novel Bak binding protein (BBP, see AAW79537), the gene encoding BBP (see AAV61499), methods for detecting substances that alter the specific binding between Bak and BBP, as well as diagnostic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Bak-binding protein and related nucleic acid, vectors, transformed cells and antibodies - are useful for modulation of apoptosis in cancer, neuro-degeneration etc., also peptide fragments of Bak that interact with the profess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell death; cancer; lymphoma; neurodegeneration; heart dicell proliferation; infection; human; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-521220/44.
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20-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Truncated Bak polypeptide Bak-delta2-TM
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                  therapeutic methods utilising BBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 53; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barr PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-SEP-1998
                                                        Local Similarity hes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bak binding protein; BBP; bbpbd-1; bbpbd-2; Bcl-2; apoptosis; death; cancer; lymphoma; neurodegeneration; heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fitzpatrick PA,
                                                                                                                                                                                                   117 AA;
                                                        Conservative
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970S-0041328
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                                                                               100.0%;
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                                                        0,
                                                                                   Score 80;
Pred. No.
                                                        Mismatches
                                                                            1.1e-06;
                                                                                                                DB 19;
                                                                                                             Length 117;
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AAR77880
IID AAR77
XX
AC AARR
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DI 21-P
DI 21-P
DI 21-P
DI STAN Cdn
KW Cdn
KW Cdn
KW Shoc
XX
KW Shoc
XX
PN WO95
                                                                       Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                   Homo sapiens
                                                                                                           Human Cdn-1(71-211).
                                                                                                                                     21-NOV-1995
                                                                                                                                                                                    AAR77880 standard; Protein; 141 AA.
                                                                                                                                                                                                                                            Lymphoma;
                                                                                                                                   (first entry)
                                                              eczema.
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W09515084-A

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Best Local S
Matches 16
                                                                                                                                                                                                                                     Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. Deletion of the N-terminal 70 amino acids of Cdn-1 improved this activity, suggesting that small, truncated Cdn-1 molecules may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
          New nucleic acid sequences encoding Cdn apoptosis modulators related vectors, transformed cells, proteins and antibodies, or diagnosis and treatment e.g. of HIV infection, reperfusion
                                                                                                                    07-OCT-1994;
30-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig.11; 66pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barr PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-1994;
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                                                       WPI; 1995-215106/28
                                                                                                                                                     30-NOV-1994;
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                                                                                                (LXRB-) LXR
                                                                                                                                                                          08-JUN-1995
                                                                                                                                                                                              WO9515084-A
                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                   Human Cdn-1(60-211).
                                                                                                                                                                                                                                                                                                                                               AAR77879 standard; Protein; 152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     potent therapeutics
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                                                                                                BIOTECHNOLOGY INC
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                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                    94US-0320157.
93US-0160067.
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93US-0160067.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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Pred. No. 1.3e-06;
Mismatches 0;
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            reperfusion injury
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2.1e-06;

Similarity

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Query Match
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                                                                                                                                                                                        New nucleic acid sequences encoding cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Pas-mediated apoptosis. Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly decreased this activity, suggesting that small, truncated Cdn-1 molecules may be potent therapeutics.
                                                                                        Cdn-1 cDNA was isolated from a human heart cDNA library using a previously isolated clone as probe. Recombinant Cdn-1 was produced in Sf9 and human colon adenocarcinoma HT99 cells. Expression of cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                 Barr PJ, Kiefer MC.
                                                                                                                                                                                                                                                                                                                                 07-OCT-1994;
30-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shock; lymphoma; eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR77876;
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                                                                            survival in response to anti-Fas-mediated apoptosis.
                                                                                                                                                      Disclosure; Fig.3A-B; 66pp;
                                                                                                                                                                                                                                                                                                          (LXRB-) LXR BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                        30-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                             1995-215106/28.
DB; AAQ95492.
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                                                    211 AA;
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93US-0160067.
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Pred. No.
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RESULT 1
AAW03668
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AAR77877
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Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                     Cdn-2 cDNA was isold. from a human placental genomic library using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino acid identity with Cdn-1 (AAR77876).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HTV; autoimmune disease; reperfusion injury; hepatitis; osteoporosis; shock; lymphoma; eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-215106/28.
N-PSDB; AAQ95493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-OCT-1994;
30-NOV-1993;
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    Human; Bak; apoptosis; latency; virus replication;
                                  Bak protein.
                                                                                                     AAW03668;
                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig.5D-E; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barr PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LXRB-) LXR BIOTECHNOLOGY INC
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                                                                                                                                    AAW03668 standard; Protein; 211 AA
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93US-0160067.
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                                                                   entry)
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Pred. No. 2.1e-06;
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Best Local S
                                                  W09633416-A1
                                                                                 Homo sapiens
                                                                                                                                                                                                 Bak-2 protein.
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                                                                                                                                                                                                                                                                    AAW03669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostic agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-APR-1995;
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16; Conser
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This Bak protein sequence represents a bc1-1 homologue which interacts with Epstein-Barr virus (EEM) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak protein and a viral protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or disport in contraction may be used as virucide, antitumour or disport in contraction may be used as virucide, antitumour or disport in contraction may be used as virucide.
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Human; Bak-2; apoptosis; latency; virus replication; Epstein-Barr virus; BHRF1; fusion protein; epitope tag; drug screening; co-precipitation; ELISA; lamunoassay; aprotein interactive trapping; virucide; antitumour; diam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening for anti-viral agents - by detecting the ability of agent to disrupt the interaction of a Bak protein and a viral
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW03669 standard; Protein; 211 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9505-0426529
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Pred. No.
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. 2.1e-06;
         ; immunoassay; antibody;
antitumour; diagnostic.
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Search completed: September 20, 2002, 10:35:58 Job time: 426~\text{sec}
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                                                                                                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                         This Bak-2 protein sequence represents a bol-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein and is capable of modulating apoptosis. The protein may be used in complete or partial form, or as an epitope tag fusion protein in a new virucide drug screening method, which involves combination of Bak-2 protein and a viral protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak-2 and viral proteins allows viral replication or lateory in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or disapped to the protein and the protein sequence of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening for anti-viral agents - by detecting the ability of an agent to disrupt the interaction of a Bak protein and a viral protein
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N-PSDB; AAT42139.
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                   diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 24pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-1995;
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|72 gqvgrqlaiigddinr 87
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                                                                                                                                                                                                                                                211 AA;
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                                                                                                                                                            0;
                                                                                                                                                        Score 80; DB 17;
Pred. No. 2.1e-06;
); M1smatches 0;
                                                                                                                                                                                        Length 211;
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a 11, Appl
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Result
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Maximum DB seq
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Perfect score:
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 protein search, using sw model
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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80
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Copyright (c) 1993 - 2000 Compugen
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                 BB
         US-09-236-388A-35
US-09-236-386A-35
US-08-440-391-2
US-08-440-391-2
US-08-908-597A-18
US-08-908-597A-18
US-08-908-597A-18
US-08-908-597A-18
US-08-108-597A-18
US-08-108-597A-14
US-08-108-597A-14
US-08-401-297A-14
US-08-471-058-23
US-08-471-058-23
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         Sequence 35, Appl.
Sequence 2, Appl.
Sequence 2, Appl.
Sequence 18, Appl.
Sequence 18, Appl.
Sequence 18, Appl.
Sequence 18, Appl.
Sequence 14, Appl.
Sequence 14, Appl.
Sequence 14, Appl.
Sequence 14, Appl.
Sequence 14, Appl.
Sequence 14, Appl.
Sequence 14, Appl.
Sequence 12, Appl.
Sequence 12, Appl.
Sequence 13, Appl.
Sequence 16, Appl.
Sequence 17, Appl.
Sequence 11, Appl.
Sequence 11, Appl.
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                                                                                                                                                                                                                                                                                                                                                    Description
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US-09-236-385A-35
                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ
US-09-236-385A-35
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GENERAL INFOCMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
                                                             Query Match
Best Local Similarity 100
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 202-942-840:
TELEFAX: 202-942-848:
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: IDM PC compatible
COMPUTER: IDM PC compatible
COMPUTER: IDM PC compatible
COMPUTER: 1DM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/236,385A

FILING DATE: 25-Jan-1999
ATTORIEX, SECRET INFORMATION:
NAME: WIXON, HEMRY N.

REGISTRATION NUMBER: 32.073

REGISTRATION NUMBER: 32.073
              N
                             1 GQVGRQLAIIGDDINR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
              GOVGROLATIGDDINR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOVEL PEPTIDES AND COMPOSITIONS WHICH MODULATE APOPTOSIS
                                                                            08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-471-057-11
US-08-440-391-3
US-08-440-391-3
US-08-440-391-16
US-08-908-597A-16
US-08-908-597A-16
US-08-908-597A-16
US-08-908-597A-16
US-08-908-597A-16
US-08-908-908-908-908-908-908-908-907A-20
US-08-908-908-907A-20
US-08-908-908-97A-20
US-08-908-385A-20
US-09-236-385A-20
US-09-236-385A-20
US-09-236-385A-20
US-09-236-385A-20
US-09-236-385A-20
                                                                0;
                                                               Score 80; DB 4;
Pred. No. 3.6e-08;
; Mismatches 0;
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                                                                                         DB 4; Length 19;
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Gaps

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; MOLECULE TYPE: PEPTIDE
SEQUENCE DESCRIPTION: SEQ ID NO: 36
US-09-236-385A-36
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Best Local Similarity
Matches 16; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                               Sequence 2,
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
ZIF: 20004
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 202-942-84
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 36
                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                APPLICANT: CHITTENDEN, Thomas D.; and APPLICANT: LUTZ, ROBERT J. REPTIDES AND COMPOSITIONS WHICH PITLE OF INVENTION: MODULATE APOPTOSIS
                                                                                                                   STATE: D. STATE: 20004
                                                                                                                                                    STREET: 14-0
CITY: Washington
                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GQVGRQLAIIGDDINR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GOVGROLATIGDDINR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMBUTER: IBM PC COMBAILINE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: RALGULIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/236.385A
FILING DATE: 25-JBN-1999
FILING DATE: 25-JBN-1999
CLASSIFEICATION: CURROWND
ATTORNEY/AGENT INFORMATION:
NAME: MIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LUTZ, ROBERT J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CHITTENDEN, Thomas D.; and
                                                                                                                                                                                                                                                                                                                                                              , Application US/08440391 5656725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 20 amino acids
                                                                                                                                                                                       E: Hale and Dorr
1455 Pennsylvania Avenue, N.W.
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3.8e-08;
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-440-391-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/08440391 Patent No. 5656725
                                                                                                                                                                                          MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPAtible
OPERATIOS YSTEM: PC-105/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-195
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MIXON, HERRY N.
REGISTRATION NUMBER: 32,073
REGISTRATION NUMBER: 37,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 16; Conservative 0
                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-9400
TELEPAX: 202-942-9494
INFORMATION FOR SEQ 1D NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHITTENDEN, Thomas D.; and APPLICANT: LUTZ, Robert J. TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH TITLE OF INVENTION: MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202-942-8400
                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1455 Penr
CITY: Washington
                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-942-8484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 12-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GQVGRQLAIIGDDINR 16
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                                                      H: 28 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Hale and Dorr
1455 Pennsylvania Avenue, N.W.
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12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Query Match Best Local Similarity Matches 16; Conserv

100.0%; Score 80; Dilarity 100.0%; Pred. No. 5. Conservative 0; Mismatches

.7e-08;

Indels

0;

Gaps

0;

Length 28;

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COMPUTER READABLE FLOWS

MEDIUM TYPEE IBM EC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PC-DOS/MS-DOS

SOFTWARE: PC-DOS/MS-DOS

SOFTWARE: PC-LOSTION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

10 ANY:

11 INCOMMINICATION:

REGISTRATION NUMBER: 12,03

REFERENCE/COCET NUMBER: 12,03

REFERENCE/COCET NUMBER: 10,4322.147

TELECOMMUNICATION INFORMATION:

TELECHN: 202-942-84400

TELECHN: 202-942-84400

TELECHN: 202-942-8450

INFORMATION FOR ESD ID NO: 2:

STOUGHCE CHARACTERISTICS:

LENGTH: 28 maino acid

TYPE: amino acid

TYPE: amino acid

TOPOLOGY: linear

TYPE: amino acid

TOPOLOGY: linear
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                                                                                                                                                                                                                                                                       RESULT 6
US-08-908-597A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-908-597A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-908-597A-2
                                                                                                                                                                                                  Sequence 18, Application Patent No. 5863795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08908597A Patent No. 5863795
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match

100.0%; Score 80; Diest Local Similarity 100.0%; Pred. No. 5.7

Matches 16; Conservative 0; Mismatches
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APPLICANT: CHITTENDEM, Thomas D.; and APPLICANT: LUTP, MODEL & PEPTIDES AND COMPOSITIONS WHICH TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH WHERE FOR PERCENCES.

MUMBER OF SEQUENCES.

ADDRESSPONDENCE ADDRESS.

DDRESSPONDENCE ADDRESS.

CITT: WASHINGTON
CITT: WASHINGTON
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TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH
TITLE OF INVENTION: MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C
ZIP: 20004
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                                                                                                                                                                                                                                18, Application US/08908597A
5. 5863795
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1455 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHITTENDEN, Thomas D.; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-908-597A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
US-09-236-385A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
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: Patent No. 6221615 
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER FANDABLE FORM:

COMPUTER: 15M pc compatible
COMPUTER: 15M pc compatible
COMPUTER: 15M pc compatible
COMPUTER: 15M pc compatible
COMPUTER: 15M pc compatible
COMPUTER: 15M pc compatible
COMPUTER: 15M pc compatible
COMPUTER: 15M pc compatible
FILING DATE: 15M pc compatible
CLASSIFICATION UNMER: U5/08/908,597A
FILING DATE: 12-MAY 1995
ATTORNEY,AGENT INFORMATION:
APPLICATION UNMER: U5/08/440,391
FILING DATE: 12-MAY 1995
ATTORNEY,AGENT INFORMATION:
RAPELSTRATION UNMERS: 32-073
RESEASTREED,COKET UNMERS: 104322.147
TELEPONUTHICATION INFORMATION:
TELEPONUTHICATION INFORMATION:
TELEPONUTH CONTON INFORMATION:
TELEPONUTH CAST UNMERS: 104322.147
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Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEPHONE: 202-942-8484
TRECEPHONE: 202-942-8484
INFORMATION FOR SEQ D NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   ZIF: 2004

COMPUTER READABLE FORM:
MEDIUM TIPE: Floppy disk
MEDIUM TIPE: Floppy disk
MEDIUM TIPE: Floppy disk
MEDIUM TIPE: Floppy disk
MEDIUM TIPE: Floppy disk
MEDIUM TIPE: Floppy disk
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ZIP: 20004
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LUTZ, Mobert J.
TITLE OF INVENTION: NOVEL PEPFIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEP: Hale and Dorr
SYREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18:
                                                                                                                                                                                                                                                                                                       ATTORNEY DOCKET NO. 104322,147CIP
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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SETEM: PC-DOS/MS-DOS
SOFTWARE: PECENTID ROTA:

COMPUTER: IBM PC compatible
OPERATING SETEM: PC-DOS/MS-DOS
SOFTWARE: PECENTID NOTA:

APPLICATION NUMBER: US/99/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION NUMBER: 25,073
ATTONEY/ACENT INFORMATION:
REGISTRATION NUMBER: 32,073
TELECOMMUNICATION INFORMATION:
TELEPRONE: 202-942-8400
TELEPRONE: 202-942-8400
TELEPRONE: 202-942-8400
INFORMATION TELEPRONE: 202-942-8400
INFORMATION TELEPRONE: 202-942-8400
INFORMATION TOR SED ID NO: 18:
SEQUENCE CHARACTERISTICS:
LEATOTH: 28 anino acids
TYPE: anino acids
TYPE: anino acids
TYPE: anino acids
TYPE: anino acids
TYPE: anino acids
TYPE: peptide
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
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US-09-2363A-18
US-09-236385A
; Sequence 18. Application US/09236385A
; Patent No. 6221615
; GENERAL INFORMATION: CHITTENDEN, Thomas D.; and APPLICANT: CHITTENDEN, Thomas D.; and LUTZ, Robert J.

**COMMANDATION: CHITTENDEN, Thomas D.; AN EXECUTION OF THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND THE PROPRIES AND TH
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TYPE: amino acid;
TOPOLOGY: linear
HOLEGULE TYPE: peptide;
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-236-385A-2
RESULT 9
PCT-US95-06122-2
Sequence 2, Application PC/TUS9606122
GENERAL INFORMATION:
APPLICANT: IMMUNOGEN, INC.
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 100.0%; Score 80; DB 4; Best Local Similarity 100.0%; Pred. No. 5.7e-08; Matches 16; Conservative 0; Mismatches 0;
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ADDRESSEE: Hals and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                           .7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 28;
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PCT-US96-06122-18
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COMPUTER READABLE FORM:

MEDIUM TIPE: Elopyy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURERNT APPLICATION DATA:

APPLICATION HORBER: PC-TUS96/06122

FILING DATE: HEREMITH

CLASSIFICATION UNBER: PTOR APPLICATION UNBER: PTOR APPLICATION UNBER: PTOR APPLICATION UNBER: US 08/440,391

FILING DATE: 12-NAY-1995
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MEDIUM TIPE: Floppy disk

MEDIUM TIPE: Floppy disk

COMPUTER: IUM PC Compatible

COMPUTER: FLOP COMPATIBLE PC CONS./MS-DOS

OPERATING SYSTEM: PC-DOS./MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: PATENTION DATA:

APPLICATION NUMBER: PCT/US96/06122

FILING DATE: HEREWITH

CLASSIFICATION NUMBER: US 08/440,391

FILING DATE: 12-MAY-195

FILING DATE: 12-MAY-195

CLASSIFICATION: NATORNAL NUMBER: PCT/US96/06122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 11043
TELECOMMUNICATION INFORMATION:
TELEPANE: 202-942-8464
TELEPANE: 202-942-8464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: IMMUNOGEN, INC.
APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: WAVEL PEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: WHICH WODDLATE APOPTOSIS
MUNDER OF SEQUENCES: 34
CORRESPONDENCE ANDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1155 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: WOCEL PEPTIDES AND C
TITLE OF INVENTION: WHICH MODULATE APOPT
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and DOTT
STREET: 1455 Pennsylvania Avenue, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                             US-08-440-391-14
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Patent No. 5
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Best Local Similarity
Matches 16; Conserv
                                                Matches
                                                               Query Match
Best Local :
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TELECHIONE: 202-942-8400
TELECRA: 202-942-8484
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION UNBER: 12,073
REFERENCE/DOCKET NUMBER: 1043
TELECOMUNICATION LIFORMATION:
TELEPHONE: 202-942-8400
                                                                                                                                                                                                                          TELEFAX: 202-942-8484 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CHITTENDEN, Thomas D.; and APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH TITLE OF INVENTION: MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C. 20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/440,391 FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                Local Similarity
les 16; Conserv
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                                                                                                                                                                                             LENGTH:
1 GQVGRQLAIIGDDINR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4, Application US/08440391 5656725
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amino acid
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1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                           36 base pairs
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ilarity 100.0%;
Conservative
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                                                               100.0%; Score 80; DB 1; 100.0%; Pred. No. 7.6e-08;
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Pred. No. 5.7e-08;
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                                                    Mismatches
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RESULT 12
US-08-908-597A-14
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                                                                                                                                                                                                                                                                    RESULT 13
US-09-236-385A-14
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                           Sequence 14, Application US/09236385A Patent No. 6221615
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH
TITLE OF INVENTION: MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 202-942-8400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D. 20004
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                            1 GOVGRQLATIGDDINR 16
                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W
                                                                                                                                                            LUTZ, Rob
TITLE OF INVENTION:
COMPUTER READABLE FORM:
                                                                                                                                                                                              APPLICANT: CHITTENDEN, Thomas D.; and
                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                         GOVGROLATIGDDINR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                              CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 80; DB 2;
100.0%; Pred. No. 7.6e-08;
                                                                                                                             Robert J.
ON: NOVEL PEPTIDES AND COMPOSITIONS WHICH MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/908,597A
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PCT-US96-06122-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application PC/TUS9606122
GENERAL INFORMATION:
APPLICANT: IMMUNGEN, INC.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 100.0%; Score 80, DB 4;
Best Local Similarity 100.0%; Pred. No. 7.6e-08;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION:
                                                                               TELEFAX: 202-942-8484
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20004
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-005/MS-005
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-942-8484 INFORMATION FOR SEQ ID NO: 14:
                                  SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
                                                                                                                       TELEPHONE: 202-942-8400
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1455
STREET: Washington
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: U. 2004
TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GQVGRQLAIIGDDINR 16
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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LENGTH: 36 base pairs
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NAME: WIXON, HENRY N.
                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: WIXON, HENRY N. REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/236,385A FILING DATE: 25-Jan-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Hale and Dorr
1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                  32,073
                                                                                                                                                                   104322.147PCT
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US-08-471-058-23
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                                                              Query Match
Best Local S
Matches 16
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Best Local Similarity
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APPLICANT: Kiefer, Michael C.

APPLICANT: Barr, Philip J.

APPLICANT: Barr, Philip J.

TITLE OF INVENTION: ROVEL APOPTOSIS MODULATING

TITLE OF INVENTION: PROTEINS, DNA ENCODING THE

TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                             TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/320
FILING DATE: 07-0CT-1994
APPLICATION UNMERER: 08/164
FILING DATE: 30-NOV-1993
ATTORNEY/ACENT INFORMATION:
NAME: Lebnhardt, Susan K
REGISTRATION NUMBER: 33,94
                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FRANCISC for Windows Version
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304-1018
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: /-
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                                                              Local Similarity
nes 16; Conserv
                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GQVGRQLAIIGDDINR 17
                   1 GQVGRQLAIIGDDINR 16
                                                                                                                                                                                          amino acid
                                                            100.0%; Score 80; DB 1; ilarity 100.0%; Pred. No. 3.8e-07; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                           08/160,067
                                                                                                                                                                                                                                                                                                                                                                                                                                          08/320,157
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                                                                                           Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEINS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 36;
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Search completed: September 20,

2002, 10:37:21

Job time: 409 sec

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GenCore version 4.5

Copyright (c) 1993 * 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:39:09 ; Search time 95.59 Seconds (vithout alignments)

16.084 Willion cell updates/sec

Pitle: US-09-544-664-30

Perfect score: B0
Sequence: 1 GyorgoLAIIGDDINR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
```

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

## SUMMARIES

	-			
C; Species: Homo sapiens (man)	ActP copper transp		29 42	
cdn-2 protein - human	ribose-phosphate p			
S58875	ribose-phosphate p			
RESULT 2	probable H+/K+-exc		26 43	
	hypothetical prote	770 2 1		
	hypothetical prote	664 2	24 43	
Db 72 GQVGRQLAIIGDDINR 87	hypothetical prote	53.8 475 2 T48031	23 43	
	probable enolase [	447 2	22 43	
Qy 1 GQVGRQLAIIGDDINR 16	phosphopyruvate hy		21 43	
	probable phosphopy	446 2	20 43	
Matches 16; Conservative 0; Mismatches 0	phosphopyruvate hy	444 2	19 43	
Best Local Similarity 100.0%; Pred. No. 3.2e-06	phytoene dehydroge			
Query Match 100.0%; Score 80; DB 2;	probable protein p		17 43.5	
	probable copper-tr	803 1		
	pilus biogenesis p	693 2	15 44	
A;Cross-references: GDB:635887	ABC-type transport	593 2	14 44	
A; Gene: GDB: BAK	probable chemorece	261 2	13 44	
C; Genetics:	sy v-atpase proteo	258 2	12 44	
A;Cross-references: EMBL:U16811; NID:g595923; PIDN:A	enolase - Helicoba	426 2	11 45	
A; Residues: 1-211 <kie></kie>	phosphopyruvate hy	426 2	10 45	
A; Molecule type: mRNA	F54F2.1 protein, -	1226 2	9 46	
A;Status: preliminary	cation transport A	915 2	8 46	
A; Accession: S58874	probable ATPase yb	834 2	7 46	
A; Reference number: S58874; MUID: 95231654	Cu(I)-translocatio	834 2	6 46	
A; Title: Modulation of apoptosis by the widely distr	probable copper-tr	834 1	5 46	
Nature 374, 736-739, 1995	H+/K+-exchanging A	833 2	4 46	
R; Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.	protein phosphatas	357 2	3 46.5	
A;Cross-references: EMBL:X84213; NID:g804984; PIDN:C	cdn-2 protein - hu	_	2 80	
A; Residues: 1-211 <far></far>	Bak protein · huma	100.0 211 2 S58873	1 08	
A; Molecule type: mRNA	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		,	
A;Status: preliminary	Description	Match Length DB ID	No. Score	
A; Accession: \$58872		Query	Result	

Copper crampporer:	E 90000		000	01.6	4	Ů
conner-transport in	500000	٥	000	2		ñ
topoisomerase IV,	E87443	N	759	51.2	41	14
twitching motility	S40037	N	682	51.2	41	ξ
methyl-accepting c	G72316	N	661	51.2	41	12
methyl-accepting c	E72379	2	656	51.2	41	î
methyl-accepting c	A72428	N	656	51.2	41	0
probable methyl-ac	F71298	ر د	654	51.2	41	99
ABC transport prot	F84172	2	642	51.2	41	88
membrane associate	H97244	N	570	51.2	41	37
methyl-accepting c	A72254	N	566	51.2	41	36
chaperonin HSP60	S22342	N	539	51.2	4-	35
methyl-accepting c	F72288	N	539	51.2	41	4
methyl-accepting c	C72291	N	530	51.2	41	ü
probable minor cap	T13091	N	447	51.2	41	2
chemotaxis protein	T44678	N	251	51.2	41	<u>=</u>
hypothetical prote	H71313	N	70	51.2	41	0

## ALIGNMENTS

man spiens (man) 996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999 997; #S5872; #S5872; #S58874 1, Harrington, E.A.; O'Connor, R.; Plemington, C.: Lutz, R.J.; Evan On of apoptosis by the Bc1-2 homologue Bak. 987; public 23765; NDI:95231653 White, J.H.M.; Martinou, I.; Raven, T.; Pun, K.T.; Grinham, C.J.; 733, 1995 101 abc1-2 homologue by interaction with adenovirus E1B 19K. Der: S58872; MUID:95231652 102 physics abc1-2 homologue by interaction with adenovirus E1B 19K. Der: S58872; MUID:95231652 103 physics abc1-2 homologue by interaction with adenovirus E1B 19K. Der: S58872; MUID:95231652 101 of apoptosis by the widely distributed Bc1-2 homologue Bak. Der: S58874; MUID:95231654 10874 10874 10875 108874; MUID:95231654 108876; Pred. No. 3.2e-06; 108876; MUID:95231654 108877 108877 108877; MUID:95231654 108878; MUID:95231654 108879; MUID:95231655 108879; MUID:95231655 108879; MUID:95231654 108879; MUID:95231655 108879; MUID:9523165 108879; MUID:9523165 108879; MUID:9523165 108879; MUID:9523165 108879	log; cdn-1 proteinrevision 01-Mar-1996 #text_change 08-Oct-1999 538874 E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; dis by the Bel-2 homologue Bak. UID:95231653 c acid sequence not shown 65: NID:9758797; PIDN:AAA93066.1; PID:9758798; Martinou, I.; Raven, T.; Pun, K.T.; Grinham, C. monlogue by interaction with adenovirus E1B 19K. UID:95231652 UID:95231652 11; NID:9804984; PIDN:CAA58997.1; PID:9804985; POWETS, V.C.; Mu, J.J.; Umansky, S.R.; Tomei, L. \$18 by the widely distributed Bcl-2 homologue Bal UID:95231654  11; NID:9595923; PIDN:AAA74466.1; PID:9595924 11; NID:9595923; PIDN:AAA74466.1; PID:9595924 11; Pred: No. 3.2e-06; DB 2; Length 211; .0%; Score 80; DB 2; Length 211; .0%; Score 80; DB 2; Length 211; .0%; Mismatches 0; Indels 0; Gaps (									
a a a	7 7 17	2 protein -	1 72	atch 100.0%; Score 80; DB 2; Length 211; cal Similarity 100.0%; Pred. No. 3.2e-06; Indels 0; Gaps 16; Conservative 0; Mismatches 0; Indels 0; Gaps	TOLIMINALY TYPE: mRNA 1-211 -KIE> erences: EMBL:016811; NID:g595923; PIDN:AAA74466.1; ENAK erences: GDB:635887	PID:9804985 S.R.; Tomei, L.D.; -2 homologue Bak.	818	nucleic acid sequence not snown L:U23765; NID:g758797; PIDN:AAA93066.1; PID:g758798 J.H.M.; Martinou, I.; Raven, T.; Pun, K.T.; Grinham, C.J.; 95	n, C.; Lutz, K.J.; EV8A,	log; cdn-1 protein revision 01-Mar-1996 #text_change 08-Oct-1999 S58874

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AR0554

HYXF-exchanging ATPase (EC 3.6.1.36) - Salmonella enterica subsp. enterica serovar Typh c:Species: Salmonella enterica subsp. enterica serovar Typh c:Species: Salmonella enterica subsp. enterica serovar Typh A:Note: this species has also been called Salmonella typhi c:Date: 09-Nov-2001 sequence_revision 09-Nov-2001 ttext_change 27-Nov-2001 c:Accession: AE0564
                                                                                          R:ParkNill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, s.; Moule, S.; O'Gaora, P. Hature 413, 648-852, 2001
A:Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica scrov A:Reference number: AB0502; PMID:11677608
A:Recession: AE0504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein phosphatase 2C homolog F11C18.60 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Daccles: Arabidopsis thaliana (mouse-ear cress) C:Date: 30-Apr:1999 #sequence_revision 30-Apr:1999 #text_change 15-Jun-2001 C:Accession: 706308 C:Accession: 706308 R:Bevan, M.: Terryn, N.: Ardiles, M.: Buysshaert, C.: Dasseville, R.: De Clewes, H.W.: Mayer, K.F.X.; Schueller, C. submitted to the Protein Sequence Database, April 1999 A;Reference number: Z15589 A;Recession: T06308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Map position: 4
A:Indp position: 4
A:Indrcons: 39/3; 61/1; 97/2: 148/3; 190/3; 232/1; 257/3; 275/2; C:Superfamily: human phosphoprotein phosphatase IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Molecule type: DAA
A:Residues: 1-357 (BEEY)
A:Cross-references: EMBL:AL049607; GSPDB:GN00062; ATSP:F11C18.60
A:Experimental source: cultivar Columbia; BAC clone F11C18
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak A;Reference number: $58874; MUID:95231654
A;Recession: $58875
A;Status: preliminary; mucleic acid sequence not shown; translation not shown A;Status: preliminary; Mucleic Acid sequence not shown; Mucleic Shown A;Residues; 1-211 <KIE>
   A:Cross-references: GB:AL513382; PIDN:CAD04983.1; PID:g16501768; GSPDB:GN00176
                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-833 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: ATSP:F11C18.60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOVGROLATIGDDINA
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Pred. No. 3.6;
4; Mismatches
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Pred, No. 3.2e-06;
""amatches 0;
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                                           R:Hayashi, T.: Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Isasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, I1-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: N90696
A;Status: preliminary
A:Molecule type: DNA
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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C;Generics:
A;Gener. 57Y0544
C:Superfamily: Bacillus probable copper-transporting ATPase yvgx; ATPase nucleotide-b
C;Keywords: hydrolase
                                Length 833
  Indels
0
Gaps
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A;Molecule type: DNA A;Residues: 1-834 cBLATY A;Cross-references: GB:AED00154; GB:U00096; NJD:91786683; PIDN:AAC73586.1; A;Experimental source: strain K-12, substrain MG1655 C;Genetics: A.; Rose, D.J.: Mau, B.: Shao, Y. Science 277, 1453-1462, 1997

N.Tille: The complete genome sequence of Escherichia coli K-12
A;Reference number: A64720; MUID:97426617
A;Accession: C64779 probable copper-transporting ATPase (EC 3.6.1.) - Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Decries decries desequence\_revision 05-Decries detect\_change 11-Jan-2000 C;Accession: C64779 G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; translation not shown PID:917866

A;Generybar
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A;Superfamily: Bacillus probable copper-transporting ATPase yvyX; ATPase nucle
C;Keywords: ATP; copper binding; hydrolase; ion transport; metal binding; phos
F;9-38/Domain: beavy-metal-associated homology (+HMAl>
F;195-31A/Domain: heavy-metal-associated homology (+HMAl>
F;195-31A/Domain: transmembrane \*status predicted (\*TMA)>
F;218-32A/Domain: transmembrane \*status predicted (\*TMA)>
F;224-558/Domain: transmembrane \*status predicted (\*TMA)>
F;438-45A/Domain: transmembrane \*status predicted (\*TMA)>
F;641-65A/Domain: AfPase nucleotide=binding domain homology (\*ATN)>
F;641-65A/Domain: AfPase nucleotide=binding domain homology (\*ATN)>
F;641-65A/Domain: AfPase nucleotide=binding domain homology (\*ATN)>
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F;640-65A/Domain: Affase nucleotide=binding domain bomology (

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Length 834;
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Gaps

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Cu(I)-translocation P-type ATPase [imported] - Escherichia coli (strain 0157:H7, C;Specites: Bscherichia coli (c;Specites: Bscherichia coli (c;Date: 18-Jul-2001 #text\_change 03-Aug-2001 C;Accession: A90696

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A:Residues: 1-834 <HAY>
A:Cross-references: GB:BA000007; PIDN:BAB33960.1; PID:gl3359994; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
C;Genetics:
A;Gene: E59537
A;Gene: E59537
C;Superfamily: Bacillus probable copper-transporting ATPase yy9X; ATPase nucleons
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: £85546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Escherichia coli
C:Date: 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E85546
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Best Local Similarity
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                                                                                                                                                                                                         1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fi
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes
A;Reference number: A82035; MUID:20406833
                                                                                                                                                                                                                                                                            R:Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Doc
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.J.; Bass, S.; Qin, H.; Dragoi, I.;
1, R.R.; McKalanos, J.J.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                           C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: H82104
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                                                              A; Experimental C; Genetics:
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A; Map position:
C; Superfamily: I
                                           A; Gene: VC2215
                                                                                  A;Cross-references: GB:AE004293;
A;Experimental source: serogroup
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A; Residues: 1-915 <HEI>
                                                                                                                                                                        A;Status: preliminary
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66.7%;
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probable copper-transporting ATPase
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                                                                                     GB:AE003852; NID:g9656766; PIDN:AAF95359.1; GSPDB:GN00 O1; strain N16961; biotype El Tor
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Potamousis,
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I.; Sellers,
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1226 <AND>
                                                                                                                                                                                                                                      submitted to the EMBL Data A; Description: Sequence of A; Reference number: $44817
                                                                                                                                                                                                                                                                                                C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001 C;Accession: $44824
                                                                                                                                                                                                                                                                                                                           F54F2.1 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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Matches
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 GVFGKQIAVVGDD 371
                            GQVGRQLAIIGDD 13
                                                                                                                                       58/2; 137/3; 179/1; 316/2; 393/1; 551/3; 597/2; 662/2; 899/3; 1178/3
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                                                                   57.5%;
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                                                                                                                          transmembrane protein
                                                                                                                                                                                                                                                         Library, September 1993 the C. elegans cosmid F
                                                                                                                                                                    NID: g388603;
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                                                           Pred. No. 17;
1; Mismatches
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G:Species: Helicobacter pylori
c;Date: 29-Nov-1995 #sequence\_revision 17-Sep-1997 #text\_change 22-Jun-1999
c;Accession: B64539; S58664
G:Accession: B64539; S58664
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.; Khalak, H.G.; Glodek, A.; McK son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser A; Authors: Mallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser A; Authors: Ad520; Mullip:97394467
A; Reference number: Ad520; Mullip:97394467
A; Recession: B64539
A; Accession: B64539 N; Alternate names: enolase phosphopyruvate hydratase (EC 4.2.1.11) - Helicobacter pylori (strains 26695 and Watthey Fraser

A; Molecule type: DNA A; Residues: 1-426 <TOM> A; Status: nucleic acid sequence not shown; translation

not

A;Cross-references: GB:AE000536; GB:AE000511; NID:92313230; PIDN:AAD07219.1; A;Experimental source: strain 26695 R:Schmitt, W: Odenbrock, S.; Heuermann, D.; Haas, R. Mol. Gen. Genet. 248, 563-572, 1995 functional characterization PID:g231

Mol. Gen. Genet. 248, 563-572, 1995 A;Title: Cloning of the Helicobacter pylori recA gene and A;Reference number: 588683; MUID:96027928 A;Accession: S58684 A; Residues: 1-25, 'I', 27-68 <SCH>A; Cross-references: EMBL: Z35478 A; Molecule type: DNA A; Residues: 1-25, 'I'

A;Gene: HP0154 C; Genetics:

C; Function: the reversible dehydration of 2-phospho-D-glyceric acid

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A;Description: catalyzes the reve A;Pathway: qlycolysis C;Superfamily: enolase C;Keywords: carbon oxyyen lyase; F;42/Binding site: magnesium 2 ( (Ser) #status pred esis; glycolysis; hydro-lyase; magnesium predicted

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gy v-atpase proteolipid PAB1189 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 *sequence_revision 20-Aug-1999 *text_change 20-Aug-1999
C;Accession: H75027
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A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Moference number: A71800; MUID:99120557
A;Accession: H71967
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H71967
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                                                                                Query Match
Best Local Similarity
7; Conserve
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A; Residues: 1-258 KAM>
A; Crosifuerences: GB:AJZ48288; GB:AL096836; NID:95458960; PIDN:CAB50662.1;
A; Experimental source: strain Orsay
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C;Superfamily: enolase
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A; Rosidues: 1-426 <ARN>
A; Rosidues: 1-426 <BLAE001453; GB:AE001439; NID:g4154651; PIDN:AAD05723.1; PID:g415465
A; Experimental source: strain J99
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C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Jun-1999
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A; Accession: H75027
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F;205,338/Active site: magnesium 1 (Asp, Glu, Asp) #status predicted
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Best Local Similarity 46.2%;
Matches 6; Conservative
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                      GEAGRGFAVVADEIRR 137
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6; Conserv
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46.2%;
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43.8%;
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Pred. No. 6.7;
4; Mismatches
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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Conservative

55.0%; 61.5%;

Score 44; DB Pred. No. 17; 3; Mismatches

2;

Length 593;

Indels

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M. Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 5, 55-76, 198
A;Title: Complete sequence and gene organization of the genome of a A;Reference number: A/1000; MUID:98344137
A;Accession: B/1213
A;Status: preliminary; nucleic acid sequence not shown; translation
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C;Species: Pyrococcus horikoshii
C;Dete: 14-Aug-1998 *sequence_revision 14-Aug-1998 *text_change 21-Jul-2000
C;Accession: B71213
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A; Residues: 1-261 <KAW>
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M.; Ohfuku, Y.; Funahashi, T.;
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A;Cross-references: EMBL:D90904; GB:AB001339; NID:g1652225; PIDN:BAA17266.1
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Jun
C;Genetics:
C;Start codon: GTG
C;Stperfamily: Escherichia coli ABC transporter mdlA; ATP-binding cassette
C;Keywords: ATP; nucleotide binding; P-loop: transport protein
F;366-560/Domain: ATP-binding cassette homology ABC>
F;383-390/Region: nucleotide-binding motif A (P-loop) C;Accession: \$75352
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; V DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellu A; Molecule type: DNA A; Residues: 1-593 <KAN> A; Cross references: EMB A;Reference number: \$74322; MUID:97061201 A;Acession: \$7555 A;Status: nucleic acid sequence not shown; translation not shown C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 02-Feb-2001 C; Species: Synechocystis sp. A; Variety: PCC 6803 ABC-type transport protein slr2019 -Synechocystis sp. the unicellular cyanobacterium NID:g1652225; PIDN:BAA17266.1; to the EMBL Data Library, June T.; Watanabe, A.; (strain PCC 6803) E.; Nakamura, Y.; Yamada, homology Synechocys PID:g165

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Rancompous. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequet Rature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen xylella fastidiosa.
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PT 01-WOV-1997 (Rel. 35, Last sequence update)

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Minimum Maximum

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hits satisfying chosen parameters:

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105224 segs, 38719550 residues

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Gapext 0.5

US-09-544-664-30 80

GQVGRQLAIIGDDINR

16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

SwissProt\_40:\*

BCL2\_FAMILY; 1.

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RESULT 2

BAY, MUNAN

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EMBO (
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MEDINE-9603131, Pubmed-852181, DOMAIN.
CINTER-9603131, Pubmed-852181, DOMAIN.
CINTER-9603131, Pubmed-852181, Houghton A.B.,
CINTER-96031131, Pubmed-852181, Houghton A.B.,
CINTER-96031131, Pubmed-852181, COMBON A.B.,
COMBON A. 14.5589-5396(1953)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 96-206 FROM N.A.
Eguchi H., Hayashi S.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ
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MEDIINE-95231653; PubMed-7715730;
MEDIINE-95231653; PubMed-7715730;
Chitcheden T., Harrington E.A., O'Connor R., Flemington
Evan G.I., Guild B.C.;
"Induction of apoptosis by the Bc1-2 homologue Bak.";
Nature 374:733-736(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95231652; PubMed-7715729;
Parrow S.N., White J.H.M., Martinou I., Raven T.,
Grinham C.J., Martinou J.C., Brown R.;
"Cloning of a bcl-2 homologue by interaction with
19K.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAK_HUMAN PRT; 211 AA. 016611; 09253; STANDARD: PRT; 211 AA. 016611; 09253; Created) 01-WOV-1997 (Rel. 35, Created) 01-WOV-1997 (Rel. 35, Last sequence update) 16-CCT-2001 (Rel. 40), Last anotation update) 16-CCT-2001 (Rel. 40), Last anotation update) 18c1-2 lumnologous antagonist/killer (Apoptosis BAKI OR BAK update) (Human), https://original.org/lines/human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
SEQUENCE
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Apoptosis: Transmembrane.
DOMAIN 74 88
DOMAIN 117 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-B-cell:
                                                                                                                                                                           STRUCTURE BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 374:731-733(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 374:736-739(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-9606;
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211 AA;
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illarity 100.
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23411 MW;
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Primates;
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BH1.
BH2.
POTENTIAL.
703875EC4DCCC1D3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 80; DB 1; L
Pred. No. 3.9e-06;
                                                                                                                                                                                                                                                                                                          BH1 and BH2,
                                                                                                                                                                                                                                                                                                                                                                    Ebb R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
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                                                                                                                                                                                                                                                                                                                                     ນ G.J.,
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-39
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RESULT 3
HAK\_MOUSE
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ID BAK\_M
AC 00873
DT 01-N0
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BAK\_MOUSE STANDARD: PRT: 208 AA 008734: STANDARD: PRT: 208 AA 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NAR-2002 (Rel. 41, Last anotation update) Bc1-2 homologous antagonist/killer (Apoptos

(Apoptosis

regulator

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Query Match Best Local S Matches 16

ch 100. 1 similarity 100. 16; Conservative

.09;

Score 80; DB 1; Pred. No. 3.9e-06; Mismatches 0;

Length 211;

0; Gaps

9

0;

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EMBL: X84213: CAA55997.1:
EMBL: U23765: AAA53066.1:
EMBL: U23765: AAA53066.1:
EMBL: U58611: AAA7466.1:
EMBL: D393017: CAB5526.1:
EMBL: D39397: BAA13606.1: JOINED.
EMBL: D89397: BAA13606.1: JOINED.
EMBL: D89397: BAA13606.1: JOINED.
PDB: 1BXL: 29-CCT-97.
INTEGER OF DEPOD2475: BCL2_family.
INTEGER OF DEPOD3475: BCL2_family.
INTEGER OF DEPOD352: BCL2.2:
EMARKT. SM00337; BCL.1.1.
                           Apoptosis;
DOMAIN
DOMAIN
DOMAIN
TRANSMEM
SEQUENCE
                                                                                                      PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                     This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions and its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                              SHILDRING LOCATION: Membrane-bound (Potential).

SHECELLILAR LOCATION: Membrane-bound (Potential).

TISSUES SPECIFICITY: EXPRESSED IN A WIDE VARRETY OF TISSUES, WITH HICHST LEVELS IN THE HEART AND SKELERAL MUSCLE.

DOMAIN: INTWCT BH3 DOMAIN IS REQUIRED BY BK. BHD, BAK, BAD AND BAX FOR THEIR FRO ADDPFOTIC ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-ACOPTOTIC MEMBRERS OF THE BCL-2 FAMILY.

SAMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                      PS01080; BH1; 1.
PS01258; BH2; 1.
PS01259; BH3; 1.
PS50063; BCL2_FAMILY;
                       ; Transmembrane;
74 88
117 136
169 184
188 205
211 AA; 23409
                         184 E
205 F
23409 MW;
                                                                                           3D-structure
BH2.
POTENTIAL.
1; A2200FE72A46D04E CRC64;
                                                                   BH3
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Best Local
_BCOLI STANDARD; PRT; 834 AA ASTCU_ECOLI STANDARD; PRT; 834 AA O59385; P78245; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                               PÉAM: PF00452; BC1-2; 1.
SMART; SM00337; BCL; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS50062; BCL:2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Gene structure, CDNA sequence, and expression of murine proapoptotic Bcl-2 family member."; Genomics 44:195-200(1997).
                                                                                                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                                                                                                            Apoptosis;
DOMAIN
                                                                                                                                                                                                                                                                                                                                              EMBL; Y13231;
HSSP; Q16611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chittenden T., Ma A., Evan G.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97446138; PubMed=9299236;
Ulrich E., Kauffmann-Zeh A., Hueb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1097161; Bak1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                        69 GQVGRQLALIGDDINR
                                                                                                            1 GQVGRQLAIIGDDINR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK
BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTI
WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SYMILARITY).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBURIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, X(L) (BY SIMILARITY).
SUBCELLULAR LOCATION: Membrane-associated (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STRUCTUS, ACCELERATES PROBRAMED CELL DEATH BY SILVING TO, AND ANTAGONIZING THE A REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG EIB 19K PROTEIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: WIDELY EXPRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                             Y13231; CAA73684.1; -. Q16611; 1BXL.
                                                                                                                                 l Similarity
15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAK.
                                                                                                                                                                                                                                                                                                            IPR002475; BCL2_family. IPR000712; BCL_2.
                                                                                                                                                                                                      Transmembrane.
71 85
114 133
1166 181
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Mouse)
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23300
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                                                                                                                                1;
                                                                                                                                                                                              BH2.
POTENTIAL.
                                                                                                                                           Pred. No.
                                                                                                                                                    Score 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hueber A.O.,
                                                                                                                                                                                    DAFC11B160C523C9 CRC64;
                                                                                                                                 Mismatches
                                                                                                                                           8.2e-06;
                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williamson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOR THEIR INTERACTION
                                                                                                                                                    Length 208;
                                                                                                                                Indels
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                                                                                                                                                              PROSITE;
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                                              TRANSMEM
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PRINTS; PROO119; CATATPASE.
PROSITE; PSO0154; ATPASE_E1_E2;
PROSITE; PS01047; HMA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00122; E1-E2_ATPase; Pfam; PF00403; HMA; 2. Pfam; PF00702; Hydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an cmail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDDJ databases.
-!- FUNCTION: INVOLVED IN COPPER TRANSPORT.
-!- CATALYTIC ACTIVITY: ATP + H(2)0 - ADP + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blattner F.R., Plunkett G. III, Bloch C.A., Perr
Riley M., Collado-Vides J., Glasner J.D., Rode C
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-K12;
Das S., Chu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (Rel. 41, Last annotation update)
Probable copper-transporting ATPase (EC 3.6.3.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001757; E1-E
InterPro; IPR001934; HMA.
InterPro; IPR001454; Hydr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EcoGene; EG13246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P04129; 1AFJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97426617; PubMed-9278503;
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                                                                                                                                                                                                                                                                          Metal-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELULIAR LOCATION: Integral membrane protein (Potential)
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(E1.E2 ATPASES). SUBFAMILY IB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U58330; AAB02268.1; -.
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                                                                                                                                                                                                                                                                                                             PS50846; HMA_2; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-profit institutions as long and this statement is not removed.
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(JUN-1996) to
                                                                                                                                                                                                                                                                                              Transmembrane;
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                                                                                                                                                                                                                                                                       Repeat;
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the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                           Phosphorylation;
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AMA 1.
HMA 2.
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Rode C.K., Mayhew G.F.,
3oeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                         ATP-binding; Copper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
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P34446;
01-FEB-1994 (Rel. :
01-FEB-1994 (Rel. :
01-MAR-2002 (Rel. :
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CONFLICT
SEQUENCE
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Bonfield J., Burton J., Connell M., Copsey T., Couper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAEEL
            HSSP; P11215; 1ABX.
WormPep; F94F2.1; CE00194.
InterPro; IPRO00413; Integrin_alpha.
Pfam; PF01839; FG-GAP; 5.
Pfam; PF00357; Integrin_A; 1.
                                                                                                                                                                                                                                                 <del>+ +</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Integrin alpha pat-2 precursor.
PAT-2 OR F54F2.1.
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                                                                                 PIR; S44824; S44824.
                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                      elegans
                                                                                                                                                                                                                                                                                                                                                              *2.2 Mb of contiguous nucleotide sequence from chromosome III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                entities requires a license agreement
                                                                                                                                                            modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                        Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                 Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           712
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                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on the buropean Bioinformatics Institute. There are no restrictions on the buropean Bioinformatics institute.
                                                                                                                                                                                                                                               FUNCTION: POSSIBLE ROLE IN CELL-CELL INTERACTIONS (BY SIMILARI SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT: ALPHA PAT ASSOCIATES WITH BETA PAT-3.
SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRQVAMVGDGIN
F00357; integrin_A; 1. PR01185; INTEGRINA.
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                                                                                                                                                                           non-profit institutions as long
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28, Last sequence up
41, Last annotation
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Pred. No. 6.
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-> R (IN REF. 1).
CF84A18FE208E6F6 CRC64;
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                                                                                                                                                              Usage
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                                                                                                                                                               and
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ALPHA PAT-2
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SIGNAL
                                                                                                                                                                                                                                                                                                                                          gastric pathogen Helicobacter pylori.";
Nature 397.16-180(1999).
    i- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate
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Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Urla-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis
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                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it the European Bioinformatics Institute.
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Bacteria; Proteobacteria; epsilon subdivision; Hel
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-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: CYTOPLASMIC
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INTEGRIN_ALPHA; 1.
Anion: Receptor; Glycoprotein; Transmembrane;
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P48285;
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MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Soutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Relson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., PitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weldman J.M., Fujii C., Bowman C., Watthey L., Wallin E.
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
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SEQUENCE
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01-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Enolase (EC 4.2.1.11) (2-phosphoslycerate dehydratase) (2-phospho-D-glycerate hydro-lyase).
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                                                                                                                                                    Thompson S.A., Blaser M.J.,
"Thompson S.A. Blaser H.J.,
"Tsolation of the Helicobacter pylori re
the recA region in resistance to low pH.
Infect. Immun. 63:2185-2193(1995).
i- CATALYTIC ACTIVITY: 2-phospho-D-glyc
                                                                                                                                                                                                                                                                               SEQUENCE OF 1-178 FROM N.A.
STRAIN-ATCC 53726 / 84-183;
MEDLINE-95286262; PubMed-7768597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENO OR HP0154.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00113; enolase;
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                                                                                                                                                                                                                                                                                                                                                                                     Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                   The complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=210;
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les 6; Conserv
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COFACTOR: MAGNESIUM IS REQUIRED FO
COFACTOR (BY SIMILARITY).
PATHWAY: GLYCOLYSIS.
SUBUNIT: HOMODIMER (BY SIMILARITY)
SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELGRQIQLVGDDL
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AGNESIUM (BY SIMILARITY).
AGNESIUM (BY SIMILARITY).
EDFA73EA6EB77BEE CRC64;
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                                                                                                                                                       phosphoenolpyruvate
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Best Local
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PRODM; PD000902: ENOLASE: 1.
PROSITE: PS00164: ENOLASE: 1.
Lyase: 61ycolysis: Magnesium; 6
ACT_SITE: 155 155 H2
METAL 242 242 M4
METAL 286 286 M4
METAL 313 313 M4
CONFLICT 26 26 V6
CONFLICT 85 85 I
                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/Announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    032220;
                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis
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299121; CAB15355.1; -. P04129; LAFJ.
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6; Conser
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MAGNESIUM (BY
MAGNESIUM (BY
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Pred. No.
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(BY SIMILARITY).
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InterPro;

BG14106; yvgx. IPR001366; Cad\_ATPase.

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RESULT
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Best Local :
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Pfam; PF00403; HMA; 2.
Pfam; PF00702; Hydrolase; 1.
PRINTS; PR00119; CATATPASE.
PRINTS; PR00940; CATPATEASEA.
PRINTS; PR00941; CATPASE.
PRINTS; PR00943; CUATPASE.
PRINTS; PR00943; CUATPASE.
PRINTS; PR00942; CUATPASE.
PRINTS; PR00946; HGSCAVENGER.
PROSTITE: PS010145; ATPASE_E1_E2; 1
PROSTITE: PS010145; ATPASE_E1_E2; 1
                                                                                                                                              CRTI_APHSP
P21134;
01-MAY-1991
01-MAY-1991
01-MAR-2002
"Cloning and nucleotide sequence of the crtI gene encoding phytoene dehydrogenase from the cyanobacterium Aphanocapsa PCC6714."; Gene 91:113-117(1990).
                                              STRAIN-PCC 6714;
MEDLINE-90382685; PubMed-2119326;
                                                                                                                            CRTI.
                                                                                                                                                                                                      APHSP
                                    Schmidt A., Sandmann
                                                          SEQUENCE FROM N.A. STRAIN-PCC 6714;
                                                                                         NCBI_TaxID=1120;
                                                                                                   Bacteria;
                                                                                                    Aphanocapsa sp.
Bacteria; Cyanobacteria;
                                                                                                                                     Phytoene dehydrogenase
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InterPro; IPR001934; HMA.
InterPro; IPR001454; Hydrolase.
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8; Conser
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; IPR000579; Cat_P_ATPaseA.

; IPR001756; Cu_ATPase.

; IPR001877; Cu_ATPase_I.

; TPR001877; Cu_ATPase_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                                             (Rel. 18, Created)
(Rel. 18, Last sequence update)
(Rel. 41, Last annotation update)
hydrogenase (EC 1.14.99-.-) (Phytoene desaturase).
                                                                                                                                                                                                                                                                                         Conservative
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COPPER (POTENTIAL).

COPPER (POTENTIAL).

COPPER (POTENTIAL).

COPPER (POTENTIAL).

PHOSHORYLATION (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

"""NESTUM (BY SIMILARITY).

"""NESTUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat;
                                                                                                 Chroococcales; Aphanocapsa
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Phosphorylation; Magnesium; ATP-binding;
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                                                                                                                                                                                                                                                                                      Score 44; DB 1; Length 803; Pred. No. 13; 2; Mismatches 2; Indels
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RESULT 10
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENO_LYCES P26300;
                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Solinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                       "Plant enclase: gene structure, expression, and Plant Cell 3:719-735(1991).
-i- CATALYTIC ACTIVITY: 2-phospho-D-glycerate -
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CV. SUPERSONIC;
MEDLINE-93044507; Pubmed-1841726;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum (Tomato).

Bukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                            van Montagu M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NP_BIND 22 49 FAD (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M55647; AAA62573.1; -. PIR; JN0084; JN0084.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 GQTGRRLQLLEFIGEDVHR 159
                                                                                                                                                                         THE DIMER (BY SIMILARITY).

PATHMAY: GLYCOLYSIS.

SUBURIT: HOMODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: Cytoplasmic.

SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GQVGRQLAI---IGDDINR 16
                                                                                                                                                                                                                                                           COFACTOR:
                                                                                                                                                                                                                                                                                                                                                        der Straeten D., Rodrigues-Pousada R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THIS ENZYME CONVERTS PHYTOENE INTO ZETA-CAROTENE VIA INTERMEDIARY OF PHYTOFILIBRE BY THE SYMMETRICAL INTRODUCTION OF DOUBLE BONDS AT THE C-11 AND C-11 POSITIONS OF PHYTOENE COFACTOR: NAD, NADP, OR FAD (FORBABLE).

SIMILARITY: BELONGS TO THE PHYTOENE DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Pred. No. 1
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444 AA
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                                                                                                                                                                                                                                                                                                                          evolution.";
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EMBL; X58108;

JQ1185;

JQ1185 CAA41115 or send an email to license@isb-sib.ch).

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RESULT
ENO2_MP
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Best Local
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. B73; TISSUE-ROOT;
MEDLINE-99063764; Pubmed-9947102;
Lal S.K., Lee C., Sachs M.M.;
Differential regulation of enclase during anaerobiosis
Plant Physiol. 118:1285-1293(1998).
-i- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-
D-glycerate hydro-lyase 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P42895;
01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
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                                                                                                                                          entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC cl
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
SEQUENCE
               ProDom; PD000902; PROSITE; PS00164;
                                                  InterPro; IPR000941; Enclase. Pfam; PF00113; enclase; 1.
                                                                                            MaizeDB;
                                                                                                                    EMBL; U17973; AAD04187.1; -.
                                        PRINTS; PR00148; ENOLASE.
                                                                              Mendel; 16623; Zeama; Pgh1; 16623
                                                                                                          HSSP; P56252;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays (Maize)
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ProDom; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000941; Enolase, Pfam; PF00113; enolase; 1.
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Mendel; 611; LYCes
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                                                                                                                                                                                                                                                      SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                               THE DIMER (BY SIMILARITY).
PATHWAY: GLYCOLYSIS.
SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                 COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
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 Glycolysis;
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                                                                                          30060;
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327
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; Enolase; 1.
; ENOLASE; 1.
s; Magnesium;
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250
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                                                                                                                                                                                                                                                    TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                           2-phospho-D-glycerate = phosphoenolpyruvate
                                                                                                                                                                                                                                                                  Cytoplasmic.
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MAGNESIUM (BY
MAGNESIUM (BY
MAGNESIUM (BY
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Pred. No.
 Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Best Local S
Matches 6
        METAL
SEQUENCE
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Q42971;
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METAL
METAL
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SEQUENCE
                                                  METAL
                                                                                                                                                                                                                                                         EMBL; U09450; AAC49173.1; -. HSSP; P56252; 1PDZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chow
                                                                                             Lyase; Glycolysis; Magnesium
ACT_SITE 164 164
                                                                                                                                           ProDom; PD000902; Enolase; 1. PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                           InterPro; IPR000941; Enolase. Pfam; PF00113; enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
                                                                             METAL
                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - I SUBCELLULAR LOCATION: CYLOPIasmic.
- I DEVELOPENTAL STAGE: EXPRESSED DURING EARLY EMBRYOGENESIS
- I SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PATHWAY: GLYCOLYSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: MAGNESIUM IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A rice early embryogenesis-specific enolase cDNA.";
(In) Plant Gene Register pGR95-084.
-i- CATALYTIC ACTIVITY: 2-phospho-D-glycerate - phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hsing Y.-I.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycerate hydro-lyase) (OSE1)
Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 EIGEQVQIVGDDL
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
02-MAR-2002 (Rel. 41, Last annotation update)
03-MAR-2002 (Rel. 41, Last annotation update)
03-MAR-2002 (Rel. 41, Last annotation update)
04-MAR-2002 (Rel. 41, Last annotation update)
05-MAR-2002 (Rel. 41, Last annotation update)
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                                                                                                 MEDLINE-21396508; PubMed-11481431;
Finan T.M., Weldner S., Wong K., Buhrmester J.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A.,
Golding B., Puehler A.;
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P58342;
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SEQUENCE 770 AA; 8
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"The complete sequence of the 1,683-kb pSymB megaplasmid from the fixing endosymbiont Sinorhizobium meliloti."; fixing endosymbiont Sinorhizobium meliloti."; for Natl. Acad. Sci. U.S.A. 99:9889-9894(2001).
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9; Conserv
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PROSITE; PS01047; HMA_1; 2.
PROSITE; PS50846; HMA_2; 2.
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modified and this statement is not removed. Usage by ar
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-: SUBCELULIAR LOCATION: INTEGRAL membrane protein (By similarity).
-: SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(E1-E2 ATPASES), SUBFAMILY IB.
-: SIMILARITY: CONTAINS 2 HMA DOMAINS.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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Mismatches
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R InterPro; IPR001757; El-E2_AffaseA.

R InterPro; IPR001757; El-E2_Affase.

R InterPro; IPR001802; Hg-Scavenger.

R InterPro; IPR001802; Hg-Scavenger.

R InterPro; IPR001845; Hyd-Olase.

R Pfam; PP00102; El-E2_ATPase; 1.

R Pfam; PP000103; HAA; 2.

R Pfam; PP000104; CATPAFASEA.

R Pfam; PR00040; CATPAFASEA.

R PRINTS; PR00940; CATPAFASEA.

R PRINTS; PR00941; CATPAFASEA.

R PRINTS; PR00941; CATPAFASEA.

R PRINTS; PR00941; CATPAFASEA.

R PRINTS; PR00941; CATPAFASEA.

R PRINTS; PR00941; CATPAFASEA.

R PRINTS; PR00941; CATPAFASEA.

R PRINTS; PR00941; CATPAFASEA.

R PRINTS; PR00941; MAA_1; 2.

R PROSITE; PS00164; HAA_1; 2.
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COPPER (POTENTIAL).

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COPPER (POTENTIAL).

PROSENORIZATION (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).
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sp.phage:*
sp.phage:*
sp.phate:*
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sp_mammal:*
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Q9mz6 ovis-piles
Q9jwz6 mis musculu
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Q9sz53 arabidopsis
Q9pz7 vibrio chol
Q9jw21 pyrococcus
Q9jx71 pyrococcus
Q9jx12 pyrococcus
Q9jx13 synechocyst
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O77738

PRELIMINARY: PRT; 80 AA.

AC 077738;

O7 01-NOV-1998 (TYENBLIFEL 08. Created)

D7 01-DEC-2001 (TYENBLIFEL 19. Last sequence update)

D7 01-DEC-2001 (TYENBLIFEL 19. Last annotation update)

D8 BAK PROTEIN (FRAMENT)

G8 BAK.

OS SUS SCROTE (Pig).

OC EDMATYOCA; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;

OC Manmalia: Butheria; Cetartiodactyla; Suina; Suidae; Sus.

RN (11)

CR MANNELTERID-9823;

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158	94	847	802	661	656	656	654	644	642	614	577	570	566	539	530	447	251	952	733	552	383	369	369	356	356	356	356	664
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Q925d2 rattus norv	Q.	Q9rrn5 deinococcus					treponema	052777 treponema p	halobact	Q9blil saturnia ja	O53050 leptospiril	Q97fd7 clostridium	Q9x1e2 thermotoga		~	064320 bacteriopha	006508 desulfuroco	097198 leishmania	Q99yg5 streptococc	Q967y5 musca domes	1	008618 rattus norv	060256 homo sapien	Q9d0ml mus musculu	Q63468 rattus norv	Q96h06 homo sapien	Q14558 homo sapien	022716 arabidopsis

## ALIGNMENTS

*Expression of spoptosis-associated genes in Albernating and Stunned Submitted (JAM-1998) to the EMBL/GenBank/DDBJ databases.  Submitted (JAM-1998) to the EMBL/GenBank/DDBJ databases.  RMBL, AJ001204; CAM-1998) to the EMBL/GenBank/DDBJ databases.  RMBL, AJ001204; CAM-1998) to the EMBL/GenBank/DDBJ databases.  INCOMENTE, INCOMENTATION HOLD FAMILY: 1.  PROSITE: PS010627 BCL2_FAMILY: 1.  PROSITE: PS01
clated genes in hibernating and stunned willy.  MBL/GenBank/DDBJ databases.  (ily.  Tolar93BD7D59C86 CRC64:  EDIAF93BD7D59C86 CRC64:  ECORE 80; DB 6; Length 80;  Fred. No. 6.38~06;  Indels 0; Gaps  Mismatches 0; Indels 0; Gaps

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Matches 15; Conservative
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InterPro: IPR002475; BCL2_7.
Prom; PF00402; BCL-2_7.
SWART; SM0037; BCL; 1.
PR0SITE; BS0062; BCL2_FAMILY; 1.
PR0SITE; PS01269; BH2; 1.
PR0SITE; PS01259; BH2; 1.
PR0SITE; PS01259; BH2; 1.
                                                                                                                           SEQUENCE FROM N.A.

STALIN-MRAI: TISSUE-NEURONAL;

STALIN-MRAI: TISSUE-NEURONAL;

MEDILINE-2128300; PubMed=11278671;

MEDILINE-2128300; PubMed=11278671;

MEDILINE-2128300; PubMed=11278671;

SUM Y.F., Yu L.Y., Saarma M., Timmusk T., Arumae U.;

Neuron-specific Bol-2 homology 3 dommin-only splice variant of Bak is anti-spopicotic in neurons, but pro-apoptotic in non-neuronal cells.";

Neuron-specific Bol-2 homology 3 dommin-only splice variant of Bak is anti-spopicotic in neurons, but pro-apoptotic in non-neuronal cells.";

J. Biol. Cinen, 276:15240-15247(2001)

J. Biol. Cinen, 276:15240-15247(2001)

J. Biol. Cinen, 276:15240-15247(2001)

J. Biol. Cinen, 276:15240-15247(2001)

J. Biol. Cinen, 276:15240-15247(2001)
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Q91WX5;
Q1-DEC-2001
Q1-DEC-2001
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N-BAK1.
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OSWASS PRELIMINARY: PRT; 163 AA.

OSWASS PRELIMINARY: PRT; 163 AA.

OSWASS PROTEIN (TEMBLICEL 15, Last sequence update)

OLDEC-2001 (TEMBLICEL 19, Last annotation update)

EAK PROTEIN (FRAGERNT).

Ovis arises (Sheap). Chordsta; Cranists; Vertebrata; Euteleostomi;

Eukaryota; Metizza; Chordsta; Cranists; Vertebrata; Euteleostomi;

Eukaryota; Metizza; Chordsta; Cranists; Vertebrata; Euteleostomi;

Eukaryota; Metizza; Chordsta; Cranists; Vertebrata; Euteleostomi;

Eukaryota; Metizza; Chordsta; Cranists; Vertebrata; Euteleostomi;

Eukaryota; Metizza; Chordsta; Cranists; Vertebrata; Euteleostomi;

Eukaryota; Metizza; Chordsta; Ruminantia; Pecora; Bovoldee;

Euyaryota; Metizza; Ovis.
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Murrby J.F., Dong Y.B., Leigh A.J., Schramuzzi R.J., Chi
"Bak in the Sheep ovary.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL, AF164518, AAR9553.1;
HSSP: Q16611; LBXL.
HSSP: Q16611; LBXL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammaila; Euthorla; Rodentia;
NCBI_TaxID=10090;
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(TrEMBLrel. 19, Last sequence update)
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         97.5%;
larity 93.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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         Score 78; DB 11;
Pred. No. 2.8e-05;
1; Mismatches (
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Pred. No. 2.1e-05;
1; Wismatches 0;
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Matches 15
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InterPro, IDPRODATS BRILZ_family.
Pfam, PFO0453 BRILZ_1.
SMART, SMO337 BRILZ_1.
PROSITE: PSS50063 BRILZ_AMMILY: 1.
PROSITE: PSS10063 BRILZ_FAMILY: 1.
PROSITE: PSS10265 BRILZ_FAMILY: 1.
PROSITE: PSS10285 BRILZ_FAMILY: 2.45:
PROSITE: PSS10295 BRILZ_FAMILY: 2.45:
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Itoh T., Itoh A., Pleasure D.
Submitted (APR-2000) to the E
EMBL; AF25504; AF71760.1;
HSSP, Q16611; 1BXL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSSESS PRELIMINARY; PRT: 357 AA.
QSSESS 101-MAY-2000 (TREMBLIEL 13, Created)
01-MAY-2000 (TREMBLIEL 13, Last sequence update)
01-DEC-2001 (TREMBLIEL 11, Last sequence update)
01-DEC-2001 (TREMBLIEL 19, Last annotation update)
PROTEIN PHOSEMATASE 20-LIKE PROTEIN (AT4631860/FILC18_60).
FILC18.60 on AT4631860.
FILC18.60 on AT4631860.
FILC18.60 on AT4631860.
Bukaryota: Viridiplantae. Streptophyta: Embryophyta: Tracheophyta: Sparmatophyta: Magnoliophyta; Eudicotyledons: Core eudicots; Rosidae: eurosids II: Brassicales; Brassicaceae: Arabidopsis.
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Q9JK59;
Q1-QCT-2000
Q1-QCT-2000
Q1-DEC-2001
BAK PROTEIN.
                                                                                                                                                                                              SEQUENCE FROM N.A.
Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.
De Cierck R., De Keyser A., Neyt P., Rouze P., Van Den Daele
Villarce R., Gielen J., Van Montagu M., Hoheisel J., Mewes H
Mayer K.F.X., Schueller C.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
MCBI_TaxID=10116;
SEQUENCE FROM N.A.
                                                                  EU Arabidopsis sequencing project;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-3702;
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(TrEMBLrel. 15,
(TrEMBLrel. 19,
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e EMBL/GenBank/DDBJ
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01-OCT-2000 (TrEM
01-DEC-2001 (TrEM
CATION TRANSPORT
                                                                                                                      SEQUENCE FROM N.A.

STRAIN-EL TOR NI6961 / SEROTYPE 01;

STRAIN-EL TOR NI6961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

MEDLINE-20406833; PubMed-10952301;

MEDLINE-20406833; PubMed-10952301;

Melloberg J.F., Elsen J.A., Nelson W.C., Clayton M.L.

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Seller

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J
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SEQUENCE
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                               HSSP; P04129; 1AFJ.
TIGR; VC2215; -.
                                                           EMBL; AE004293;
                                                                                         cholerae.";
                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                              Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                       Nature 406:477-483(2000)
                                                                                                     "DNA sequence of both chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., Bekyser A., Neyt P., Rouze P., Van Den Dacle H., Villaroel R., Gielen J., Van Montagu M., Newes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C_domain
Pfam; PF00481; PP2C; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GQVG-RQLAIIGDDINR 16
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SM00331; PP2C_SIG; 1.
E; PS01032; PP2C; 1.
CE 357 AA; 39203 MW;
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IPR000579; Cat_P_ATPaseA
IPR001757; E1-E2_ATPase.
                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
SPORT ATPASE, E1-E2 FAMILY.
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                                                         AAF95359.1;
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057733; PRELIMINARY; 057733; 01-AUG-1998 (TrEMBLrel. 0: 01-AUG-1998 (TrEMBLrel. 0: 01-DEC-2001 (TrEMBLrel. 1: 261AA LONG HYPOTHETICAL C: PH1970.
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InterPro; IPRO01454; Hydrolase.
InterPro; IPRO0150; Hyothlet_c
InterPro; IPRO010150; Hyothlet_c
Pfam; PF00122; E1-E2_ATPase; 1.
Pfam; PF00403; HMA; 3.
Pfam; PF00702; Hydrolase; 1.
PRINTS; PR00940; CATPATPASEA.
PRINTS; PR00946; HGSCAVENGER.
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Q1-MAY 2000 (TrEMBLrel. 1
Q1-MAY 2000 (TrEMBLrel. 1
Q1-DEC-2001 (TrEMBLrel. 1
SY V-ATPASE PROTEOLIPID.
                                                                                                                                                                                                       SEQUENCE 258 AA;
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InterPro; IPR004090; Me_chemotaxis.
Pfam; PF00015; MCPsignal; 1.
                                                                                                                                                                                                                                                                          "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.", submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AJZ48288; CAB50662.1: -
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Archaea; Euryarchaeota;
NCBI_TaxID=29292;
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_ATPase; 1.
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          CHEMORECEPTOR PROTEIN
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Last sequence update)
Last annotation updat
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Pred. No.
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Pred.
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"Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
Complete
SEQUENCE
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Archaea; Euryarchaeota;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SMART; SM00283; MA; 1.
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InterPro; IPR004089; Chemotaxis_transducer
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                                                                                                                                                                                                                                                                                                                  "Structural analysis of a Sequence features of the TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko T., Kato T., !
Submitted (MAY-2000)
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                              PubMed-10907853;
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261 AA;
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63.0 KDA PROTEIN).
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EMBL/GenBank/DDBJ data
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Horikoshi K.,
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P73239;
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Conrad A., Hornischer K., Kauer G., Loehnert T.-H., N
Reichelt J., Scharfe M., Schoen O., Bargues M., Terol
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
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Miyajima N., Hirosawa M., Sugiura
Hosouchi T., Matsuno A., Muraki /
Shimpo S., Takeuchi C., Wada T.,
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Bacteria; Cyanobacteria; C
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ATP-binding; cc
                                                                                   PROSITE;
                                                                                                                          Pfam; PF00664; ABC_membrane; Pfam; PF00005; ABC_tran; 1. SMART; SM00382; AAA; 1.
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EMBL; D90904; BAA17266.1;
InterPro; IPR003593; AAA.
InterPro; IPR003193; ABC_transporter_tmem.
InterPro; IPR003149; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
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mes 7; Conserv
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AC069473; AAG51057.1;
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Sato S., Kotani H., Tanaka
., Hirosawa M., Sugiura M.,
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    Complete proteome;
93 AA; 65761 MW; )
                                                                                   ABC_TRANSPORTER; 1.
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, Sugiura M., Sasamoto S., Kimura T.,
Muraki A., Nakazaki N., Naruo K., Ok
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         DA48CE3D0EDAC6C9 CRC64;
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MEDILINE-20365717; PubMed-10910347;
Simpson A.J.G., Rethach F.C., Arryd J.E., Bala G.S., Baptista C.S., Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S., Barros M.R., Alves L.M.C., Araya J.E., Bove J.M., Briones M.R.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A. A., Camargo L.E.A., Carraro D.M., Carrer L.G., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coultino L.L., Cristofani M., Dias-Neto E.D., Docena C., El-Dorry H., Facincani A.P., Ferralara A.J.S., Ferrelara V.C.A., Ferro J.A., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Garnier M., Goldman G.H., Goldman M.L., Kemper E.L., Kitajima J.P.,
                                                                                                                                                                                                                                                                                              O9PC32 PRELIMINARY;
O9PC32;
01-OCT-2000 (TrEMBLrel. 15,
01-DCT-2001 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structural analysis of Arabidopsis thaliana chromosome submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases EMBL, AR002031; BAD9804.1; -
Interpro; IPRO0531; TonB_boxC.
PROSITE: PS00430; TOMB_DEPENDENT_REC_1; UNKNOWN_1.
SEQUENCE 608 AA; 67925 MM; 75B5DF42E697586C CRC64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                        NCBI_TaxID=2371;
                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                     Xylella fastidiosa
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hes 8; Conserv
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7; Conserv
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Pred. No.
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Pred. No.
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A Nhani A. Jr. Nobrega F.G., Nunes L.R., Oliveira M.A.,
Add Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
Adde Rossa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
Add a Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
Add Solva A.C.R., da Silva A.M., da Silva F.R., Silva M.A., Jr.,
Add Solva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
Add Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
AVALlada H., Van Slvya M.A., Verjovski Almeida S., Vettore A.L.,
AVALlada H., Van Slvya M.A., Verjovski Almeida S., Vettore A.L.,
AVALlada H., Van Slvya M.A., Verjovski Almeida S., Vettore A.L.,
AVALLAGA M.A., Zatz M., Meidanis J., Setubal J.C.;
AN TENDOMOLI, AAF84755.1;
BENBL, REDOMOLI, AAF84755.1;
BENBL, REDOMOLI, AAF84755.1;
BENBL, REDOMOLI, AAF84755.1;
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Best Local Similarity
Matches 7; Conser
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OB1716;
O1-NOV-1998
O1-NOV-1998
O1-DEC-2001
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                                                                                                                                                           Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstaad M.E., Felblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0260; CHEMTRNSDUCR. SMART; SM00283; MA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004089; Chemotaxis_transducer
InterPro; IPR004090; Me_chemotaxis.
Pfam; PF00015; MCPsignal; 1.
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Lemos E.G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                              STRAIN=CV. COLUMBIA; MEDLINE=20083487; PubMed=10617197;
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                                   Submitted (MAR-2000)
                                                       Lin
                                                                       SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
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SEQUENCE FROM N.A
                                                                                                                            Nature 402:761-768(1999).
                                                                                                                                                thaliana."
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Lemos M.V.F., Lopes S.A.,
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Last annotation updat
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Pred. No.
                                   EMBL/GenBank/DDBJ databases
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Mismatches
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RA Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Tortumi M.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Wiranda M.,
RA Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
RA Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
RA Shinn P., Theologis A.,
RA Shint P., Theologis A.,
RY "Full Length cDNA of gene F27C12.1/At2g25070 (G1:4559345).";
RI Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

BMBL; AC006585; AAD23006.1: -.
DR EMBL; AC006585; AAD23006.1: -.
DR EMBL; AC006585; AAD23006.1: -.
DR H.S.P. p58313; LAGO.
DR InterPro: IPR01022; PP2C.
DR InterPro: IPR01923; PP2C_domain.
DR Ffam; PP00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS01032; PP2C, 1.
InterPro; IPR000759; Adridx_reductase.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR0001327; FAD_pyr_redox.
InterPro; IPR000133; Moxy_FAD_binding.
InterPro; IPR002038; Moxy_FAD_binding.
InterPro; IPR002013; Pyridine_redox_2.
InterPro; IPR001010; Pyr_redox_.
InterPro; IPR001010; Pyr_redox_.
InterPro; IPR001010; Pyr_redox_.
InterPro; IPR001042; Mng_mnoxygenase.
Pfam; PF0149; FAD_binding_3; I.
Pfam; PF0149; FAD_binding_3; I.
Pfam; PF0149; FAD_binding_3; I.
Pfam; PF0149; FAD_binding_3; I.
Pfam; PF0149; FAD_binding_3; I.
Pfam; PF0149; FAD_Binding_3; I.
Pfam; PF0149; FAD_Binding_3; I.
Pfam; PF0149; FAD_Binding_3; I.
Pfam; PF0149; FAD_Binding_3; I.
Pfam; PF0149; FAD_Binding_3; I.
Pfam; PF0149; PR00411; PNDRDTASEI.
PRINTS; PR00411; PNDRDTASEII.
R PRINTS; PR00420; RNGMNOXGNASE.
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STRAIN-MAFF203099;
MEDLINE-21082930; PubMed-11214968;
MEDLINE-21082930; PubMed-11214968;
MEADAKO T., Nakamura Y., Sato S., Asamizu E., Kato T.
Watanabe A., Idesawa K., Ishikawa A., Kawashima K.,
Watanabe A., Idesawa C., Kohara M., Matsumoto M., M.
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., M.
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., M.
Takeuchi C., Yamada M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
PROBABLE FAD-DEPENDENT MONOOXYGENASE.
                                                                                                                                                                                                                                                                                                              Mesorhizobium lot1.";
DNA Res. 7:331-338(2000)
EMBL; AP002997; BAB48792.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobium loti (Mesorhizobium loti).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group:
Phyllobactoriaceae: Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                        Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 GORGWRELAVLGDKMNK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GQVG-RQLAIIGDDINR
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9: Conser
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355 AA; 3
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Pred. No. 40
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Sugimoto M.,
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RESULT
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Best Local
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Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Burrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9CD42 PRELIMINARY; PRT; 447 AA.

O9CD42;
O1-GYPENBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ENOLASE (EC. 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
                                                                                                                            PRINTS; PRO0148; ENOLASE.
PRODOM; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
COmplete proteome; Glycolysis;
SEQUENCE 447 AA; 47250 MW;
                                                                                                                                                                                                  InterPro; IPR000941; Enolase
Pfam; PF00113; enolase; 1.
                                                                                                                                                                                                                              -i- PATHWAY: GLYCOLYSIS.
-i- SUBGUNIT: HOMODIMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
EMBL; AL583917: CAC29763.1;
-HSSP; P00024; 4ENL.
Leproma; ML0255;
                                                                                                                                                                                                                                                                                                                                                                          "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Corynebacterineae; NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium leprae.
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319
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Pred. No.
                                                                      Score 43; DB
Pred. No. 63;
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                                                                                                                             Lyase; Magnesium 63F03867DAA230B8
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Job time: 1663 sec

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Pred. No. is the number of results predicted by chance to have of score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1_/SIDS1/gcgdata/h
2: /SIDS1/gcgdata/h
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length: 2000000000
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7: //SIDSI/gcgdata/hold-genesed/geneseq-embl/AA1985.DAT: *
8: //SIDSI/gcgdata/hold-genesed/geneseq-embl/AA1987.DAT: *
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9: //SIDSI/gcgdata/hold-genesed/geneseq-embl/AA1989.DAT: *
9: //SIDSI/gcgdata/hold-genesed/geneseq-embl/AA1999.DAT: *
10: //SIDSI/gcgdata/hold-genesed/geneseq-embl/AA1999.DAT: *
11: //SIDSI/gcgdata/hold-genesed/geneseq-embl/AA1999.DAT: *
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13: //SIDSI/gcgdata/hold-genesed/geneseq-embl/AA1993.DAT: *
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Gapop 10.0 , Gapext 0.5
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81
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Copyright (c) 1993 - 2000 Compugen Ltd
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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SUMMARIES

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AAB37032 AAY05411 AAW06298 AAY96323 AAB70373 AAB70373 AAB705430 AAY705430 AAY705430 AAY71406 AAY34119

BC12 polypeptide B Human BAXTAM3 doma GD domain region f Mammalian Bax BC1-BAX BH3 consensus BC12 polypeptide B Human BAX BH3 doma Human neuroprotect Human truncated Ba Human Bax Brotetan Human Bax Brotetan

New peptide conjugates for modulating apoptosis or for inhibiting

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WPI; 2	φ.	(UYJE-	07-APR-	06-APR-	12-0CT	WO20005	Homo s	Cytostatic; cardiant; I apoptosis; colorectal; melanoma; stroke; myo	Bcl2 p	28-FEB-2001	AAB37032;	1 32 AB370		45	44	2 2	4 0	4 0	о С	37	დ თ ნი თ	34	w u	ω - Δ	30	298	27	26 5 5	24	22	21	20	18	17	15	14	12	
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379325/6	ang J	V JEFFERSON	); 99US-	ν.		-A1.	•	ic; neurop; Bcl-2 sus modulatial; gastri; lymphocy myocardial	ide	(firs		tandard;			87.7														100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
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í P	Z,	THOMAS	02.	352.				ve; ly; ell sma kem	lin l	3		•-			21																							
	Shan S, Lu Z;	S.				•		protective; anti-HTV; viruolde; cerebro; uperfamily; BH3 domain; cell death agon: lon; B cell lymphome/leukemia 2; cancer: ic; non-small lung; renal; thyroid; neuytic leukemia; neurodegenerative disordil infarction.	peptide #32.			16 AA.	ALIGNMENTS	AAY70817	AAY70816	AAB85171	AAW06296	AAR37034	AAY05412	AAB35128	AAB74122 AAB74125	AAY70828	AAW87808	AAY05434	AAR71407	AAB37007 AAY70819	AAY70824	AAY05426 AAH37033	AAY39263	AAY78512	AAB50539	AAB48286 AAB35199	AAB74126	AAB74121	AAY70827	AAW87809	AAY05435	
or inhihiting p								ebroprotective; agonist; Bad; ancer; prostate; neuroblastoma; sorder; AIDS;						tec	Human neuroprotect	BH3 domain of Bax	<b>Q</b> 1	BC12 polypeptide B	Human BAX BH3 doma	Murine Bax. Mus s	Murine bcl-2 assoc	Mouse BAX alpha pr	Murine Bcl-2 assoc	Mouse BAX protein	Murine Bax protein	Mouse neuroprotect	Mouse neuroprotect	Mouse BAX BH3 doma	Coding region of c	Truncated Bax amin	Human Bax protein	pψ	ğ	Human bcl-2 associ	uman B		uman BAX protein	

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The invention relates to a peptide conjugate having the formula:

(R X)n Peptide where n = 1-10; X = CoO, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where ct the functional group of the side chain is NH2 or OH; or X = 0 or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or COOH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one correctly optionally concentrated with a 1-5C straight or branched chain alkyl group, or benzyl optionally concentrated with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ABB37001-1837058 represent examples cof the peptide option of the conjugate is The peptides represent analogues of a Bel-2 superiamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the ceil death agonist Bad. The peptides conjugate is useful for modulating apoptosis in the cells of a subject, or for creversing B cell lymphoma/leukemia 2 (Bel-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bel-2 conjugate is useful for modulating apoptosis in the cells of a subject, or for creversing B cell lymphoma/leukemia 2 (Bel-2)-mediated blockage of conjugate afflicted with a cancer characterized by cancer cells that cancer cells afflicted with a cancer characterized by cancer cells that cancer conjugate is useful for treating a conjugate is also useful for treating and conjugate is a conjugate is a subject afflicted with a cancer characterized by cancer cells that cancer cells and conjugate is a conjugate is a conjugate is a subject afflicted with a cancer characterized by cancer cells that cancer conjugate is a conjugate is a conjugate is a subject afflicted with a cancer characterized by cancer cells that cancer conjugate is a subject afflicted with a cancer characterized by cancer cells that cancer includes prostate, colorectal, gastric, and non-tymphocytic leukemia. The peptide conju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY05411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoprollferative condition; arthritis; autoimmune disease; therapy.
Korsmeyer SJ
                                                                                                                                                  07-0CT-1997;
26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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treating neurodegenerative disorders, stroke,
                                                                         (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                 22-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100
nes 16; Conservative
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Pred. No. 9.3e-07;
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The term GD domain refers to a protein domain first identified in Bak and shown to be essential for the interaction of Bak with Bcl-x(L) and for Bak's cell killing function: and to peptides and/or molecules capable of mimicking its structure and/or function. The present sequence represents a GD domain corresponding to amino acid residues 52-77 of Bax. An antibody raised against a GD domain may be used to screen a cDNA expression library for clones comprising cDNA inserts encoding immunocrossreactive proteins. Truncated GD domain peptides have been shown to maintain the protein binding and cell killing function exhibited by wild type Bak. These molecules may induce apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a bcl homology domain 3 (BH3 domain) of the invention, derived from a prospoptotic member of the BCL2 family. The BH3 polypeptide can be used in a method for promoting apoptosis in a target cell respectially where the cell is a cancer cell a virus infected cell or an autoantibody producing cell. The BH3 polypeptide can be used in therapeutic compositions for treating disease including cancer, other lymphoproliferative conditions, arthritis, inflammation, and autoimune diseases, which may result from the down regulation of cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide(s) comprising GD domains - have similar activities to wild type Bak, and cause cellular apoptosis for treatment of viral
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                                                                                                                      The present sequence is the mammalian Bax Bcl-2 homology domain 3 (BH3) domain, which was used in a sequence alignment with the same domain of a putative version of the mammalian apoptosis regulator BBC3, which was designated BBC3-ORF2. The BBC3 protein, nucleic acids and antibodies are suitable for use in promoting cell death or for preventing apoptosis in malignant cells and those causing autoimmune diseases.
                                                                                                                                                                                                                                       Mammal; apoptosis; cell death; BBC3; apoptosis promotion; Bax; apoptosis inhibition; malignant cell; autoimmune disease.
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The present invention describes an isolated or synthetic polypeptide (RI) comprising a less than full length maino acid sequence of a mutant CC Bcl-XL/Bol-2 associated cell death regulator polypeptide (RAD) or its correct mutant sequence, which contains amino acid substitutions at Seril8 of a human RAD, Seris5 of a mutante RAD (longer mutane BAD) or Seril3 of a mutante RAD (sorter mutane RAD). (I) has immunostimulant, neuroprotective, contropte, antischaemic, vulnerary, cytostatic, antivital, contropte, antischaemic, vulnerary, cytostatic, antivital, contropted and an apoptosis inducer or inhibitor. BAD polypeptides and contropted and an apoptosis inducer or inhibitor. BAD polypeptides and copolynucleotides can be used for screening candidate compounds and drugs correctivity that promote cell survival or apoptosis. Other uses include conducing or inhibiting apoptosis in a cell. Candidate compounds contentified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischaemic cell (long), reperfusion cell death, wound healing, cancer, viral infections, content of the present sequence represents a Bc1-family member consistency inventions as sequence which is used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises maino acid substitutions at Seril8, Seri55 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bcl-XL/Bcl-2 associated cell death regulator; DAD; mutant; apoptosis; immunostimulant; neuroprotective; nootropic; antischaemic; vulnerary; cyrostatic; antiviral; antiarthritic; antisinfammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death, reperfusion cell death, arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
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  Sequence
                                            present invention.
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RESULT
AAB37006
ID AAB3
                                                                                                                                                                                                                                                                                                                  The invention relates to a peptide conjugate having the formula:

(C (R-X))-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH; the functional group is attached to the C-terminus of the peptide, or a side chain for the peptide, or a side chain for the peptide, where the side chain functional group is COOH CC or two double bonds, cyclobuty, cyclopentyl, cyclobaxyl containing one CC or two double bonds, cyclobutyl, cyclopentyl, cyclopexyl cyclopexyl cyclopexyl, cyclopexyl, cyclopexyl cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyclopexyl, cyc
                            Query Match
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                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                      conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders. Armitrad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 18; Page 17; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptide conjugates for modulating apoptosis or for inhibiting ceil lymphoma/leukemia 2 (BL-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huang
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                                                                                                                                                                                                                         immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-679325/66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stroke; myocardial infarction.
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        16;
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                                                                                                                                                                         27
    Conservative
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                            100.0%;
                                                                                                                                                                                                                                 neurodegenerative disorders, (AIDS), stroke or myocardial
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Score 81; DE
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Human neuroprotective truncated BAX protein, tBAX78

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                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                      This sequence represents a bcl homology domain 3 (BH3 domain) of the invention, derived from a proapoptotic member of the BCL-2 family. The BH3 polypeptide can be used in a method for promoting apoptosis in a target cell, especially where the cell is a cancer cell a virus infected cell or an autoantibody producing cell. The BH3 polypeptide can be used in therapeutic compositions for treating disease including cancer, other lymphoproliferative conditions, arthritis, inflammation, and autoimmune diseases, which may result from the down regulation of cell death
                                  31-JUL-2000 (first entry)
                                                           AAY70818;
                                                                                  AAY70818 standard; Protein; 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoproliferative condition;
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                Example 10; Fig 17a; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        Bcl homology domain 3 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-1997;
26-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis; autoimmune disease; therapy
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                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                     Score 81;
Pred. No.
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                     2e-06;
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                                                                                                                                                                                                                  Length 34;
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a specifically claimed truncated BAX protein tBAX78 which inhibits neuronal apoptosis induced by trophic factor deprivation. The protein consists of first 78 amino acids of human BAX alpha, that includes the N-terminal region and BH3 domain. It lacks the BH1, BH2 and C-terminal region are the transmembrane domain so the full-length BAX alpha. The tBAX protein lacking only the transmembrane domain has been shown to have anti-apoptotic activity. The transmembrane domain has been shown to have anti-apoptotic activity.
                                                                                                                                                                                                                                                                                                                                                                                      AAY34149 standard; Protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 33; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
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                                                     Doma in
                                                                                                                           Homo sapiens
                                                                                                                                                                              Apoptosis;
                                                                                                                                                                                                                             Human truncated Bax protein
                                                                                                                                                                                                                                                                                   30-NOV-1999
                                                                                                                                                                                                                                                                                                                                      AAY34149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spinal cord injury, head trauma and stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               poptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100 es 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kklseclkrigdelds
                                                                                                                                                                              adenovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 AA;
                                                                                                                                                                                                                                                                                (first entry)
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                                               Location/Qualifiers 59..101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                              dimeric; Bcl-2;
                         "Portion of BH3 domain essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO.
                                                                                                                                                                              p53; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
4.8e-06;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 78.
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                         for dimerisation"
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RESULT 1
AAR71406
ID AAR7
XX
AAC AAR7
XX
XX
BY
AC Huma
XX
DE Huma
XX
KW Huma
KW apop
KW prolk
KW apop
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                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon. Jesulting in a truncated protein. However, the domain responsible for its function is still present in the truncated protein. Bax (Bc1-2 associated x protein) is a proapoptotic member of the Bc1-2 gene family. CC Bax functions as a primary response gene in the p53-regulated apoptotic pathway. The Bax gene promoter has 4 p53 binding sites and the CC expression of Bax is upregulated at the transcriptional level by p53, and CC Bax mRNA, and protein expression have been shown to increase following induction of p53. Bax protein can function as homodimer; or it can neterodimerise with other Bc1-2 gene family members such as the entispophoric protein Bc1-2. Heterodimerisation of Bc1-2 family members model. This code is useeptibility of a cell to undergo apophosis. If Bc1-2 is in excess, however, Bax homodimers predominate and cell death via the "rhoostat" model. This can excess, however, Bax homodimers predominate and cell death is inhibited. If Bax is classified and a complete station in its monomeric form to accelerate cell death. Use of novel ademovital vectors containing this Bax gene may can function in its monomeric form to accelerate cell capite arcest and/or apoptosis in malignant cells carrying p53 cmutations. In addition, Bax overexpression could provide the apoptotic call cycle arcest and/or apoptosis in malignant cells carrying p53 cmutations. In addition, Bax overexpression could provide the apoptotic carrying p53 without the need for p53 itself.
                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line; apoptosis; membrane-associated cytoplasmic protein; B cell; T cell; proliferation; cell cycle proyression; Bax; apoptotic cell death; apoptosis; cytokine; death repressor; BHI; BH2; cancer therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a human truncated Bax protein. The CDNA contains a single base deletion relative to the wild-type (ARX19764), causing a frameshift which leads to translation of a premature stop causing a frameshift which leads to translation of a premature stop
                                                                                                                                      15-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 26; Page 148-149; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New adenovirus vectors, used for killing or inhibiting the growth cells and for treating cancers \,\cdot\,
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                                                                                              Human Bax protein
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                                                                                                                                                                                                                AAR71406 standard; Protein; 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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16; Conser
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                                                                                                                                                                                                                                                                                                                                                                                        Score 81; DB 20;
Pred. No. 8.3e-06;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 131;
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RESULT 11
AAY34150
ID AAY341
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AC AAY341
XX
DT 30-NOV
DT 30-NOV
XX
LDE Human
XX
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                                                                                                                                                                                                                                                                                                             Considered with the human Bax protein. Bax is a protein which is associated with the human bc1-2 alpha and beta proteins, the sequences of which are given in AR7104-05 respectively. bc1-2 is encoded by a prote-oncogene and is capable of inhibiting appropriate in many comprehensive protein and is thought to function by enhancing the survival of hematopoletic cell systems. bc1-2 is a 26 kb membrane-associated cycloplasmic protein and is thought to function by enhancing the survival of proliferation of these cell types. bc1-2 has not been shown to directly promoting comprehensive to inmitting concentrations of II-3. bc1-2 has been shown to directly promote cell cycle progression nor does it necessarily alter the dose reponse to limiting concentrations of II-3. bc1-2 has been shown to commend the protein progression nor does it necessarily alter the dose considerates approach cell into a least induced by cytokine deprivation in an accelerates approach cell into and it also accs to counter the death repressor accelerates approach cell into sell death induced by cytokine deprivation in cell into between bc1-2 and Bax determines cell sustitution or deletion in the BHI or BH2 domains. This makes the substitution or deletion in the BHI or BH2 domains. This makes the connear therapy, controlling hyperplasias and eliminating self-reactive connective constrained by a proposition of the BHI or BH2 domains. The immunocaned connect therapy, controlling hyperplasias and eliminating self-reactive constitution bot 21s beneficial in treatment and diagnossis of immunocal deficiency diseases, including AIDS and neurodegenerative and ischaemic cell seast.
                                                                                                                                                                                                                  Ouery Match 100
Best Local Similarity 100
Matches 16; Conservative
                           Human wild-type Bax protein
                                                    30-NOV-1999 (first entry)
                                                                              AAY34150;
                                                                                                    AAY34150 standard; Protein; 192 AA
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                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methods for producing and identifying mutant bcl-2 proteins - that lack death repressor activity and/or lacks binding to Bax.
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N-PSDB; AAQ97606.
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25-MAY-1994;
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                                                                                                                                                                  192 AA;
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94US-0248819
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                                                                                                                                                                                                                    Score 81; DB 16;
Pred. No. 1.2e-05;
); Mismatches 0;
                                                                                                                                                                                                                                           Length 192;
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Best Local
               Human BAX protein sequence
                                        02-JUL-1999
                                                                 AAY05435
                                                                                        AAY05435 standard; peptide; 192
                                                                                                                                                                                                                                                                    Sequence
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N-PSDB: AAZ19764.
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                                                                                                                                                                             1 KKLSECLKRIGDELDS 16
                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                    192
                                                                                                                                                                                                      100.0%;
ilarity 100.0%;
Conservative 0
                                        (first entry)
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                                                                                                                                                                                                       0,
                                                                                                                                                                                                                    Score 81;
Pred. No.
                                                                                           2
                                                                                                                                                                                                       Mismatches
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1.2e-05; DB 20; 0;

Length 192;

0; Gaps

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This sequence represents human wild-type Bax protein. A naturally coccurring mutant protein (ANY34149) was also isolated. Bax (Bcl-2 associated X protein) is a proapoptotic member of the Bcl-2 gene family. CC Bax functions as a primary response gene in the p53-regulated apoptotic ceptiway. The Bax gene promoter has 4 p53 binding sites and the ceptival of Bax is upregulated at the transcriptional level by p53, and CC expression of Bax is upregulated at the transcriptional level by p53, and CC pathway. The Bax sprotein expression have been shown to increase following induction of p53. Bax protein can function as homodimer; or it can heterodimerise with other Bcl-2 gene family members such as the antisymphototic protein Bcl-2. Heterodimerisation of Bcl-2 family members provides a means of controlling call death via the "rhoostat" model. This can be provided a means of controlling call death via the "rhoostat" model. This compose is that the relative amounts of Bcl-2 and Bax determine the susceptible to apoptosis following exposure to an apoptotic stimulus. The cases, however, Bax homodimers predominate and cell death is inhibited. If Bax is conceptible to apoptosis following exposure to an apoptotic stimulus. Additionally, Bax can function in its monomeric form to accelerate cell cell cycle arrest and/or apoptosis in malignant cells carrying p53 cultations. In addition, Bax overexpression could provide the apoptotic cell cycle arrest and/or apoptosis in malignant cells carrying p53 cultations. In addition, Bax overexpression could provide the apoptotic cell cell could provide the apoptotic cell cell cycle arrest and/or apoptosis in malignant cells carrying p53 cultations. In addition, Bax overexpression could provide the apoptotic cell cycle arrest and/or apoptosis in malignant cells carrying p53 contained the apoptotic cell cycle arrest and/or apoptosis in malignant cells carrying p53 contained the apoptotic cell cycle arrest and/or apoptosis in malignant cells carrying p53 contained cells carrying p53 cells cell
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RESULTANA RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RABBOTAN RA
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Best Local Similarity
Matches 16; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 21c; 104pp; English.
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26-SEP-1997;
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                           US5856171-A
                                                                                                          Domain
                                                                                                                                                              Domain
                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                      Human; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator; ''
bcl-2-related function; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW87804 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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97US-0060133
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                                                                                                                                                          Location/Qualifiers 97..118
                                                                                                                                      /note-
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100.0%; Pred. No. 1.2e-05;
tive 0; Mismatches 0;
                                                                               "BH2 domain"
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RESULT 14
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Best Local :
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26-AUG-1993;
25-MAY-1994;
                                                                                        10-NOV-1994;
26-AUG-1993;
25-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human Bc1-2 associated protein designated Bax. The Bax protein is used in a composition which comprises a bc1-2 family member polypeptide, a naturally occurring Bax polypeptide and an antibody that binds to the Bax polypeptide. The composition is used to identify modulators of bot-2-related function, e.g. substances that inhibit binding of Bax to bc1-2, which would be potentially useful as drugs for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA composition encoding bcl-2 two-hybrid and reporter system - for identifying modulators of bcl-2 function
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DNA composition encoding bcl-2 two-hybrid and
                                                                                                                                                           05-JAN-1999.
                                                                                                                                                                                US5856171-A
                                                                                                                                                                                                                            Human; Bc1-2 associated protein; Bax; bc1-2; antibody; modulator;
bc1-2-related function; apoptosis.
                                                                                                                                                                                                                                                            A human Bc1-2 associated protein designated
                                                                                                                                                                                                                                                                                                          AAW87809;
                                                                                                                                                                                                                                                                                                                                AAW87809 standard; Protein; 192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                       WPI; 1999-105119/09
                                            Korsmeyer
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                                                                                                                                                                                                      Homo sapiens
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                                                                  (UNIW ) UNIV WASHINGTON
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Pred. No. 1.2e-05;
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 reporter system
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identifying modulators of bcl-2 function

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Best Local Similarity 100.0%;
Matches 16; Conservative (
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                                                                                                                                                      WPI;
   Disclosure; Page 35-36; 43pp; English
                                                            Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders -
                                                                                                                                                                                                               Johnson
                                                                                                                                                                                                                                                                       (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                22-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; truncated BAX protein; tBAX; BAX alpha; BCL-2 family; head trauma; neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive; apoptosis; tratment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; stroke; pro-apoptotic; PCD; programmed cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human BAX alpha protein.
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                                                                                                                                                                                                           Easton R;
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169..188
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/note- *BCL-2 Homology domain
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Pred. No. 1.2e-05;
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                                                                            Query Match
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                                       1 KKLSECLKRIGDELDS 16
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
          protein search, using sw model
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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81
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/J/iaa/5a_COMB.pep:*
/cgn2_6/ptodata/J/iaa/6a_COMB.pep:*
/cgn2_6/ptodata/J/iaa/backfilesi.pep:*
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US-09-36-388A-26
PCT-USS6-66122-26
US-08-440-391-13
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PCT-USS6-66122-21
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PCT-USS6-66122-21
US-08-798-897-22
US-08-798-897-22
US-08-798-898-231-2
US-08-798-898-331-348-39
US-08-337-6468-331-2
US-08-337-6468-331-2
US-08-856-531-2
US-08-856-531-3
US-08-856-531-3
US-08-856-531-3
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Sequence 40, Appl
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-	ω	Sequence	US-08-856-034		192	96.3	78	3
Appl	Θ	Sequence	2 US-08-856-531-8		192	96.3	78	42
Appl	w	Sequence	2 US-08-856-531-3		192	96.3	78	1
-	ω	Sequence	2 US-08-337-646A-8		192	96.3	78	40
		Sequence	2 US-08-337-646A-3		192	96.3	78	39
Appl	œ	Sequence	1 US-08-248-819A-8		192	96.3	78	38
Appl	w	Sequence	1 US-08-248-819A-3		192	96.3	78	37
•	œ	Sequence	1 US-08-112-208C-8	h -	192	96.3	78	36
Appl	w	Sequence	1 US-08-112-208C-3		192	96.3	78	35
Appl	5	Sequence	4 US-09-037-742B-9		221	100.0	81	34
Appl	ø	Sequence	1 US-08-616-732A-9		221	100.0	81	33
5, App	25	Sequence	5 PCT-US95-04600-25		192	100.0	81	32
Appl	9	Sequence	4 US-08-927-326-9		192	100.0	81	μ
App1	'n	Sequence	4 US-08-927-326-2		192	100.0	81	ö
Appl	7	Sequence	4 US-09-127-048-7		192	100.0	81	9
s, App.	Ŀ	Sequence	3 US-08-471-057-13		7.6T	100.0	18	82

## ALIGNMENTS

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RESULT US-09-235-385A-40 US-09-235-385A-40 S-09-235-385A-40 S-09-235-385A-40 S-09-235-385A-40 S-09-235-385A-40 S-09-235-385A-40 US-09-235-385A-40 US-09-235-
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEO ID NO:
US-09-236-385A-40
                                                                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REALABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: HEM PC Compatible
COMPUTER: HEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-199
CLASSIFICATION: CHOKOWID
ATTORNEY/AGENT INFORMATION:
NAME: WIXDN. HENRY N.
HEGISTRATION NUMBER: 32.073
REGISTRATION NUMBER: 32.073
REGISTRATION NUMBER: 32.073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHNE: 202-942-8400
TELEPAX: 202-942-8484
INFORMATION FOR SED ID MO: 40
SEQUENCE CHARGITRIFFICS:
                                              1 KKLSECLKRIGDELDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES, 41
CORRESPONDENCE ADDRESS:
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STRIE: D.C.
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH MODULATE APOPTOSIS
KKLSECLKRIGDELDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20 amino acids
                                                                                                                                                                        Conservative
                                                                                                                                                      100.0%; sr
100.0%; pr
                                                                           16
                                                                                                                                                                  Score 81; DB 4;
Pred. No. 4.1e-07;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY DOCKET NO. 104322.147CIP
                                                                                                                                                                             0
                                                                                                                                                                                                                                                         Length 20;
                                                                                                                                                                             Indels
                                                                                                                                                                             0
                                                                                                                                                                             Gaps
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CURRENT APPLICATION DATA 41.25
CURRENT APPLICATION DATA 40.391
APPLICATION NUMBER: U$/08/440,391
FILLING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION UNMBER: 104322.147
TELECHMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEPHONE: 202-943-8400
TELEPHONE: 202-943-8400
TELEPHONE: 202-943-8400
TELEPHONE: 202-943-8400
SEQUENCE CHARACTERISTICS:
LENGTH: 26 anino acids
TYPE: anino acids
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TYPE: data 250-104-8600
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Patent No. 565672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 100.0%; Score 81; DB 1; Best Local Similarity 100.0%; Pred. No. 5.4e-07 Matches 16; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08440391 Patent No. 5656725
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: CHITTE
APPLICANT: LUTZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CHITTENDEN, IMPRICANTS AND COMPOSITIONS WHICH TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH TITLE OF INVENTION: MODULATE APOPTOSIS NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSES: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IMM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
                                                                                                                                 STREET: 1:--
STREET: Washington
CITY: Washington
STATE: D.C.
STATE: 20004
ZIP: 20004
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COCEMBASE AND THE PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: U. Z
                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 KKLSECLKRIGDELDS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKLSECLKRIGDELDS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                 E: Hale and Dorr
1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08440391
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHITTENDEN, Thomas D.; and
                                                                                                                                                                                                                                                                                                                                                                                                                           Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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; MOLECULE TYPE: US-08-908-597A-6
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US-08-908-597A-6
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; MOLECULE TYPE: peptide
US-08-440-391-24
                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/08/440
PILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 10,43
TELECOMMUNICATION INFORMATION:
TELECHNOLICATION: 10FORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                   TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHITTENDEN, FINANCE AND COMPOSITIONS WHICH TITLE OF INVENTION: MOVEL PROPTIDES AND COMPOSITIONS WHICH TITLE OF INVENTION: MODULATE APOPTOSIS NUMBER OF EQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSE: Hale and Dore
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-POS/MS-POS
SOFTWARE: PALENLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1455
CITY: Washington
CTATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,0
                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 100.0%;
Local Similarity 100.0%;
nes 16; Conservative 0
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FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6, Application US/08908597A
5. 5863795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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amino acid
                                                                   26 amino acids
                  peptide
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                                                                                                                                                                             104322.147
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Pred. No. 5.4e-0
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0

Query Match

100.0%;

Score 81;

DB 2;

Length 26;

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SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
NOLECULE TYPE: peptide
US-08-908-597A-24
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US-09-236-385A-6
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                                                                                          Sequence 6, Application US/09236385A Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and LUTZ, Robert J.
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: U5/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY, AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE, DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CHTTENDEN, Thomas D.; and APPLICANT: LUT2, KODETT J. TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH TITLE OF INVENTION: MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 530
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CITY: Washington
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                                                                                                                                                                                                                                                              1 KKLSECLKRIGDELDS 16
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NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
                                                           TITLE OF INVENTION: NOVEL PEPTIDES AND MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                        100.0%; Score 81; DB 2; ilarity 100.0%; Pred. No. 5.4e-07; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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Mismatches
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ches 0;
                                                                            COMPOSITIONS WHICH
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-236-385A-6
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US-09-236-385A-24
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Best Local S
Matches 16
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GENERAL INFORMATION:
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TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEO ID NO: 6:
SEQUENCE CHARACTERISTICS:
  TELEPHONE: 202-942-84
TELEPAX: 202-942-8484
THEORNATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-705/MS-DOS
SOFTWARE: Patentin Release $1.0, Version $1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: CONKNOWN>
ATTORNEY/AMENT INFORMATION:
NAME: WIXON, HERRY N.
NAME: WIXON, HERRY N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 100.0%; Score 81; DB 4; Local Similarity 100.0%; Pred. No. 5.4e-07; pes 16; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KKLSECLKRIGDELDS 16
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FILING DATE: 25-Jan-1999
CLASSIFICATION: CLASSIFICATION: CUBROOM>
ATTORNEY/ACENT INFORMATION:
NAME: MIZON, HENRY N
REGISTRATION NUMBER: 32,073
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MEDIUM TYPE: Floapy disk
COMPUTER: HBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOPTWARE: Patentin Release #1.0/
                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CHITTENDEN, Thomas D.; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1455 Pennsylvania Avenue, CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
STATE: D.C.
                                                                                                 REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Hale and Dorr STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 26 amino acids
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                                                           202-942-8400
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                                                                                               ATTORNEY DOCKET NO. 104322.147CIP
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RESULT 9
PCT-US96-06122-24
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TOPOLOGY: linear;
MOLECULE TYPE: peptide
PCT-US96-06122-6
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PCT-US96-06122-6
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Sequence 24, Application PC/TUS9606122 GENERAL INFORMATION:
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                                                                                                                                                                                  Matches
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Best Local :
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INFORMATION FOR SEQ 1D NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMENTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURENT APPLICATION NUMBER: PCT/US96/061
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY /AGENT INFORMATION:
NAME: NIXON, HENRY N.
REGISTRATION UNMBER: 32,073
REFERENCE/DOCKET NUMBER: 10-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL PERTIDES AND COMPOSITIONS TITLE OF INVENTION: WHICH MODULATE APOPTOSIS NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1455 Peni
CITY: Washington
                                                                                                                                                                             Match 100.0%; Score 81; DB 5; Local Similarity 100.0%; Pred. No. 5.4e-07; Nes 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 100.0%; Score 81; DB 4;
Local Similarity 100.0%; Pred. No. 5.4e-07;
hes 16; Conservative 0; Mismatches 0;
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                                                                                                             6 KKLSECLKRIGDELDS 21
                                                                                                                                              1 KKLSECLKRIGDELDS 16
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1455 Pennsylvania Avenue, N.W.
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                                                                                                                                                                                                                 Length 26;
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PCT-US96-06122-24
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Best Local Similarity 100.0%; Pred. No. 5. 4e-07;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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TELEPAX: 202-942-8484
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: EC-DOS/MS-DOS
OPERATING SYSTEM: EC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILLING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                              APPLICANT: CHITTENDEN, Thomas D.; and APPLICANT: LUTZ, ROBERT J.

TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH TITLE OF INVENTION: MODULATE APOPTOSIS NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS: ADDRESS: HALE and Dorr STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION UNMEER: 32,073
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTMARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US96/06122
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
                                                                                                                                                                                  CILA.
STATE: D.C.
20004
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                                                                                                                                                                                                                          CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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CITY: Washington
CLASSIFICATION:
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TELECOMMUNICATION INFORMATION:

202-942-8400

REFERENCE/DOCKET NUMBER:

TELEPHONE:

ATTORNEY/AGENT INFORMATION

NAME: WIXON, HENRY N. REGISTRATION NUMBER:

32,073

104322.147

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                                                                                 US-08-908-597A-13
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US-08-908-597A-13
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GENERAL INFORMATION:
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Best Local Similarity
Matches 16; Conserv
Query Match
Best Local Similarity
Matches 16; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1455 - CITY: Washington STATE: D.C. of the 20004
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: U5/08/440,391

FILING DATE: 12-MAY-1995

FILING DATE: 12-MAY-1995

ATTORNEY AGENT INFORMATION:

NAME: MIXON, HENRY N.

REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CHITTENDEN, Thomas D.; and APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH TITLE OF INVENTION: MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KKLSECLKRIGDELDS 16
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1455 Pennsylvania Avenue, N.W
100.0%; hilarity 100.0%; Conservative 0;
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               Score 81;
Pred. No.
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Pred. No. 7.2e-07;
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 Mismatches
               7.2e-07;
                                   DB 2;
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TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-236-385A-13
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PCT-US96-06122-13
Sequence 13, Application PC/TUS9606122
GENERAL INFORMATION:
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Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
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SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20004

COMPUTER READABLE FORM:

COMPUTER: READABLE FORM:

COMPUTER: LIM PC compatible

COMPUTER: SYSTEM: PC-DOS/M5-DOS

OPERATING SYSTEM: PC-DOS/M5-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

COMPUTER PATENTION DATE: US-09/236,385A

FILTMO DATE: 25-Jan.1999

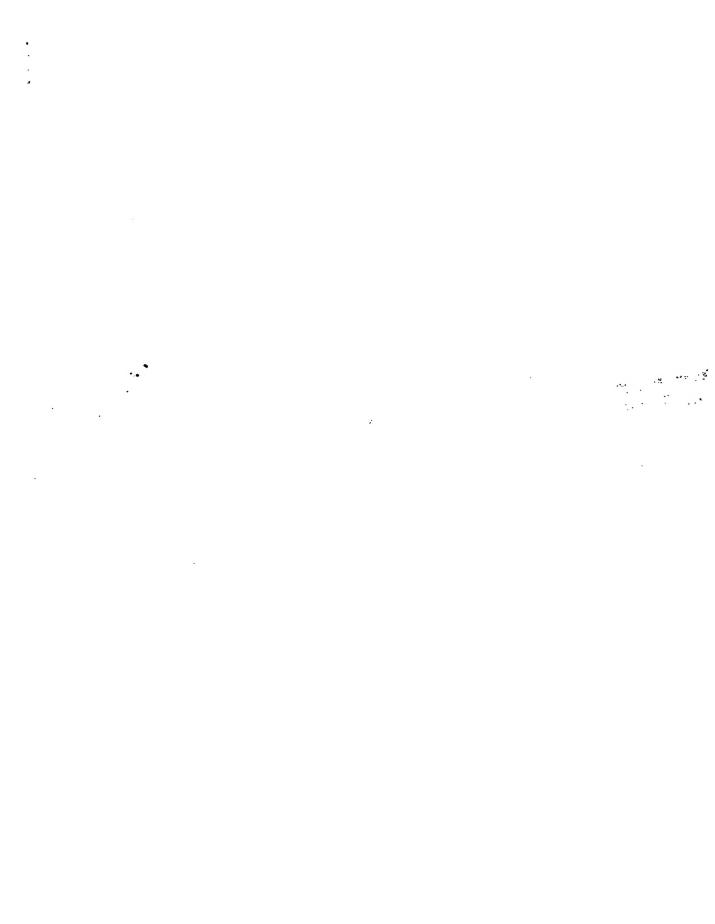
ATPORISSIFICATION: "COMPATION: SYSTEM: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DATE: PS-DAT
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                                                                                                                                                                                            STREET: 1455 Pent
CITY: Washington
                                                                                                                                                                STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
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                                                                                                                                20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 202-942-8484
TELEFAX: 202-942-8484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 34 amino acids
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Pred. No. 7.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100
Best Local Similarity 100
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22,
                                                                                                                         CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/08/798,897
FILING DATE: FEBRUARY 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.01400
TELEPOAMUNICATION INFORMATION:
TELEPOAMUNICATION INFORMATION:
TELEPOAMUNICATION INFORMATION:
TELEPOAMUNICATION INFORMATION:
TELEPOAMUNICATION INFORMATION:
TELEPOAM: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5789201
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Guastella, John
TITLE OF INVENTION: Gennes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS: 53
ADDRESSEE: STERME, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-D
SOFTWARE: PATENTIN Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8480
TELEFAX: 202-942-8484
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NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                   COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE: HEREW
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                     STRANDEDNESS:
TOPOLOGY:
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                                       amino acid
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                     not relevant
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n Release #1.0, Version #1.25
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100.0%; Pred. No. 7.2e-07;
tive 0; Mismatches 0;
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COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COSC/MS-COS
SOFTMARE: Detentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/978.523
FILING DATE: herewith
CLASSIFICATION: 424
PIOR APPLICATION WHEER: US 08/799.897
FILING DATE: Pebruary 11, 1997
CLASSIFICATION WHEER: US 08/799.897
FILING DATE: Pebruary 11, 1997
CLASSIFICATION WHEER: 32,83
ATTORNEY/AGENT INFORMATION:
NAME: Esmond. Robert W.
REGISTRATION NUMBER: 1483.0140002
FELECOMMUNICATION INFORMATION:
TREEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTENISTICS:
LENGTH: 42 amino acids
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US-08-978-523-22
Search completed: September 20, 2002, 10:37:21 Job time: 409 sec
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                                                                                                                                                                               Matches
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APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Codd
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 100.0%; Score 81; DB 1; Local Similarity 100.0%; Pred. No. 8.9e-07; Mismatches 0; Mismatches 0;
                                                                                                  27
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les 16; Conserv
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STREET: 1100 New York Avenue, N.W., Suite 600
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                                                                                                  KKLSECLKRIGDELDS 42
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                                                                                                                                                                             100.0%; Score 81; DB 2; ilarity 100.0%; Pred. No. 8.9e-07; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                      Length 42;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
      seq length: 0
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Match
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      PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
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Gapop 10.0 , Gapext 0
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81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
      DB
      A47538
A47538
B47538
B47538
B55252
F562235
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(without alignments)
16.084 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283138
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ser/thr protein ki
alpha-actinin - sl
hypothetical prote
2-amino 4-hydroxy-
gene 28 protein
anthramilate phosp
myo-incsitol 1-pho
dihydrolipoamida
hypothetical prote
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fructose-1,6-bisph
hypothetical prote
hypothetical prote
hypothetical prote
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probable arom prot
malate dehydrogena
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hypothetical prote
GrpE protein - Syn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bax-delta protein
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## ALIGNMENTS

KKLSECLKRIGDELDS 16	RESULT 1 JC7255 Bax delta protein - human C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: University (man) C.Date: 09-un-2000 **sequence_revision 09-Jun-2000 **text_change 17-Nov-2000 C.Accession: JC7255 R.Schmitt, E.; Paquet, C.; Beauchemin, M.; Dever-Bertrand, J.; Bertrand, R. Biochem Biophys. Res. Commun. 270, 858-879, 2000 A.Teltle: Characterization of Bax-delta, a cell death-inducing isoform of Bax. A.Reference number: JC7255 A.Reference number: JC7255 A.Residues: 1-179 <sch> A.; Residues: 1-179 <sch> A.; Experimental source: cancer promyelocytic cells A.; Experimental source: cancer promyelocytic cells C.; Comment: This protein, a member of the Bc1-2 family, has a proapoptotic effect. It C.; Superfamily: bc1 transforming protein</sch></sch>
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A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map postition: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer
                                                                                                                                                              A; Gene: bax
C; Superfamily:
                                                                                                                                                                                                                                                                                               Cell 74, 609-619, 1993
A;Title: Bel-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates
A;Reference number: A4753B; MUID:93364978
A;Accession: b4753B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 74, 609-619, 1993
A;Title: Bol-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates A;Reference number: A47538; MUID:93364978
A;Accession: B47538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bcl-2-associated protein x, beta splice form - human N;Alternate names: BhA; programmed cell death membrane protein x beta c;Species: Homo sapiens (man) c;Datc: 03-May-1994 #sequence_revision 03-May-1994 #tcxt_change 17-Nov-2000 C;Datc: 03-May-1994 #sequence_revision 03-May-1994 #tcxt_change 17-Nov-2000 C;Datc: 04-7594 #sequence_revision 03-May-1994 #tcxt_change 17-Nov-2000 C;Datc: 04-7594 #sequence_revision 03-May-1994 #tcxt_change 17-Nov-2000 C;Datcuston 1847518
В
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A: Residues: 1-192 <OLT>
A: Cross-references: GB:L22472
                                                                                                                                                                                                                                                                                                                                                                                             bcl-2-associated protein x'- mouse
N;Alternate names: BAX; programmed cell death membrane protein x
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #Sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Accession: D47538
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A;Residues: 1-218 COLT>
A:Cross references: (B:LL2474; NID:g388167;
A:Note: the amino end of the mature protein
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Best Local Similarity
Matches 16; Conserv
                                                                                           Query Match
Best Local
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Best Local Similarity
Matches 16; Conserv
                                                                         Matches
  57
                                                                       Local Similarity
nes 15; Conserv
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                                1 KKLSECLKRIGDELDS 16
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ilarity 100.0%;
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ilarity 100.0%;
Conservative 0
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                                                                                       96.3%;
93.8%;
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                                                                       Score 78; DB 2;
Pred. No. 4.9e-05;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 81; DB 2; Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 81; DB 2;
Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN:AAA03620.1;
is blocked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                         0
                                                                                                           Length 192;
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                                                                       Gaps
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                                                                ٥,
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                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE006641;
C;Genetics:
A;Gene: SSO3207
                             FADOAA actinin - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 22-Jun-1999
C;Accession: $00103; A29006
R:Noegel A: Witke, W.; Schleicher, M.
FEBS Lett, 221, 391-396, 1987
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                                                                                                                                                                     RESULT
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A; Residues: 1-669 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                            3 LSECLKRIGDELDS 16
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                                                                                                                                                                                                                                                                                                 Similarity
7; Conserv
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                                                                                                                                                                                                                                                                                                                   50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NID:g13816645; PIDN:AAK43304.1; GSPDB:GN00155
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A.Title: Expression of members of the bc1-2 gene family in the immature rat onstitutive bc1-2 and bc1-xlong messenger ribonucleic acid levels.

A.Reference number: 153295; NUID:95129487

A.Accession: 153295

A.Status: preliminary; translated from GB/ENBL/DDBJ

A.Residues: 1-133 (MES)

A.Residues: 1-133 (MES)

A.Gross-references: EMBL:U32098; NID:9975869; PIDN:AAA75200.1; PID:9975870

C.Gennetics:
A.Gene: bax

C.Superfamily: bc1 transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: BAX; programmed cell death membrane protein x C:Species: Rattus norvegicus (Norway rat) C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 03-Nov-2000 C;Accession: 15325 R;Tilly. J.L; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, Endocrinology 136, 232-241, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bcl-2-associated protein x - rat (fragment)
2
                          Score 75; DB 2;
Pred. No. 0.0001;
Mismatches
0
                                                        Length 133
                                                                                                                                                                                                                                                                                                                                                                                                                              the immature rat ovary: eq levels.
0
Gaps
0
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M. Jong, I.; Jeffrles, A.C.; Kozeta, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Recession: A90506 ser/thr protein kinase, probable [imported] - Sulfolobus solfataricus C; species: Sulfolobus solfataricus C; pacies: 34-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001 C; Accession: A90506 .J.; Ch Redder

7; Score 49; DB Pred. No. 6.9; Mismatches 2 Length 669; 0; Gaps

0;

A;Title: Calcium-sensitive non-muscle alpha-actinin contains EF-hand structures and A;Reference number: 500103; MUID:87304850

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A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 92-359, 'P',361-500, 'T',502-505 <WIT>
A:Cross-references: EMBL:X04324; NID:g7702; PIDN:CAA27855.1; PID:g929034
C:Csuperfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin
C:Keywords: actin binding, calcium binding; duplication; EF hand; homodimer
F:212-36/Domain: alpha-actinin actin-binding domain homology <ACT>
F:266-377/Domain: spectrin/dystrophin repeat homology <SP1>
F:386-493/Domain: spectrin/dystrophin repeat homology <SP2>
F:502-607/Domain: spectrin/dystrophin repeat homology <SP3>
F:502-607/Domain: spectrin/dystrophin repeat homology <SP3>
F:502-607/Domain: spectrin/dystrophin repeat homology <SP3>
F:616-717/Domain: spectrin/dystrophin repeat homology <SP4>
F:730-762/Domain: calmodulin repeat homology <EF1>
F:766-798/Domain: calmodulin repeat homology <EF1>
                                                                                                           C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Peb-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Bjourson, A.J.; McReynolds, A.D.K.; Wright, submitted to the Protein Sequence Database, M. Reference number: S64218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein VCL202w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein G1253 C;Speciles: Saccharomyces cerevisiae C;Speciles: Saccharomyces cerevisiae C;Date: 17-May-1996 #Sequence_revision 17-May-1996 #text_change
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A; Accession: A29006
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A; Molecule type: mRNA
A; Residues: 1-862 <NOE>
                   R;Alm, R.A.; Ling, L.S.L.; Moir, Ives, C.; Gibson, R.; Merberg, Nature 397, 176-180, 1999
                                                                                             C; Accession: F71868
                                                                                                                                                                                     hypothetical protein jhp0948 -
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A;Experimental source: strain S288C
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A; Residues: 1-500 <BJO>
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     A; Title:
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Best Local S
Matches 9
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Best Local
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nes 9; Conser
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Genomic sequence comparison of two
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9; Conser
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87
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                                             D.T.; King, B.L.;
D.; Mills, S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
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                                                                                                                 12-Feb-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                     No .
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18;
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unrelated isolates of the human
                                                                                                                                                                                  pylori
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Мау 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                             Jiang,
                                                                 Brown,
                                                                                                                                                                                  (strain J99)
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                                          E.D.; Doig, P.C.;
Q.; Taylor, D.E.; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-Oct-1999
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gastric path
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                                                                                                                                                                                                                                             R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldred; Qiu, D.; Spadafora, R.; Vicalre, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Ji ki, S.; Church, G.M.; Danlels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997

M;Tille: Complete genome sequence of Methanobacterium thermoautotrophicum Delta A;Reference number: A6900; MUDI:98037514

A;Accession: E69057
                                                                                                                                                                                                                                                                                                                                                                                                                                   molybdopterin-guanine dinucleotide biosynthesis mobA related protein - Metha
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec:1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
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                                                                                                                                     A;Cross-references: GB:AE000803; GB:AE000666; A;Experimental source: strain Delta H
                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-213 <M
                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               Accession: E69057
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<HTM>

sequence

not shown;

translation

not

erzbowski, J.; Gibson, R.; Jiwa P.; Noelling, J.; Reeve, J.N.

J.; Aldredge, T son, R.; Jiwani,

Ξ fu Methanobacteri

NID:g2621179; PIDN:AAB84649.1; PID:g262

53.1%;

Score 43; Pred. No.

DB 21;

2;

Length

213;

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C;Superfamily: heat shock protein grpE
C;Superfamily: heat shock; stress-induced
                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-197 <NIM>
                                                                                                                                                                                                                                               A; Accession: PC2235
                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 201, 466-471, 1994
A;Title: Identification of dnak multigene family in
A;Reference number: PC2156; MUID:94257019
                                                                                                                                                                                                                                                                                                       C;Date: 20-Feb-1995 #sequence_revision C;Accession: PC2235; PC2156 R;Nimura, K.; Yoshikawa, H.; Takabashi,
                                                                                                                                                                                                                                                                                                                                                         GrpE protein -
C; Species: Syne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: jhp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A71800; MUID:99120557
A;Accession: F71866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1 '92 <ARN>
A;Cross-references: GB:AEE001524; GB:AE001A;Experimental source: strain J99
                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                               A;Cross-references: DDBJ:D28550; NID:g507816; PIDN:BAA05902.1; PID:d1006452; PID:g507
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                                                                        Query Match
Best Local
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Best Local
                                                           Matches
120
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                          1 KKLSECLKRIG 11
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8; Conser
                                                         Similarity
8; Conser
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                                                         Conservative
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                                                       Score 43;
Pred. No.
2; Mismato
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                                                           Mismatches
                                                                                                                                    protein
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                                                         0;
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94

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A; AGCess.v...
A; Molecule type: DNA
A; Residues: 'L', 2-339 <HO2>
A; Residues: 'E', 2-339 <HO2>
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R;HOnka, E.; Fabry, S.; Niermann, T.; Palm, P.; Hensel,
submitted to the EMBL Data Library, February 1990
A;Reference number: S08689
A;Accession: S08689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Honka, E.; Fabry, S.; Niermann, T.; Palm, P.; Hensel, R. Eur. J. Biochem. 188, 623-632, 1990
A;Title: Properties and primary structure of the L-malate dehydrogenase from A;Reference number: S08981; MUID:90235834
A;Accession: S08981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-217 <KAW>
A; Residues: 1-217 <KAW>
A; Cross-references: GB: AP000004; NID: g3236131; PIDN: BAA30147.1; PID: g3257464
A; Experimental source: strain OT3
A; Experimental source: strain OT3
A; Mote: this accession replaces an interim accession for a sequence replaced by GenBank
A; Mote: this accession replaces an interim accession for a sequence replaced by GenBank
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A;Title: Complete sequence and gene organization of the genome of a hyperathermophilic A;Reference number: A71000; MUID:98344137
A;Accession: E71098
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                     8
                                                             Query Match
Best Local Similarity
Watches 10; Conserve
                                                                                                                                                                                        A;Start codon: TTG
G;Superfamily: malate dehydrogenase ylbC
G;Keywords: oxidoreductase: tricarboxyllc acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Methanothermus fervious
C:Date: 21. Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Sep-1998
C:Accession: S08981; S08689
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C;Superfamily: aroM protein
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C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: E71098
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A; Residues: 1-339 <HON>
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C; Species: Pyrococcus horikoshii
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320 KKLVEKLKEIADELN 334
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hes 7; Conservation
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Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.;
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                                                                                                     Score 43; DB 2; Length 339; Pred. No. 32;
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Pred. No.
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Best Local Similarity
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103 KVVECLKRIG-KLD

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10:39:12

2 KLSECLKRIGDELD 15 10;

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Mismatches

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Score 42.5; Pred. No. 52;

DВ

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Length 460;

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Gaps

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C;Accession: AF1909
R;Kaneko, T; Nakamura, Y; Wolk, C;P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N; Shimpo, S; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabatz DNA Res. B, 205-213, 2001
A;Tille: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF1909
A;Status: preliminary
A;Molecule type: DNA
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R;Nolling, J; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C96964
A;Accession: C96964
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SAM dependent methyltransferase related to tRNA(uracyl-5-)-methyltransferase (trma fa C:Species: Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
Tevision 14-Sep-2001 #text_change 14-Sep-2001
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-460 <KUR>
A;Cross-roferences: GB;AE001437; PIDN:AAK78502.1; PID:g15023386; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCCB24
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streptococc mycoplasma saccharomyc klebsiella

drosophila rattus norv homo sapien arabidopsis

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
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Y380_METJA
Y095_METJA
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YDK9_SCHPO
ATPF_BACHD
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Y258_METJA
DDX4_MOUSE
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RA Reyes A., COCKORILL S...

RI Increased ratio of bc1-2/bax expression is associated with bovine relations of bc1-2/bax expression is associated with bovine relations virus-induced leukemogenesis in cattle.";

RI Virology 242:184-192(1998).

CC LONG THE ACOPTOSIS REPRESSON BCL-2 OR ITS ADEMOVIRUS SHOWLOGE ELB 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C. C. CACTIVATION OF CORSPASE. J. AND THERREBY APOPTOSIS. BAX DEFICIENCY CC LEADS TO LYMPHOLD HYPERPLASIA AND MALE STEATLITY. BECAUSE OF THE CC. CESSATION OF SPERM PRODUCTION (BY SIMILARITY).

CC LISUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2, ELB 19K PROTEIN, BCL-X(L), MCL-1 AND AI (BY SIMILARITY).

CC LISUBURIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2, ELB 19K PROTEIN, BCL-X(L), MCL-1 AND AI (BY SIMILARITY).

CC LISUBURIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2, ELB 19K PROTEIN, BCL-X(L), MCL-1 AND AI (BY SIMILARITY).

CC LISUBURIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2, ELICING. CONTAINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE EXPLICITION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).

CC LOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND BAX FOR THEIR FRO-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).

CC LOMAIN: THE BCL-2 HOMOLOGY DOMAIN 1 (BH1).

CC LOMAIN: SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

CC LISUBLERITY: BELONGS TO THE BCL-2 FAMILY.

CC LISUBLERITY: BELONGS TO THE BCL-2 FAMILY.
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                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboral between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce modified and this statement is not removed. Usage by
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STRAIN=HOLSTEIN; TISSUE=Thymus;
MEDLINE-98162580; PubMed=9501056;
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Mammalia, Eltheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
Bovidae: Boyinae, Bos.
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15-UUL-1999 (Rel. 38, Last sequence update)
15-UUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last amoutation updat apoptosis regulator BAX, membrane isoform a
    InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl-2; 1.
                                                             EMBL; U92569; AAC48806.1; HSSP; Q07817; IMAZ.
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HMA1_CUCSA
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ITERMATION: ACCELBRATES PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVARUS (HOMOLOG ELB 19K PROTEIN, INDUCES THE RELEASE OF CYTOCHROME C, ACTIVATION OF CASPAGE-3, AND THEREBY APOPTOSIS.

ITSUBUNIT: FORMS HOMODIMERS AND HETEROBIMERS TOGETHER WITH BCL-2, ELB 19K PROTEIN, BCL-X(L), MCL-1 AND AL.

SUBCELLULAR LOCATION: Membrane-bound.

ALTERNATIVE PRODUCTS: THE MEMBRAKE ISOFORM ALPHA AND THE THREE CYTOPIASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPICITION.

ALTERNATIVE SPICITION:

TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.

TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.

THEN THEIR PRO-APOPTOTIC ACTIVITY AND POR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                           BAX.";
Blood
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MEDLINE-9800607; Pubbed-95331611;
ME1jerink J.P.P., Mensink E.J.B.M., Wang K., Sediak T.W.,
Sloetjes A.W., de Witte T., Waksman G., Korsmeyer S.J.;
"Hematopoietic malignancies demonstrate loss-of-function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chittenden T., Flemington C., Houghton A.B., Ebb Elangovan B., Chinnadurai G., Lutz R.J.;
"A conserved domain in Bak, distinct from BH1 and death and protein binding functions.";
pupo J. 14:5589-5596(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93364978; PubMed=8358790;
Oltval Z.N., Milliman C.L., Korsmeyer
"Bcl-2 heterodimerizes in vivo with a
accelerates programmed cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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PROSITE; PS01268; BH2; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis regulator BAX, membrane BAX.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     accelerates programmed Cell 74:609-619(1993).
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Pred. No.
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isoform alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВН2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mediates cell
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                                                                                                                                                                                                                                                                                                                                                                                                                   mutations
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                                                                                                                                                                                                                                                                                            RESULT 3
BAXB_HUMAN
                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 16
MEDLINE-93364978; PubMed-8358790;
Oltval Z. N., Milliman C.L., Korsmeyer S.J.;
"BGL-2 heterodimerizes in vivo with a conse
accelerates programmed cell death.";
Cell 74:609-619(1993);
-i- PUNCTION: ACCELERATES PROGRAMED CELL DE
ANTAGONIZING THE APOPTOSIS REPRESSOR BE
HONOLOG EIB 19K PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; BCL_2.
Pfam; PF00452; BCL-2; 1.
SMART; SM00337; BCL; 1.
SMOSITE: PS50062; BCL2_FAMILY; 1.
PROSITE: PS501080; BH1; 1.
PROSITE: PS01258; BH2; 1.
PROSITE: PS01259; BH3; 1.
                                                                                                                                                                                                       Apoptosis BAX.
                                                                                                                                                                                                                                                       BAXB_HUMAN
Q07814;
Q1-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
TRANSMEM
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an omail to license agreement.
                                                                                                                                                                                                              01-FEB-1995 (Rel. 31,
01-FEB-1995 (Rel. 31,
16-OCT-2001 (Rel. 40,
Apoptosis regulator BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L22473; AAA03619.1;
PIR; A47538; A47538.
HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SMISS-PROT entry is copyright. It is produced through
between the Swiss Institute of Bloinformatics and the get
the European Bioinformatics Institute. There are no restr
                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                 SEQUENCE FROM N.A.
TISSUE-B-cell;
                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APOPTOSIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 600040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ÷
                                                                                                                                                                                                                                                                                                                                            57 KKLSECLKRIGDELDS 72
                                                                                                                                                                                                                                                                                                                                                                       <u>س</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
DISEASE: DEFECTS IN BAX BAF FOUND IN SOME PATIENTS WIT
ACTTE LYMPHODLASTIC LEUKEMIA.
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: BCONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
                                                                                                                                                                                                                                                                                                                                                                     KKLSECLKRIGDELDS 16
                                                                                                                                                                                                                                                                                                                                                                                              16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Alternative splicing; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
98
150
172
                                                                                                                                                                (Human).
letazoa; Chordata;
ltheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118
165
165
192

    Last sequence up
0, Last annotation
BAX, cytoplasmic i

                                                                                                                                                                                                                                                                                                                                                                                                                                                            21184
                                                                                                                                                                                                                                                       Created)
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BH2.
POTENTIAL.
G -> R (IN
LEUKEMIA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId-VAR_007809
                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                         Score 81; DB 1;
Pred. No. 7e-06;
                                                                                                                                                                                                                                                                                   PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            6C0CDB0A7DEE4994
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
    HETERODIMERS
                                                                                                                                                                                                                                            update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IN T-CELL
                                                                                                                                                                                                                     n update)
                                                                            s.J.;
                                                                                                                                                                                                                                                                                 218
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                           BCL-2
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                                                                                                                                                                                                                     beta.
                                                                                                                                                                                                                                                                                                                                                                                                0;
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    TOGETHER
                             S BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACUTE LYMPHOBLASTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                             homolog,
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 192
                           BINDING
ITS ADE
      HIIM
                                                                             вах,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yh a collaboration - EMBL outstation -
                                        TO,
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                                                                                                                                                                                                                                                                                                                                                                                                0,:
    BCL-2
                                                                             that
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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SUBCELLULAR ALTERNATIVE

TEIN, BCL-X(L), MCL-1 AND A1.

LOCATION: Cytoplasmic.

RENODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE BY

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BAXA_MOUSE
ID BAXA_M
AC Q07813
AC Q07813
DT 01-FEB
DT 16-CCT
DE Approx
GN Mus mu
OC Eukary
OC Mammal
OX NCB1_1
RN [1]
RN [1]
RN [1]
RN [1]
RN STRAUE
RC STRAUE
RC STRAUE
RC STRAUE
RC STRAUE
RC T acceta
RT acceta;
CC -!- Et
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/dimounce/or send an email to license@isb-sib.ch).
             "BC1-2 heterodimerizes in vivo with a accelerates programmed cell death."; Cell 74:609-619(1993).
                                                                   STRAIN=C57BL/6 X DBA/2;
MEDLINE=93364978; PubMed=8358790;
                                                                                                                                                                                                                                       Q07813;
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART: SM00337; ECL; 1.
PROSITE; PS01000; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE: PS01259; BH3; 1.
PROSITE: PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                            01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                                                                                 BAXA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis; Alternative splicing. DOMAIN 59 73 BH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; Q07817
MIM; 600040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L22474; AAA03620.1;
PIR; B47538; B47538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as modified and this statement is not removed. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                SEQUENCE FROM N.A
                                                                                                                          NCBI_TaxID=10090
                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                              Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                1 KKLSECLKRIGDELDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.

DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD

BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACT

WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a careen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC ISOFORMS, ALTERNATIVE SPLICING.
    FUNCTION:
                                                                                                                                                                                                                                                                                                                                      KKLSECLKRIGDELDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q07817; 1MAZ
                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                              regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
                                                                                                                                                                                         (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
egulator BAX, membrane isoform alpha.
                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                  (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98
150
   ACCELERATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA,
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
165
                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24220 MW;
                                                                                                                                                                                                                                                                                                                                      72
   PROGRAMED
                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH1
                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                      Score 81; DB 1;
Pred. No. 7.9e-06;
                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            F69DCD70F960192F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
   CELL
                                                                                                                                                                                                                                                                 192
                                        S.J.;
conserved homolog,
                                                                                                                                                                                                                                                                 ξ
   DEATH
   BY BINDING TO,
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THEIR INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions on
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                                          Ваx,
                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                outstation
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Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Rodentia;

Sciurognathi; Muridae; Murinae; Rattus Craniata; Vertebrata; Euteleostomi;

Rattus norvegicus (Rat).

MEDLINE=96178771; PubMed=8600029

SEQUENCE FROM N.A. NCBI\_TaxID=10116;

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RESULT
BAXA_RAT
RRA OCC OCS GDT DT AC
                                                                                                                                                                                                                                                                                                                                                                                                                     Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
SEQUENCE
                                                                                                                                                                                                  063890; 062995; 064383;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- DOMAIN: INVACT BH3 DOMAIN IS REQUIRED BY BIK, BID. BAI BAX FOR THEIR INV.

WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

-i- SIMILARITY: CONTAINS 1 BCL-2 HOWOLGGY DOMAIN 1 (BH1).

-i- SIMILARITY: CONTAINS 1 BCL-2 HOWOLGGY DOMAIN 2 (BH2).

-i- SIMILARITY: CONTAINS 1 BCL-2 HOWOLGGY DOMAIN 3 (BH3).

-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                 Apoptosis regulator BAX,
                                                                                                                                                                                                                                                                                                BAXA_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apoptosis;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01080; PROSITE; PS01258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000712; | Pfam; PF00452; Bcl-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KKLSECLKRIGDELDS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CESSATION OF SPERM PRODUCTION.
SUBURIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
SUBCELLULAR LOCATION: Membrane-bound.
ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALDHA AND THE TAUTHERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALDHA AND THE TAUTHERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALDHA AND THE TAUTHERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALDHA AND THE TAUTHERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALDHA AND THE TAUTHERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALDHA AND THE TAUTHERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALDHA AND THE TAUTHERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALDHA AND THE TAUTHERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE TAUTHERNATIVE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN AND THE PROTEIN ALDHA AND THE PROTEIN ALDHA AND THE PROTEIN AND THE PROTEIN AND THE PROTEIN AND THE PROTEIN AND THE PROTEIN AND THE PROTEIN AND THE PROTEIN AND THE PROTEIN AND THE PROTEIN AND TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANYAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADEMOVIRUS HOMOLOG EILB 19K PROTEIN INDUCES THE RELEASE OF CYTOCHROME C. ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:99702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00337; BCL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS01259; BH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 AA;
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98
150
172
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BH2; 1
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165
192
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93.8%;
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                                                                                                                                                                                 membrane isoform alpha.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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InterPro, IPRO00712; Bcl_2.
Pfam; PF00452; Bcl_2; 1.
SMART; SM00337; Bcl; 1.
SMART; SM00337; Bcl; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The E1B 19K protein blocks apoptosis by interacting with and inhibiting the p53-inducible and death-promoting Bax protein."; Genes Dev. 10:461-477(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Madison D.L., Pfeiffer S.E.;
"Cloning of the 3' end of rat bax-alpha and corresponding developmental down-regulation in differentiating primary, cultured
                                                                               Apoptosis;
                                                                                                                                                                                                              EMBL: U49729; AAC26327.1; -.
EMBL: U59184; AAC52998.1; -.
EMBL: U32098; AAA75200.1; -.
EMBL: S75511; AAC60700.2; -.
EMBL: S75517; LAAZ.
                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBI outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligodendrocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 75-192 FROM N.A.
                                                                                                                                                                                                                                                                                          entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                      DOMAIN
                                                                                                                                                                                     InterPro; IPR002475; BCL2_family. InterPro; IPR000712; Bcl_2.
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                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TIS
HIGHEST LEVELS IN THE TESTIS AND OVARY.

DOMALN: INTACT H3 DOMAIN IS REQUIRED BY BIK, BID, BAN
DOMALN: IS REQUIRED BY BIK, BID, BAN
BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INT
WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Membrane-bound.
ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE
CYTOPLASMIC PROTEINS BETA AND GAMMA ARE
 ; Transmembrane; / 59 73 98 118 150 165 172 192 72 72 76 76 126 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220:183-186(1996).
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                                                                                             Alternative
BH3.
BH1.
BH2.
POTENTIAL.
S -> N (IN
L -> M (IN
C -> Y (IN
                                                                                             splicing
   REF.
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Best Local
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01-NOV-1988 (Rel. 0
16-OCT-2001 (Rel. 4
Alpha-actinin, non-
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                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBUNIT: HOMODIMER, ANTIPARALLEL.
-1- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
-1- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
-1- SIMILARITY: CONTAINS 2 EP-HAND CALCIUM-BINDING DOMAINS.
-1- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Noegel A., Witke W., Schleicher M.;
"Calicium-sensitive non-muscle alpha-actinin contains EP-hand structures and highly conserved regions.";
FEBS Lett. 221:391-396(1987).
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P05095;
Pfam; PF00307; CH; 2.
Pfam; PF00036; efhand; 2.
Pfam; PF00435; spectrin; 4.
SMART; SM00033; CH; 2.
SMART; SM00054; EFh; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                          EMBL; Y00689; CAA68685.1; -. EMBL; X04324; CAA27855.1; -. PIR; S00103; FADOAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the ED
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InterPro; IPR001589; Actinin_act_bind
InterPro; IPR001715; Calponin_hom.
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                                                                                                                    InterPro; IPR002017;
                                                                                                                                        InterPro; IPR002048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57
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192 AA;
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09, Last sequence update)
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n-muscular (F-actin cross
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                                                                                                                    Spectrin.
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Pred. No. 2.1e-05;
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-> E (IN REF. 1)
7B3CD198D56DF589
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cross linking protein).
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RESULT 7
ARO8_YEAST
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CONFLICT
CONFLICT
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CA_BIND
                                                                                                                                the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-SIGMA 1278B;
MEDLINE-98151783; PubMed-9491083;
Iraqui I., Vissers S., Cartiaux M., Urrestarazu A.;
"Characterisation of Saccharomyces cerevisiae ARO8 and ARO9 genes encoding aromatic aminotransferases I and II reveals a new aminotransferase subfamily ", and the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of th
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P53090;
01-CCT-1996 (Rel. 34, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
15-DEC-1996 (Rel. 37, Last annotation update)
Aromatic amino_acid aminotransferase I (EC 2.6.1.-).
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PROSITE; PS00020; ACTININ_2;
PROSITE; PS50021; CH; 2.
PROSITE; PS00018; EF_HAND; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
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Transferase; Aminotransferase SEQUENCE 500 AA; 56177 MW;
                                                                 EMBL; Y13624; CAA73946.1; ... EMBL; 272724; CAA96914.1; ...
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SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
EF-HAND 1 (BY SIMILARITY).
EF-HAND 2 (BY SIMILARITY).
EF-HAND 2 (BY SIMILARITY).
F- P (IN REF. 2).
I - T (IN REF. 2).
MW; 15608ADB71213226 CRC64;
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Pred. No.
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RESULT 9
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GRPE_SYNP7
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30-MAY-2000
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01-NOV-1997
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Nimura K., Yoshikawa H., Takahashi H.;
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                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Probable molybdopterin-guanine dinucleotide
                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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"Identification of dnaK multigene family in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechococcus sp.
                                                                                                                      026246;
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HSSP; P09372; 1DKG.
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-!- SIMILARITY: BELONGS TO THE GRPE FAMILY
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NCBI_TaxID-145262
[1]
                       Archaea; Euryarchaeota;
Methanothermobacter.
                                              MOBA OR MTH143.
Methanobacterium thermoautotrophicum
                                                                                                                                 MOBA_METTH
                                                                                                                                                                                                                                                                                                                           Heat shock; Chaperone.
                                                                                                                                                                                                                                                                                                                                        Pfam; PF01025; GrpE; 1.
PROSITE; PS01071; GRPE; 1.
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(Rel. 35, Last sequence update)
(Rel. 39, Last annotation update)
(HSP-70 cofactor) (Fragment).
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dinucleotide b
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C 082514; Q9FMW2;

AC 082514; Q9FMW2;

AC 082514; Q9FMW2;

DT 16-CCT-2001 (Rel. 40, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Adenylate kinase (EC 2.77.4.3) (ATP-AMP transphosphorylase).

DE ADK1 OR ATTGG53400 OR MLE2.3.

OS Arabldopsis thallana (Mouse-ear Creas).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnollophyta; eudicotyjedons; core eudicots; Rosidae;

Aurosids II; Brassicales; Brassicaceae; Arabldopsis.
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RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothler B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M.,
RA Daniels C.J., Mao J.-T., Rice P., Noelling J., Reeve J.N.;
ROMPIET Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.';
J. Bacteriol. 179:7135-7155(1997).
CC --- FUNCTION: LINKS A GUANOSINE S'-PHOSPHATE TO MOLYDDOPTERIN (MPT)
FORMING MOLYBDOPTERIN GUANINE DINUCLEOTIDE (MGD) (BY SIMILARITY).
CC --- SUBCELLULAR LOCATION: CYCOPLASMIC (BY SIMILARITY).
CC --- SUBCELLULAR LOCATION: CYCOPLASMIC (BY SIMILARITY).
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MOlybdenum coffactor blosynthesis; GTP-binding; Complete proteome SEQUENCE 197 AA; 21556 MW; 6AE029D2B0AD8619 CRC64;
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                       physically assigned P1 clones.";
DNA Res. 4:401-414(1997).
                                                                                  Sequence features
                                                                                                                                                           MEDLINE=98162728; PubMed=9501997;
Nakamura Y., Sato S., Kaneko T.,
                                                                                                                                                                                                                          STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                    adenylate kinase.";
                                                                                                                                                                                                                                                                                                                                                        Weers B., Thornburg R.; "Characterization of the cDNA and gene
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                               "Structural analysis of Arabidopsis Sequence features of the regions of
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                          (In) Plant Gene Register
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RESULT 11

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Matches 9; Conser
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EMBL; AB007649; BAB08805.1; -.

RESP; POTJ10; LAXY.

Mendel; 33102; Arath; 2711; 33102.

Mendel; 33102; Arath; 2711; 33102.

Mendel; 33102; Arath; 2711; 33102.

Mendel; 33102; Arath; 2711; 33102.

Mendel; 33102; Arath; 2711; 33102.

PEGAN; PF00005; PR000550; Adenylatekinase; 1.

PRODOM; PD000657; Adenylatekin: 1.

PROSITE; PS00113; ADENYLATE_KINASE; 1.

PROSITE; PS00113; ADENYLATE_KINASE; 1.

PROSITE; PS00113; ADENYLATE_KINASE; 1.

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                                                                                                                                                                          J. Bacteriol. 182:3688-3692(2000)
1- FUNCTION: Acts on oxaloacetate, sulfopyruvate but not on pyruvate.
Has a higher selectivity for the coenzyme NADH than for NADPH.
-!- CATALYTIC ACTIVITY: (S)-malate + NAD(P)(+) - oxaloacetate +
                                                                                                                                                                                                                                                                                                                           Graupner M., Xu H., White R.H.; "Identification of an archaeal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE STRAIN-V24S / DSM 2088; MEDLINE-90235834; PubMed-2110059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanothermus fervidus. Archaea; Euryarchaeota; Methanothermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation updat Malate/L-sulfolactate dehydrogenase (EC 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Honka E., Fabry S., Niermann T., Palm P., Hensel R., "Properties and primary structure of the L-malate dehydrogenase the extremely thermophilic archaebacterium Methanothermus ferviceur J. Biochem. 188:623-632(1990).
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                                                                                                                                                                                                                                                                                               "identification of an archaeal 2-hydroxy acid dehydrogenase catalyzing reactions involved in coenzyme biosynthesis in methanoarchaea.";
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20309698;
                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION
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CATALYTIC ACTIVITY: ATP + AMP - ADP + ADP.
SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
   SUBUNIT: Homodimer.
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                    CATALYTIC ACTIVITY:
                                                                                        NAD(P)H.
                                                                                                                                                    NAD(P)
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                                                                                                                    (R)-sulfolactate
   Cytoplasmic.
THE LDH2/MDH2
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Pred. No. 8.6;
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(EC 1.1.1.37) (EC 1.1.1.82).
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-i- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN
-i- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kondo M., Sutou S.;
"Cloning and molecular characterization of cDNA encoding a mous
male-enhanced antigen-2 (Mea-2): a putative family of the Golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ol-NOV-1997 (Rel. 35, Created)
Ol-NOV-1997 (Rel. 35, Last sequence update)
I5-DEC-1998 (Rel. 37, Last annotation updat
Golgin-160 (Male-enhanced antigen-2) (MEA-2
COLGA3 OR MEA-2.
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P55937;
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                                                 EMBL; D78270; BAA19612.1;
HSSP; P18852; ISCG.
MGD; MGI:96958; Golga3.
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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PIR; S08981; S08981.
InterPro; IPR003767; ldh_2.
Pfam; PF02615; ldh_2; 1.
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   Spermatogenesis; Developmental protein DOMAIN 201 204 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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ween the Swiss Institute of Bioinformatics and the Eb
Buropean Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                  TESTIS DEVELOPMENT. PROBABLY IDENTICAL WITH THE SE DETECTABLE MALE ANTIGHN (SDM).

TISSUE SPECIFICITY. HIGHLY EXPRESSED IN TESTIS. THE FOUND IN SPERMATIDS DURING SPERMATOGENESIS. NO EXPENDED CELLS, SPERMATOGONIA, OR SPERMATOCYTES.

SIMILARITY: HIGH. TO HUMAN GOLGIN-150.

CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-19 OR
                                                                                                                                                        equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9063644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No.
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(MEA-2).
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RA Harris B., Ansorge W., Brandt P., Givell L.A., Rieger M., Meller M., Reichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M., Ra Kreis M., Delseny M., Pulgdomenech P., Watson M., Schmidtheini T., Ra Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Ra Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Langham S.-A., McCullagh B., Bilham I., Robben J., Langham S.-A., McCullagh B., Bilham I., Robben J., Ra Van der Schweren J., Grymonprez B., Chuang Y.-J., Vandenbussche F. Ra Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Bareken M., Weller B., Chuang Y.-J., Vandenbussche F. Ra Holzer E., Brandt A., Feters S., van Staveren M., Dirkse W., Bernest E., Brandt A., Fedepausch M., Lamberth S., Van den Daele H., Ra Holzer E., Brandt A., Fedepausch M., Lamberth S., Van den Daele H., Ra Pereiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., Ra Pereiser S., Bergert J., Cronin A., Quall M., Bray-Allen S., Ra Ra Ra Ra Harls H., Raperst J., Cronin A., Quall M., Bray-Allen S., Ra Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Ra Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Ra Pettett A., Rajandream M., Maarse A.C., Schaefer M., Glmm M., Lochnert T.-H., Ra Dose S., de Haan M., Maarse A.C., Schaefer M., Glmm M., Lochnert T., H., Ra Petter S., Pitter S., Ra Berger C., Puchs M., Petranna B., Granderath K., Dauner D., Herzl A., Meumann S., Argiriou A., Vitale D., Liguori R., Pirayandi E., Ra Massenet O., Ouigiey F., Clabauld G., Muendlein A., Felber R., Ra Gabel C., Puchs M., Petranna B., Granderath K., Dauner D., Hezzl A., Berger P., Cooke R., Berger C., Monfort A., Casacuberta E., Pitares A., Purayandi E., Maraner D., Heave N., Vandenbol M., Bargues M., Terol J., Jesse T., Ra Gabel C., Pether R., Vandenbol M., Bargues M., Terol J., Jesse T., Ra Petrez P., Peber S., Francs P., Bielke C., Francs P., Bielke C., Francs P., Bielke C., Francs P., Bielke C., Francs P., Bielke C., Francs P., Bielke C., Francs P., Bielke C., Fran
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16-0CT-2001 (Rel. 40). Last annotation update)
Cytochrome p450 71A27 (EC 1.14-7-).
CYP71A27 OR AT4G20240 OR FC1C12.160.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta: Sparmatophyta: Magnollophyta: ediocytyledons; core eudicots; Rosidae; eurosids: II; Brassicales; Brassicaceae; Arabidopsis.
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Pred. No.
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Query Match
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Matches
                                                                      STRAINS-3A.1. DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FlixGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstook K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nauyen D.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.F., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
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Q57825;
Q1-NOV-1997
Q1-NOV-1997
16-OCT-2001
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EMBL; AL161552; CAB79024.1; ALT_FRAME.
InterPro; IPRO01128; Cyt_P450.
Pfam; Pr00957; p450; 1.
PROMITS; PRO0385; P450; 1.
PROMITS; PRO0385; P450.
Oxidoreductase; Monooxygenase; Transmembrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                         Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                            MJ0380
                                                          jannaschii
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                      Methanococcus
                                                                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
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[2]
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thaliana."
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SIMILARITY: BELONGS TO THE CYPTOCHROME P450 FAMILY.
CAMPION: REF.I SEQUENCE DIFFERS FROM THAT SHOWN DUE TO WRONG EXON
PREDICTIONS FROM THE GENOMIC DESQUENCE. THE PERDICTION MIX UP
CYPTIAZT WITH CYPTIAZB. THERE IS FURTHERWORE A FRAMESHIFT IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENOMIC SEQUENCE.
SWISS-PROT entry is copyright.
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16-OCT-2001 (
Hypothetical
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitsGerald L.M., Clayton R.A., Gocayne J.D.,
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Overbeck R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidmann J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschil."
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as ins content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                        Hypothetical protein; SEQUENCE 126 AA; 1.
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Search completed: September 20, 2002, 11:04:34 Job time: 1631 sec



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(without alignments)
16:075 Million cell updates/sec
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Copyright (c) 1993 - 2000 Comp
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Ophyd7 homo sapien
Ophyd7 homo sapien
Ophk13 rattus norv
Ophu13 rattus norv
Ophu13 sulfolobus
Ophu18 sulfolobus
Ophu18 sulfolobus
Ophu18 sulfolobus
Ophu18 mus musculu
Ophu17 arabidopsis
Opeun5 mus musculu
Ophu17 homo musculu
Ophu17 homo musculu
Ophu17 helicobacte
Ophu18 human immun
Ophu17 helicobacte
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Q9uqd6 homo sapier
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1 KKLSECLKRIGDELDS 16
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## ALIGNMENTS

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O9GMG7:
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ECL2-ASSOCIATED PROTEIN BAX (FRACMENT)
                                                                                                                                                                                                                                                                                           TISSUE-OVARY;
Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.,
"Bax in the sheep ovary";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AR163774, AAF98242.1; -.
EMSD; Q07817; IMAZ.
BSSP; Q07817; IMAZ.
                                                                                                                                                                           Pfam; PF00452; BC1:2; 1.
SMART; SM00337; BCL; 7.
PROSITE; PS50062; BC12_FAMILY;
PROSITE; PS01080; BH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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InterPro; IPR000712; Bcl_2.
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16917 MW;
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ative 0;
  Score 81; DB 6;
Pred. No. 2e-05;
Mismatches
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KKLSECLKRIGDELDS

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Q9UQD6;
Q1-MAY-2000
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Shi B., Triebe D., Kajlji S., Iwata K.K., Bruskin A., I
Shi B., Triebe D., Kajlji S., Iwata K.K., Bruskin A., I
Shi B., Triebe D., Kajlji S., Iwata K.K., Bruskin A., I
Shi B., Triebe D., Kajlji S., Iwata K.K., Bruskin A., I
Shi B., Triebe D., Kajlji S., Iwata K.K., Bruskin A., I
Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi S., Shi 
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01-JUN-2001
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 270:868-879(2000). EMBL; AF247393: AAF71267.1; -. HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-20237095; PubMed-10772918;
Schmitt E., Paquet C., Beauchemin M., Dever-Bertrand J., Bertrand Schmitt E., Paquet C., Beauchemin M., Dever-Bertrand J., Bertrand Tcharacterization of bax-sigma, a cell death-inducing isoform of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS50062: BCL2_FAMILY: PROSITE: PS01080: BH1: 1. PROSITE: PS01259: BH3: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                PROSITE; PS50062; BCL2_FAMILY; PROSITE; PS01080; BH1; 1. PROSITE; PS01259; BH3; 1.
                                                                                                                                       Pfam; PF00452; Bcl-2;
SMART; SM00337; BCL; 1
                                                                                                                                                                                                         InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; Bcl_2.
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    19718 MW;
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Pred. No. 2.2e-05
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    5802B0AC73B2E4CE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bertrand R.;
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Best Local Similarity
Matches 16; Conser
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Best Local :
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Q98U13;
Q1-JUN-2001 (
Q1-JUN-2001 (
Q1-DEC-2001 (
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                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE*21107661; PubMed*11158585;

Finklelstein C.V., Lewellyn A.L., Maller J.L.;

Finklelstein C.V., Lewellyn in Xenopus embryos activates multiple

"The midblastula transition in Xenopus embryos activates multiple

pathways to prevent apoptosis in response to DNA damage.";

proc. Natl. Acad. Sci. U.S.A. 98:1006-1011(2001).

Proc. Natl. Acad. Sci. U.S.A. 98:1006-1011(2001).
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01-OCT-2000 (TERMILTE). 15, Last sequence update)
01-DEC-2001 (TERMILTE). 19, Last annotation update
BAX PROTEIN SPLICE VARIANT K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRO02475; BCL2_family.
InterPro; IPRO02712; Bcl_2.
Pfam; PF00452; Bcl_2; 1.
SMART; SM00337; BCL; 1.
PROSITE; PS05062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jin K., He X., Greenberg D.A., Simon R.P., Graham Submitted (FEB-2000) to the EMBL/GenBank/DDBJ data EMBL, AF23993; AF30411.1; HSSP: Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAX.
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    Interpro; IPR002475; BCL2_family.
Interpro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KKLSECLKRIGDELDS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKLSECLRRIGDELDN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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PS01080; BH1; 1.
PS01258; BH2; 1.
173 AA; 19661 MW; F1
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1 (TrEMBLrel. 1
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llarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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17,
19,
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Last annotation update)
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pred. No. 0.00022;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F19A45BCF642C34F CRC64;
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Best Local S
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Best Local S
Matches 1
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Cell Death Differ. 7:509-510(2000).

EMBL: AP31015; AAF66960.1; -

HSSP, P53563; 1AF3;

InterPro; IPR0072475; BCL2_family.

InterPro; IPR007712; BCL2.

InterPro; IPR007712; BCL2.

R Pfam; PF00452; BCL2.

R SWART; SW00337; BCL; 1.

R PROSITE: P550062; BCL2_FAMILY; 1.

R PROSITE: P50062; BCL2_FAMILY; 1.

STOURNCE 192 AA; 21401 MW; 8A71.
                                                                                                                                                                                                                                                         Q9DVM1;
Q9DVM1;
Q9DVM1;
Q1-MAR-2001 (TrEMBLrel. 1
Q1-MAR-2001 (TrEMBLrel. 1
Q1-MAR-2001 (TrEMBLrel. 1
Q1-MAR-7001 (TrEMBLrel. 1
PXGRF72 PEPTIDE.
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01-OCT-2000
01-OCT-2000
01-DEC-2001
BAX.
BAX.
SPRAIN-K1;
SPRAIN-K1;
SPRAIN-K1;
SPRAIN-K1;
Hablimoto Y., Hayakawa T., Ueno Y., Fujita T.,
"Sequence analysis of the Plutella xylostella q
Virology 275:358-372(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
hctinopteryqli; Neopteryqli; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                               Plutella xylostella granulovirus.
Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00337; BCL; 1.
PROSITE; PS50062; BCL2_FAMILY;
SEQUENCE 221 AA; 24251 MW;
                                                                                                                                                                                                                                          PXORF72
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MEDLINE=20373792; PubMed=10917738;
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                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                          NCBI_TaxID=98383;
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87 KRLSECLRKIGDELDA 102
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                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Last annotation updat
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Pred. No. 0.06
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 69;
Pred. No.
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8A71A630A56FDC32
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36DBA2E2240793FA CRC64;
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0.062;
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                                                     granulovirus
                                                                       Sano Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 192;
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                                                                                                                                                                                                 Granulovirus
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                                                  Matsumoto
rus genome.
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C STRAIN-ATCC 35092 / DSM 1617 / P2;

C STRAIN-ATCC 35092 / DSM 1617 / P2;

X MEDLINE-21332296; PubMed-11427726;

X MEDLINE-21332296; PubMed-11427726;

X She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

A She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

A Mayez M.J., Chan-Meiher C.C.-Y., Clausen I.G., Curtis B.A.,

A Melikamp-de Jong I., Jeffiles A.C., Kozera G.J., Medina N., Peng X.,

A Heikamp-de Jong I., Jeffiles A.C., Kozera G.J., Medina N., Peng X.,

A Heikamp-de Jong I., Jeffiles A.C., Kozera G.J., Medina N., Peng X.,

A Heikamp-de Jong I., Schenk M.E., Theriault C., Tolstrup N.,

A Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

A Charlebois R.L., Doolittle W.F., Duguet M., Gasterland T.,

A Garrett R.A., Ragan M.A., Sensen C.M., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.

PT PTC. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

BR ENTE-PTC: 1TR0010719; Euk.pkinase.

BR InterPtc: 1TR0010719; Euk.pkinase.
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Q97018;
01-OCT-2001
01-OCT-2001
01-OCT-2001
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smarr; SM00220; S_TKC; 1.
smarr; SM00218; Terk; 1.
smarr; SM00219; TyrKC; 1.
pR0SITE; PS50011; PROTEIN_KINASE_DOM; 1.
Kinase; Transferase; Complete proteome.
SEQUENCE 669 AA; 77369 MM; 8E0FADD7739F0888 CRC64;
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InterPro;
                                                                        099KZ6; PRELIMINARY; PRT; 485 AA.
099KZ6; O1-JUN-2001 (TEMBLrel. 17, Created)
01-JUN-2001 (TEMBLrel. 17, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
SIMILAR TO ZINC FINGER PROTEIN ANC_ZH01.
Mus musculus (Mouse)
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Eutaleostoni;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulfolobus solfataricus
Archaea; Crenarchaeota;
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SSO3207.
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InterPro; IPR001245; Tyr_pkinase
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KITECLKIINDEMD
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7; Conserv
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9; Conser
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18, Last sequence update)
18, Last annotation update)
PUTATIVE (EC 2.7.1.).
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Pred. No. 13;
7; Mismatches
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13;
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0979F5: 01-OCT-2001 (TrEMBLrel. 18, C
01-OCT-2001 (TrEMBLrel. 18, L
01-OCC-2001 (TrEMBLrel. 19, L
DNA-DIRECTED RNA POLYMERASE A
TYG1233699.
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OPFIN7 PRELIMINARY; PRT; 2376 AA.
09FIN7; OFFIN7; OFFINAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLREL. 16, Last sequence update)
01-MAR-2001 (TrEMBLREL. 16, Last senotation update)
CENOMIC DNA, CHROMOSOME 5, TAC CLONE:K16H17.
Arabidopsis thallana (Mouse-ear cress).
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InterPro; IPR000822; 2nf-C2H2.
pfam; PP00096; zf-C2H2; 9.
SMART; SM00355; Znf-C2H2; 9.
PROSITE; PS00026; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS00026; ZINC_FINGER_C2H2_2; 5.
DNA-Binding; Metal-Binding; Zinc-finger.
DNA-Binding; Metal-Binding; Zinc-finger.
SEQUENCE 485 AA; 55678 MM; 52428549C27A2E4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S., Kawashima T., Amano N., Koike H., Yamazaki M., Kanehori K., Kawashima T., Yamamoto Y., Aramaki H., Makino K., Suzuki K., Narchaeal adaptation to higher temperatures revealed by gen sequence of Thermoplasma volcanium.", Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000). EMBL; AP000995; BAB60348.1; ThterPro; IPR002879; RNA_POLA2. Pfam, PP01854; RNA_POLA2. SEQUENCE 508 AN; 56949 MW; OB17ABCBFE0118FE CRC64;
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STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINE-20570466; PubMed-11121031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoplasma volcanium. Archaea; Euryarchaeota; Thermoplasma.
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Pred. No. 28;
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RA Arakawa T. Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochlwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochlwa H.,
RA Fleischmann W., Gasterland T., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Jali D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., J., Balt C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N. H.,
RA Gustincich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,
Ra Mordone P., Rhng B., Ringwald M., Rodriguez I., Sakamoto N.,
Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K. H., Weltz C., Whitteker C., Wilming L.,
RA Hyusahizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Q9CVN5;
Q1-JUN-2001
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Sequence features of the regions of 1,081,958
physically assigned Pl and TAC clones.";
DNA Res 5.379-391(1998).
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota: Metazoa: Chordata:
Mammalia: Eutheria: Rodentia:
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Asamizu E., Sato
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11-JUN-2001 (TEEMBLYE1. 17, Last annotation updat)
1700095F04RIK PROTEIN (FRAGMENT).
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Oyaokenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Oyaokenbush J.,
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RA Kuehl P., Lewis S., Matsuo W., Aono H., Baldarelli K., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli K., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli K., Barsh G.,
RA Biake J., Boffelli D., Bojunga N., Czarninci P., de Bonaldo M.F.,
RA Biake J., Bolt C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Hyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaetts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hyushaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Q9YRQ6;
Q9YRQ6;
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01-MAY-1999
01-DEC-2001
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Q1-JUN-2001
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EMBL: AK007078: BAB24853 1. .
MGD: MGI:1914606; I700095F048ik.
SEQUEENCE 303 AA; 35853 MW; D4AA3952B5C1058
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01-JUN-2001 (TrEMBLrel.
1700095F04RIK PROTEIN.
                                                                                                                                                         Viruses; Retroid viruses; NCBI_TaxID=11676;
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                                            SEQUENCE FROM N.A. STRAIN=GP-513;
                                                                                                                                                                                                      Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
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         MEDLINE * 99180152; PubMed * 10082115;
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"HIV type 1 V3 domain serotyping and genotyping in Gauteng,
"Engelbrecht S., Smith T.L., Kasper P., tao., ..., ...
"HIV type 1 V3 domain serotyping and genotyping in Gauteng,
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JHP0948.
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Nature 397:176-180(1999).
EMBL; AE001524; AAD06526.1; ..
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MEDILINE-99120557; PubMed-9923682;

Alm R.A., Ling L.-S.L., Woir D.T., King B.L., Brown E.D.,

Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.

Tummino P.J., Carnso A., Uria-Nickelsen M., Mills D.M., It

Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E.,

Trust T.J.;
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## ALIGNMENTS

## RESULTA AAB37017 ID AAB3 XX AAB3 XX BC12 XX Cytc KW Coltc KW Coltc KW mela KW mela KW mela KW MO2( KW MO2( XX UOC) KW OCOLtc KW MO2( XX UOC) KW OCOL KW MO2( XX UOC) KW OCOL KW MO2( XX UOC) XX UCC) XX UOC) stroke; myocardial Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; Bc12 polypeptide BH3 domain peptide #57 28-FEB-2001 (first entry) AAB37057; AAB37057 standard; peptide; 17 infarction. AA

Huang Z, 07-APR-1999; 06-APR-2000; 2000WO-US09352 WO200059526-A1 cardiant; Bc1-2 superfamily, BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastom; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; (UYJE-) UNIV JEFFERSON THOMAS. 12-OCT-2000 Homo sapiens. Wang J, 99US-0128202. Zhang Z, Shan ş 'n Z

New peptide conjugates for modulating apoptosis or for inhibiting

WPI; 2000-679325/66.

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CC (Rx)n-peptide where n = 1-10; X = C-0. When the Kx group is attached to the N-tcerminus of the peptide, or a side chain of the peptide where ct the functional group of the side chain of the peptide, or a side chain of the peptide, or a side chain of the peptide, or a side chain of the peptide, where the side chain functional group is containing one crown double bonds, cyclobutyl, cyclopentyl, cyclopentyl optionally concerning one ct wo double bonds, cyclobutyl, cyclopentyl, cyclopexyl optionally concerning one concerning one cyclopexyl potionally concerning one cyclopexyl potionally concerning one cyclopexyl potionally concerning one cyclopexyl potionally cyclopexyl potionally cyclopexyl potionally cyclopexyl potionally cyclopexyl potionally cyclopexyl potionally cyclopexyl potionally cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclopexyl proprior cyclope
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                                                                                                                                              07-OCT-1997;
26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH3 domain; cell death agonist; bc1 homology domain; BC1-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoprolliferative condition; arthritis; autoimmune disease; therapy.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the BH3 domain of human BAK. The invention relates to a bcl homology domain 3 (BH3 domain), derived from a proapoptotic member of the BCL-2 family. The BH3 polypeptide can be used in a method for promoting apoptosis in a BH3 polypeptide can be used in a method for promoting apoptosis in a target cell, especially where the cell is a cancer cell a virus infected cell or an autoantibody producing cell. The BH3 polypeptide can be used in therapeutic compositions for treating disease including cancer, other lymphoproliferative conditions, arthritis, inflammation, and autoimmune diseases, which may result from the down regulation of cell death
                                                                                                                                                                                                                                      New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bel-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
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                                                                                                                                                                               Claim 18;
                                                                                                                                                                                                                                                                                                                                                                                                                      Huang 2,
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16; Conserv
                                                                                                                                                                               Page 18; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Wang J, Zhang Z,
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The invention relates to a peptide conjugate having the formula:  $(R-X)_{n}$ -peptide where n=1-10; x=C=0, when the R-X group is att to the N-terminus of the peptide, or a side chain of the peptide the functional group of the side chain is NH2 or OH; or X=0 or when the R-X group is attached to the C-terminus of the peptide.

attached

where

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cs side chain of the peptide, where the side chain functional group is COOH CONH2; and R = 2.48C alkyl or alkoxy, 2-14C alkylenyl containing one CC or two double bonds; cyclobutyl, cyclobentyl, cyclobentyl optionally CC monosubstituted with a 1-5C straight or branched chain alkyl group, person of the peptide with a 1-5C straight or branched chain of the conjugate. The peptides represent examples CC alkyl group, or benzyl. The peptides with a 1-5C straight or branched chain of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptcais in the cells of a subject or for creversing B cell lymphoma/leukemia 2 (Bcl-2) mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a cubject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, conjugate is also useful for treating disorders characterized by cancer cells that conjugate is also useful for treating disorders characterized by cancer cells that conjugate is also useful for treating disorders characterized by cancer cells that conjugate is also useful for treating disorders characterized by cancer cells that conjugate is also useful for treating disorders characterized by cancer cells conjugate is also useful for treating disorders, acquired conjugate is also useful for treating disorders characterized by cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer cells cancer c
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The present sequence was used in an example illustrating an invention relating to an antimycin derivative which modulates apoptosis by binding to a Bcl-2 family protein and preferentially induces apoptosis in a cell which over-expresses the Bcl-2 family protein. The antimycin derivative is used in treating an apoptosis-sasociated disease and for inducing apoptosis. It is also useful for treating neoplasia and drug
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                                                                                                                                                                                                                                                                                                      Example 6; Page 41; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   Novel antimycin derivatives that bind to antiapoptotic Bcl-2 family protein, useful for modulating the apoptotic state of a cell -
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                                                                                                                                            The present sequence is the mammalian Bak Bcl-2 homology domain 3 (BH3) domain, which was used in a sequence alignment with the same domain of a putative version of the mammalian apoptosis regulator BBC3, which was designated BBC3-ORF2. The BBC3 protein, nucleic acids and antibodies are suitable for use in promoting cell death or for preventing apoptosis in malignant cells and those cau
                                                                                                                                                                                                                                                        Novel polynucleotide encoding a BBC3 protein which is useful for modulating apoptosis, especially in the treatment of cancer and autoimmune diseases .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammal; apoptosis; cell death; BBC3; apoptosis promotion; Bak; apoptosis inhibition; malignant cell; autoimmune disease.
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ilarity 100.0%;
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RESULT
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                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mutant Bcl-XL/Bcl-2 Associated Ccll Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or Serl13 -
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CC (R-X)n-peptide where n = 1-10; X = C=0, when the K-X group is attached CC to the N-terminus of the peptide, or a side chain of the peptide where ct the functional group of the side chain of the peptide, or a side chain of the peptide, or a side chain of the peptide, or a side chain of the peptide, or a side chain of the peptide, or a side chain of the peptide, or a side chain of the peptide, or a side chain of the peptide, or a side chain of the peptide, or a side chain of the peptide, or a side chain of the peptide, or a side chain side chain alkyl group is COOH CC or two double bonds, cyclobutyl, cyclopentyl, cyclobatyl petionally group, or bends, cyclobatyl, cyclopentyl, cyclopentyl containing one CC of the peptide did in a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ABB37001-837058 represent examples CC of the peptide portion of the conjugate and the special strain and confer chain alkyl group, or benzyl. The peptide corresponding to amino acids 72-97 of CC the BH3 domain off the cell death agonist BEd. The peptide conjugate is cuseful for modulating apoptosis in the cells of a subject, or for creversing B cell lymphoma/leukemia 2 (BCl-2) mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bel-2 confusion. In particular, the peptide conjugate is useful for treating a concer concer cells. The peptide conjugate is subject afflicted with a cancer characterized by cancer cells that acroes Bel-2 and the peptide conjugate is subject to subject afflicted with a cancer characterized by cancer cells that conjugate is also useful for treating a subject or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating a group or conjugate is also useful for treating a group or conjugate is also useful for treating a group or conjugate is also useful for treating a group or conjugate is also useful for treating a group or conjugate is also useful for treating a group or conjugate is also useful for treating a group or conjugat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (BLI-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
Sequence
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                                                                                                                                                                                                                                                                   The term GD domain refers to a protein domain first identified in Bak and shown to be essential for the interaction of Bak with Bcl-x(l) and for Bak's cell killing function; and to peptides and/or molecules capable of minicking its structure and/or function. The present sequence represents a GD domain corresponding to amino acid residues 67-94 of Bak. An antibody raised against a GD domain may be used to screen a common corresponding to amino acid residues 67-94 of immunocrossreactive proteins. Fruncated GD domain peptides have been shown to maintain the protein binding and cell killing function exhibited by wild type Bak. These molecules may induce apoptides have carbibited by wild type Bak. These molecules may induce apoptosis in tumours. 4.9. follicular lymphoma, which depend on high levels of Bcl-2 for their continued growth and survival. GD domain mimetics that inhibit Bcl-2 may be selectively toxic to of Bcl-2 for their continued growth and survival. GD domain mimetics of infected cells.
                                                                                                                                                                         Query Match
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                           AAW79535;
                                                    AAW79535 standard;
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 52; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide(s) comprising GD domains - have similar activities to wild type Bak, and cause cellular apoptosis for treatment of viral
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                                                                                                                     ggvgrqlaiigddinr 21
                                                                                                                                                 GQVGRQLAIIGDDINR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 follicular lymphoma; tumour; p53; antibody.
                                                                                                                                                                                                                                              28
                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lutz
                                                     Protein;
                                                                                                                                                                                      94.18;
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                                                       117
                                                                                                                                                                           0;
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                                                                                                                                                                                      Score 80;
Pred. No.
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                                                                                                                                                                           Mismatches
                                                                                                                                                                                     DB 17; I
2.6e-07;
                                                                                                                                                                                                    Length 28;
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Best Local Similarity
Matches 16; Consert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Bak-binding protein and related nucleic acid, vectors, transformed cells and antibodies - are useful for modulation of apoptosis in cancer, neuro-degeneration etc., also peptide fragments
                                                                          Cdn-1; apoptosis modulator: adoptive immunotherapy; therapy; HIV
autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-521220/44
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20-MAR-1997;
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           W09515084-A
                                   Homo sapiens
                                                             shock; lymphoma; eczema.
                                                                                                                   Human Cdn-1(71-211)
                                                                                                                                             21-NOV-1995
                                                                                                                                                                       AAR77880;
                                                                                                                                                                                                 AAR77880 standard; Protein; 141 AA.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 53; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Bak that interact with the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Truncated Bak polypeptide Bak-delta2-TM
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                                                                                                                                                                                                                                                                                             2 GOVGRQLATIGDDINR 17
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                                                                                                                                             (first entry)
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97US-0041328
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                                                                                                                                                                                                                                                                                                                  94.18; Suc
100.08; Pr
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Pred. No.
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1.3e-06;
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heart disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 94.
Best Local Similarity 100
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. Deletion of the N-terminal 70 amino acids of Cdn-1 improved this activity, suggesting that small, truncated Cdn-1 molecules may be potent therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid sequences encoding cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injur
                                               New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-1994;
30-NOV-1993;
                         etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shock; lymphoma; eczema
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30-NOV-1993;
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93US-0160067.
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93US-0160067.
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Pred. No. 1.6e-06;
0; Mismatches 0;
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                                                                                                                                                                                   Cdn-1 cDNA was isolated from a human heart cDNA library using a previously isolated clone as probe. Recombinant Cdn-1 was produced in Sf9 and human colon adenocarcinoma HT29 cells. Expression of Cdn-1 in WT-LZ lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Ras-mediated apoptosis. Deletion of the W-terminal 59 amino acids of Cdn-1 only slightly decreased this activity, suggesting that small, truncated Cdn-1 molecules may be potent therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-215106/28.
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30-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  shock; lymphoma;
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93US-0160067
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                                Score 80;
Pred. No.
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                                                      Length 211;
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GOVGROLATIGDDINR

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RESULT 1
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ID AAW0
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DT 22-F
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DE Bak
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KW Huma
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                                                                                                                                                                                                                    Matches
                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                   Cdn-2 cDNA was isold from a human placental genomic library using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino acid identity with Cdn-1 (AAR77876).
                                                                                                                                                                                                                                                                                                                         New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
Human; Bak; apoptosis; latency; virus replication;
                  Bak protein
                                                                            AAW03668 standard;
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                              Disclosure; Fig.5D-E; 66pp; English.
                                                                                                                                                                                                                                                                                                                    etc.
                                                                                                                                                                                                                                                                                                                                                                                               Barr PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                 (LXRB-) LXR BIOTECHNOLOGY INC
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30-NOV-1993;
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                                                         AAW03668;
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                                                                                                                                                                   16; Conservative
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93US-0160067,
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                                                                            Protein;
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thes 0;
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This Bak protein sequence represents a bcl-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may be used in complete or partial form, or as an epitope tag fusion protein, an anew virucide drug screening method, which involves combination of Bak protein and a viral protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELTSA. Interaction of Bak and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or inhibit the interaction may be used as virucide, antitumour or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epstein-Barr virus; BRRF1; fusion protein; epitope tag; 
Epstein-Barr virus; BRRF1; fusion protein; mmunoassay; antibody; 
protein interactive trapping; virucide; antitumour; diagnostic.
                                                                                                                                                                                                                                                                                                                             Screening for anti-viral agents - by detecting the ability of an agent to disrupt the interaction of a Bak protein and a viral
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-485886/48
N-PSDB; AAT42138.
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Sequence
                                 diagnostic agents.
                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 24pp; English.
                                                                                                                                                                                                                                                                                                             protein
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  211 AA;
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Query Match
Best Local S
Matches 16
                            Local Similarity 100 mes 16; Conservative
2 GQVGRQLAIIGDDINR 17
                                      94.18;
                            Score 80; DB 17; ; Pred. No. 2.5e-06; 0; Mismatches 0;
                                                 Length 211;
                              Indels
                              0;
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AAW03669;
                       AAW03669 standard; Protein; 211
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RESULT 1
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AC AGW Human; Bak-2; apoptosis; latency; virus replication; Epstein-Barr virus; BHRF1; fusion protein; epitope tap; drug screening; co-precipitation; ELISA; immunoassay; antibody; protein interactive trapping; virucide; antitumour; diagnostic. 24-OCT-1996 W09633416-A1 Homo sapiens

Bak-2 protein 22-FEB-1997

(first entry)

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                                                                                                                                                                                                                      Search completed: September 20, 2002, 10:35:59 Job time: 427 sec
                                                                                                                                        Query Match 94.1%;
Best Local Similarity 100.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                 This Bak-2 protein sequence represents a bol-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak-2 protein and a viral protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak-2 and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for anti-viral agents - by detecting the ability of an agent to disrupt the interaction of a Bak protein and a viral protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-485886/48.
N-PSDB; AAT42139.
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barr PJ. Kiefer MC;
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Pred. No.
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        score greater than and is derived by a
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2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
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PCT-US96-66122-14
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	Sequence 10, Appl	Sequence 38, Appl	Sequence 20, Appl	Sequence 10, Appl	Sequence 20, Appl	Sequence 10, Appl	Sequence 20, Appl	Sequence 10, Appl	Sequence 16, Appl	Sequence 3, Appli	Sequence 16, Appl	Sequence 3, Appli	Sequence 16, Appl	Sequence 3, Appli	Sequence 16, Appl	Sequence 3, Appli	•	Sequence 11, Appl

## RESULT 1 US-09-236-385A-35 ; MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ US-09-236-385A-35 Sequence 35, Application US/09236385A Patent No. 6221615 GENERAL INFORMATION: APPLICANT: CHITTENDEN, Thomas D.; and LUTZ, Robert J. INFORMATION FOR SEQ ID NO: 35: SEQUENCE CHARACTERISTICS: COMPUTER READABLE FORM: MEDIUM TYPE: FLOPY disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-POS/MS-POS SOFTWARE: PATENTIAN FRIESE #1.0, Version #1 CURRENT APPLICATION NUMBER: US/09/236,385A APPLICATION NUMBER: US/09/236,385A FILING DATE: 25-Jan-1999 CLASSIFICATION: CUNKNOWN> ATTORNEY/AGENT INFORMATION: NAME: WIXON, HENRY NO. REGISTRATION NUMBER: 32,073 REGISTRATION NUMBER: 32,073 CORRESPONDENCE ADDRESS: ADDRESSEE: Hale and Dorr TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH MODULATE APOPTOSIS TELECOMMUNICATION INFORMATION: NUMBER OF SEQUENCES: STREET: 1455 Pennsylvania Avenue, N.W. CITY: Washington TELEPHONE: 202-942-8400 TELEFAX: 202-942-8484 STATE: D.C. TOPOLOGY: linear LENGTH: 19 amino acids amino acid Ð 6 NO: ATTORNEY DOCKET NO. 104322.147CIP 35 #1.25

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Conservative

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Mismatches

94.1%;

Score 80; DB 4; 1; Pred. No. 3.7e-08

Length 19

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TYPE: mains acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO:

US-09-236-385A-36
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APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ. ROBERT J.
APPLICANT: LUTZ. ROBERT J.
APPLICANT: LUTZ. NOVEL PEPTIDES AND COMPOSITIONS WHICH
TITLE OF INVENTION: MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
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TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
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ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                              STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE: D.C. STATE:
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nes 16; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION MADER: US/09/236,385A
FILING DATE: 25-Jan-199
FILING DATE: 25-Jan-199
CLASSIFICATION: CUBKNOWND
ATTORNEY/AGENT INFORMATION:
NAME: MIXON, HENRY N.
REGISTRATION NUMBER: 32,073
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TELEPHONE: 202-942-8400
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MEDIUM TYPE: Floppy disk
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Pred. No.
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-440-391-18
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US-08-440-391-18
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                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER: IBM PC COMPARIBLE
COMPUTER: IBM PC COMPARIBLE
COMPUTER: TIME PC COMPARIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARIBLE PARIBLE
SOFTWARE: PARIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILLING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTONNEY_AGENT INFORMATION:
REGISTRATION HENRY N.
REGISTRATION UMBER: 32,073
REGISTRATION UMBER: 32,073
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TELEPAX: 202-942-8484
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 maino acid
TYPE: amino acid
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Best Local Similarity 100.0%;
Matches 16; Conservative
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TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHITTENDEN, Thomas D.; and APPLICANT: LUTZ, ROBERT J. ROPEL GONPOSITIONS WHICH TITLE OF INVESTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH TITLE OF INVESTION: MOULLATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
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ZIP: 20004
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1455 Pennsylvania Avenue, N.W.
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5.9e-08;
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Best Local Similarity Matches 16; Conserv

94.1%; Score 80; DB 1; L ilarity 100.0%; Pred. No. 5.9e-08; Conservative 0; Mismatches 0;

Length 28

Indels

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Gaps

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-908-597A-2
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GENERAL INFORMATION:
                                                                                                                                                          Patent No.
                                                                                                                                                             Sequence 18, Application US/08908597A Patent No. 5863795
                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-OOS/MS-DOS
SOFTWARE: RatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                     APPLICANT: CHITTENDEN, Thomas D.; and APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH TITLE OF INVENTION: MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LUTZ, ROBERT J.
TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH
TITLE OF INVENTION: MODULATE APOPTOSIS
UNBBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1411
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                      Local
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                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                     Similarity 100.0%;
16; Conservative
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E: Hale and Dorr
1455 Pennsylvania Avenue, N.W
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1455 Pennsylvania Avenue, N.W.
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                                                                                                                                                                                                                                                                                                                                                      94.1%; Score 80; DB 2; I
100.0%; Pred. No. 5.9e-08;
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Best Local
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US-08-908-597A-18
                                                                                                                                                                    APPLICATION NUMBER: US/08/440,391
APPLING DATE: 12-MAY-1995
APPORNEY, AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REGISTRATION GUMBER: 32,073
PELECOMMUNICATION INFORMATION: TELEFONE: 202-942-8400
TELEFONE: 202-942-8408
INFORMATION FOR SEG ID NO: 18:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: L. 20004
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
               Local Similarity 100.0%;
                                                                                                                       amino acid
)GY: linear
                                                                                                                                                           28 amino acids
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
                                                                                                      peptide
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                 Score 80;
pred. No.
0;
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  Mismatches
                 DB 2; L
. 5.9e-08;
                                   Length 28;
Indels
  0;
Gaps
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2 GOVGROLATIGDDINR 17 |||||||||||||||| |6 GOVGROLATIGDDINR 21

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S-09-38-38-A-2
Sequence 2, Application US/09236385A
PATENT NO. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENNEN, Thomas D.; and
APPLICANT: CHITTENNEN, Thomas D.; and
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1,455 Pennsylvania Avenue, N.W.
CITY: Washington
STRIE: D.C.
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AFFLICATION NUMBER: 05/97/250,3834

FILING DARFE: 25-Jan-1999

ATTOREY/ACENT INFORMATION:

NAME: MIXON, HENRY N.

REGISTRATION NUMBER: 32,073

REGISTRATION INFORMATION:

TELEPHONE: 202-942-8400

TELEPHONE: 202-942-8404

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

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SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-236-385A-18
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US-09-236-385A-18
US-09-236-385A-18
Sequence 18. Application US/09236385A
Patent No. 6221615
CENERAL INFORMATION:
                                                                                                         PCT-US96-06122-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-236-385A-2
Sequence 2, Application PC/TUS9606122 GENERAL INFORMATION: IMMUNOGEN, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Matches 16; Conserv
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Best Local :
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TELEPHONE: 202-942-8400
TELEPAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 25-Jan-1999
CLASSIFICATION: dUnknown>
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                            GOVGRQLAIIGDDINR 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CHITTENDEN, Thomas D.; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 41
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CITY: Washington
STATE: D.C.
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100.0%; Pred. No. 5.9e-08;
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 28;
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ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32,073

REFERENCE/DOCKET NUMBER: 1043:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-947-840

TELEPHONE: 202-947-840

TELEFERE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acid

TYPE: 28 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application PC/TUS9606122 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
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SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/nern
FILING DATE: HERPUTT"
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
                                                                                                                                                                                          SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA
APPLICATION NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
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                                                                                                                            CLASSIFICATION:
                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
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CITY: Washington
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1455 Pennsylvania Avenue, N.W.
                                                                                                                                                             HEREWITH
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                                                                                                                                                                                                                                                                           Release #1.0, Version #1.25
                                                                                                                                                                                          PCT/US96/06122
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3. 5.9e-08;
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US-08-440-391-14
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                                                                                                                                          US-08-440-391-14
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                                                                    Query Match
Best Local
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Patent No. 5656725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 16; Conserv
                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: CHITTE:
APPLICANT: LUTZ,
                                                                                                                                                                                                                                                                             ATTODNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 1047
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                             TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LUTZ, ROBERT J.
TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH
TITLE OF INVENTION: MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C
STATE: D.C
STATE: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Palanners
                                                     Local Similarity
hes 16; Conser
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                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1455 Penn
CITY: Washington
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                              TYPE:
                                                                                                                                                                                                        LENGTH:
  2 GOVGROLATIGDDINR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 GQVGRQLAIIGDDINR 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08440391
                                                                                                                                                                                                                                                                202-942-8484
                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                           linear
                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US/08/440,391
12-MAY-1995
                                               100.0%; F.
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; Pred. No. 5.9e-08
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                                                                    Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                   104322.147
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                                                     Mismatches
                                               DB 1; Lc...
o. 7.9e-08;
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                                                                                                                                                                                                                                                                               RESULT 13
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                                                                                                                                                                                                      Sequence 14, Application US/09236385A Patent No. 6221615 CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08908597A Patent No. 5863795
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: CHITTENDEN, 7
APPLICANT: LUTZ, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: U$/08/440,391

FILING DATE: 12-MAY-1995

FILING DATE: 12-MAY-1995

ATTORNEY/AGENT IMPORMATION:

NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32,073

REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LUTZ, ROBERT J.
TITLE OF INVENTION: MODULATE APOPTOSIS
TITLE OF INVENTION: MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 202-942-8484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32,073 REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                  2 GQVGRQLAIIGDDINR 17
                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
ZIP: 20004
COMPUTER READABLE FORM
                                                                                                                                    TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH MODULATE APOPTOSIS
                                                                                                                                                                                         APPLICANT: CHITTENDEN, Thomas D.; and
                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                CITY: Washington
STATE: D.C.
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1455 Pennsylvania Avenue, N.W
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                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                           LUTZ,
                                                                                                                                                                           Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                    94.1%; Score 80; 100.0%; Pred. No.
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DB 2; L 5. 7.9e-08;

Length 36;

0, Gaps

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; molecule TYPE: peptide
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-236-385A-14
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GENERAL INFORMATION:
APPLICANT: IMMUNOSEN, INC.
TITLE OF INVENTION: WOVEL PEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                 TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1455.
STREET: Washington
STATE: D.C.
ZIP: 20004
ZIP: 20004
                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
08/440,391
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 12-MAY-1995 CLASSIFICATION:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: HEREW
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COMPUTER: IBM DC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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NAME: WIXON, HENRY N.
                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 32,073
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1455 Pennsylvania Avenue,
                                                                        36 base pairs
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US-08-471-058-23
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PCT-US96-06122-14
                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 94.J
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/471,058
EILING DATE: 06-JUN-1995
CLASSIFICATION UNMER: 006-JUN-1995
CLASSIFICATION UNMER: 08/320,157
APPLICATION UNMER: 08/320,157
FILING DATE: 07-0CT-1994
APPLICATION UNMER: 08/30,067
FILING DATE: 09.NOV-1993
ATTORNEY/ACENT INFORMATION:
NAME: 1 Lebhart Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23,
                                                                                 Query Match
                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acid
                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                               TELEFAX: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 755 PAGE
CITY: Palo Alto
STATE: CA
                                                                      Local
                                                                                                                                                         LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                          NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                           2 GOVGROLATIGDDINR 17
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GOVGROLATIGDDINR 17
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5770443
                                                                    Similarity
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linear
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100.0%; F1
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PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
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Pred. No.
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Pred. No.
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                                                                  DB 1: Length 141;
4e-07;
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Search completed: September 20, 2002, 10:37:21

Job time: 409 sec



Title: Perfect score: Sequence:

BLOSUM62

Run Š

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Post-processing: Minimum Match 08
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length: 2000000000
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    Match 100%
first 45 summaries
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S58875
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T03267
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H82104
S44B2104
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G82618
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A90696
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(without alignments)
17.089 Million cell updates/sec
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cdn-2 protei
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  RESULT 2
$58875
cdn-2 protein - 1
C;Species: Homo:
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MyAlternate names: bc1-2 homolog; cdn-1 protein

C;Species: Homo sapiens (man)

C;Date: 15-Feb-1996 #sequence_revision O1-Mar-1996 #text_change O8-Oct-1999

C;Accession: S58973; S58872; S58874

R;Chittenden, T.; Harrington, E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G

Rature 374, 733-736, 1995

Astrile: Induction of apoptosis by the Bc1-2 homologue Bak.

A;Reference number: S58873; MUID:95231653
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Molecule type: mRNA
A;Residues: 1-211 <CHIP
A;Cross-references: EMBL:U23765; NID:g75879; PIDN:AAA93066.1; PID:g758798
A;Cross-references: EMBL:U23765; NID:g758797; PIDN:AAA93066.1; PID:g758798
A;Cross-references: EMBL:U23765; NID:g758797; PIDN:AAA93066.1; PID:g758798
A;Cross-reference number: S58872; MUID:g5231652
A;Reference number: S58872; MUID:g5231652
A;Accession: S58872; MUID:g5231652
A;Accession: S58872; MUID:g5231652
A;Accession: S78872
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-211 <FRNA
A;Residues: 1-210; PID:g804984; PIDN:CAA58997.1; PID:g804985
A;Molecule type: mRNA
A;Residues: 1-210; PID:g804984; PIDN:CAA58997.1; PID:g804985
A;Cross-references: EMBL:X84213; NID:g804984; PIDN:CAA58997.1; PID:g804985
A;Cross-references: EMBL:X84213; PID:g804984; PIDN:CAA58997.1; PID:g804985
A;Cross-references: EMBL:X84213; PID:g804984; PIDN:CAA58997.1; PID:g804985
A;Cross-references: EMBL:X84213; PID:g804985
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A;Cross-references: EMBL:X84213; PID:g804985
A;Cross-references: EMBL:X84213; PID:g804985
A;Cross-references: EMBL:X84213;
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S58873
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A;Cross-references: GDB:635887
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A; Residues: '1-211 <KIE>
A; Cross-references: EMBL: U16811;
                                                                                                                                                                                                                                                                                                                                                                                                            A: Fittle: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak. A: Reference number: $58874; MUID:95231654
A: Accession: $58874
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                                                                                                                                                                                     Query Match 94.1%;
Best Local Similarity 100.0%;
Matches 16; Conservative
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                                                                                                                                  2 GQVGRQLATIGDDINR 17
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- human
o sapiens
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    (man)
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$76964

T136964

T12291

C72291

C72291

F72288

F72284

A72254

H97244

H9724

H9724

F84172

F711298

A72379

G72316
                                                                                                                                                                                                                                                                                                                                      NID:g595923; PIDN:AAA74466.1;
                                                                                                                                                                                     Score 80; DB 2; L, Pred. No. 5.4e-06; 0; Mismatches 0;
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Result

Score

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Database

Listing

4::: PIR\_71:\*
1: pir1:\*
2: pir2:\*
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4: pir4:\* Maximum Minimum

DB

seq

Searched: Scoring table:

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H+/K+-exchanging ATPase (EC 3.6.1.36) - Salmonella enterica subsp. enterica (Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 C:Accession. AED564 (C:Accession.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Accession: T06308
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, ewes, H.W.; Mayer, K.F.X.; Schneller, C. submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15589
A;Accession: T06308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Date: 15-Feb-1996 #sequenco_revision 01-Mar-1996 #text_change 21-Jul-2000 C:Accession: 858875 R:Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Nature 374, 736-739, 1995
                                                                                                                             Asturbors: Parry C.; Quall, M.; Rutherford, K.; Simmonds, M.; Authors: Parry C.; Quall, M.; Rutherford, K.; Simmonds, M.; A;Title: Complete genome sequence of a multiple drug resistant A;Reference number: AB0502; PMID:11677608
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A:Reference number: 558074; MUID:95231654
A:Accession: 558075
                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-833 <PAR>
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A;Experimental source: cultivar Columbia; BAC clone f11C18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A: Molecule type: DNA
A: Residues: 1-357 <BEV>
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        A;Cross-references: GB:AL513382;
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                                                                                                                                                                                                                                                                                                                                           James, K.D.; Thomson, N.R.;
in, A.; Davis, P.; Davies, R.
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0; Mismatches
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PIDN:CAD04983.1; PID:g16501768; GSPDB GN00176
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pred. No. 3.2;
5; Mismatches
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5.4e-06;
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Affanor ybak

C.Superfamily: Bacillus probable copper-transporting ATPase yvgX; ATPase nucle
C.Superfamily: Bacillus probable copper-transporting ATPase yvgX; ATPase nucle
C.Supvords: ATP; copper binding; hydrolase; jon transport; metal binding; phose
F: 9-38/Domain; heavy-metal-associated homology (HMAL)
F: 105-134/Domain; transmembrane #status predicted CTM1>
F: 218-234/Domain; transmembrane #status predicted CTM2>
F: 224-568/Domain; transmembrane #status predicted CTM3>
F: 438-454/Domain; transmembrane #status predicted CTM3>
F: 438-454/Domain; transmembrane #status predicted CTM3>
F: 631-64/Domain; transmembrane #status predicted CTM3>
F: 648-484/Domain; ATPase nucleotide-binding domain homology (ATN)>
F: 648-785/Domain; ATPASE nucleotide-b
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             A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Recession: A99696
                                                                                            gasawara, N.; Yasunaga, T
DNA Res. 8, 11-22, 2001
A;Title: Complete genome
                                                                                                                                    C; Accession: A90696
R; Hayashi, T.; Makino,
gasawara, N.; Yasunaga,
DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                        Cull)-translocation P-type ATPase [imported] - Escherichia coli (strain O157:H7, C;Species; Escherichia coli (strain O157:H7, C;Species; Escherichia coli (strain O157:H7, C;Spate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
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A;Residues: 1-834 <BLAT>
A;Coss-references: GB:AB000154; GB:U00096; NID:q1786683; PIDN:AAC73586.1;
A;Experimental source: strain K-12, substrain MG1655
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C;Species: Escherichia coli
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A; Gene: STY0544
C; Superfamily: Bacillo
C; Keywords: hydrolase
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A;Status: preliminary
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Best Local S
Matches 8
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asunaga, T.;
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Pred. No.
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A;Status: Pre-.....A;Status: Pre-....A;Status: Pre-....A;Rolecule type: DNA
A;Rosidues: 1-915 <HEI>A;Rosidues: 1-915 <HEI>A;Cross-references: GB:AED004293; GB:AED03852; NID:g9656766;
A;Cross-references: GB:AED004293; GB:AE003852; NID:g9656766;
A;Cross-references: GB:AED004293; GB:AED004293; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004294; GB:AED004
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
A;Accession: H82104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cation transport ATPase, E1-E2 family VC2215 [imported] - Vibrio cholerae (strain N16961 C;Species: Vibrio cholerae C;Species: Vibrio cholerae C;Species: Vibrio cholerae C;Spate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001.
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85546
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A;Cross-references: GB:BA000007; PIDN:BAB33960.1; PID:g13359994; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                      A; Map position: 1
C; Superfamily: Ba
                                                                                                                                                                       A; Gene:
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C;Species: Escherichia coli
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C;Superfamily: Bacillus probable copper-transporting ATPase yvgX; ATPase nucleotide-bind
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Potamousis, K.; A
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S58684
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A;Gene:
                              phosphopyruvate hydratase (EC 4.2.1.11)
N;Alternate names: enolase
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Helicobacter pylori
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ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-263 <KUR>
A; Cross-references: GB:BA000018; PID:913700986; PIDN:BAB42282.1;
A; Experimental source: strain N315
                                                                                                                                                                                                                                                                                    A;Title: whole genome sequencing of meticillin resistant Stapylococcus aureus A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F89890
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A;Molecule type: DMA
A;Residues: 1-1226 <AND>
A:Cross-references: EMBL:L23645; NID:g388603; PID:g388605
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submitted to the EMBL Data
A; Description: Sequence of
                                                                                                                                                                                                                                                                                                                                                                                   C.Accession: F89890

C.Accession: F98990

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F89890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein SA1030 [imported] -
C; Species: Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F54F2.1 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                   A; Status: preliminary
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A; Accession: S44824
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9; Conserv
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7; Conser
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the C. elegans cosmid F54F2.
                                                                      Score 45;
Pred. No.
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3; Mismatches
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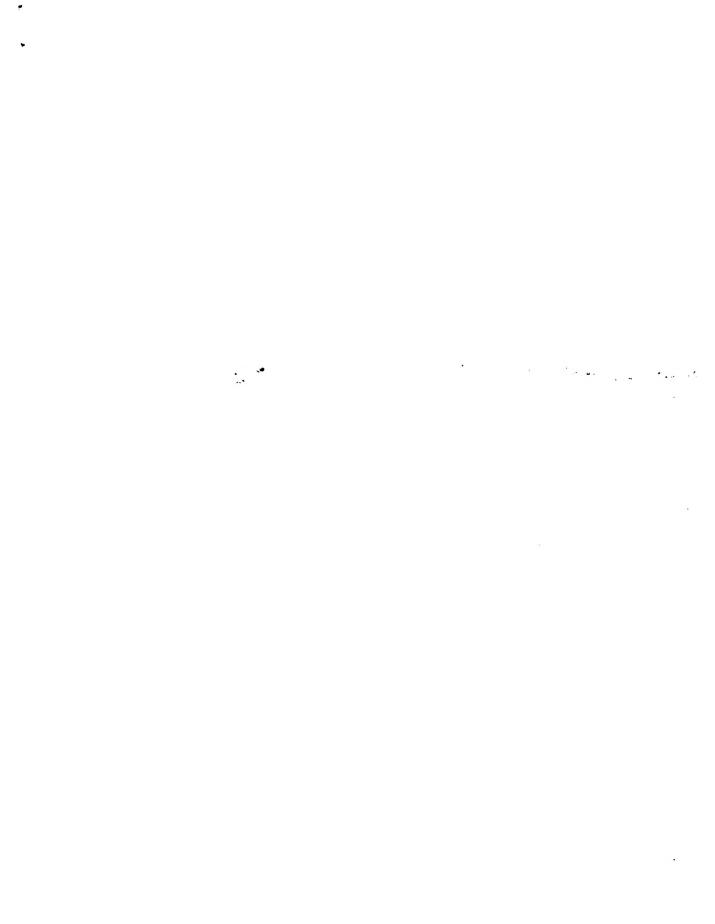
- Helicobacter pylori (strains 26695 and

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A;Roccession: Bowled Sequence not shown; translation not shown A;Roccession: Down A;Roccession: Notes nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Roccides: 1-426 <TONA
A;Roccides: 1-426 <TONA
A;Roccides: 1-426 <TONA
A;Roccides: Caba, AB000536; GB:AE000511; NID:g2313230; PIDN:AAD07219.1; PID:g231323
A;Roccide control of A;Roccides: Caba, S63-572, 1995
A;Roccide: Cloning of the Helicobacter pylori recA gene and functional characterization of A;Roccide: Cloning of the Helicobacter pylori recA gene and functional characterization of A;Roccide: Cloning of the Helicobacter pylori recA gene and functional characterization of A;Roccide: Cloning of the Helicobacter pylori recA gene and functional characterization of A;Roccide number: S58683; MUID:96027928
A;Rocleon: Lype: DNA
A;Roccide: 1-25;11,27-68 <SCH>
A;Roccide: 1-25;11,27-68 <SCH>
A;Roccide: 1-25;11,27-68 <SCH>
A;Roccide: 1-25;11,27-68 <SCH>
A;Roccide: 1-25;11,27-68 <SCH>
A;Gene: HP0154
C;Genetics:
A;Gene: HP0154
C;Function:
A;Bescription: Catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phose constraintly: enclass cription: Catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phose cide controls: Catalors catalyzes and predicted file controls: Catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors catalors 
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G:Data: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Jun-1999
G:Accession: H71967
G:Accession: H71967
G:Accession: H71967
G:Accession: R.J. L.S. L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; rves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557
A;Accession: H71967
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                                                                                                                                                                                                                                                                                                 A;Residues: 1-426 <ARN>
A;Cross-references: GB:AE001453; GB:AE001439; NID:g4154651; PIDN:AAD05723.1; PID:g415465
A:Experimental source: strain J99
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A;Molecule type: DNA
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C/Species: Helicobacter pylori
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Best Local Similarity 40...
Conservative
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hes 6; Conserv
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6; Mismatches
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Mature 402, 761-766, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: H84643
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C;Specias: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 *sequence_revision 02-Feb-2001 *text_change 15-Jun-2001
C;Accession: H84643
C;Date: 14-Aug-1998 *sequence_revision 14-Aug-1998 *text_change
C;Accession: B71213
R;Rawarrabayasi, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino,
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
7; Conserv
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A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1189
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A; Accession: H75027
A; Status: preliminary
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C;Speciles: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: H75027
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A;Map position: 2
C;Superfamily: human phosphoprotein phosphatase
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C;Genetics:
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M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; T
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.;
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A; Residues: 1-258 <KAW>
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A; Residues: 1-355 <STO>
                                                                                                                                probable chemoreceptor protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
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6; Mismatches
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Pred. No. 8
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hen, M.; Vanaken, S.E.; Umayam, L.; Tailon,
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       Y.; Hino,
Yamazaki,
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A:Pile: Complete sequence and gene organization of the genome of a hyper-thermophilic of A:Recession: B71213
A:Rocession: B71213
A:Status: preliminary; nucleic acid sequence not shown; translation not shown photosic by the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the
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14.631 Million cell updates/sec
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                        013014 homo sapien 01661 homo sapien 01661 homo sapien 016734 mus musculu (59385 escherichia p3446 caenorhabdi (92ha4 staphylococc 92mm6 helicobacte p48285 helicobacte p48285 helicobacte p21134 aphanocapas p26300 lycopersico p42895 esa mays (m 042971 oryza satiy 01960 caenorhabdi p58342 rhizobium m 093543 rhizobium m 093543 rhizobium m 093543 rhizobium m 093546 treponema p p97720 mesocricetu p58371 rhizobium m 08356 treponema p p97720 mesocricetu opsien p5812 clostridium p26821 clostridium p26821 clostridium p26821 clostridium p26821 caulobacter 016922 aplysia call p87426 drosophila drasafum social p87426 drosophila p45444 enericella p78716 fusafum social p78716 fusafum social p78716 gallus gallus gallus gallus p55169 gallus gallus p87116 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716 fusafum social p78716
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BAK2_HUMAN
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	39	39	39	39	39	39	39	39	39	39	39	39	
	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	
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PI TOMBUTO	CNG_ICTPU	CNG3_CHICK	CNG3_MOUSE	ODO2_MYCTU	ENO_RICCO	ENO1_HEVBR	ENO_ALNGL	ENO_VIBCH	ENO_THEMA	ENO_PYRAB	DCUP_CAUCR	YDA8_SCHPO	
	P55934 ictalurus p		Q9jjz8 mus muscul	Q10381 mycobacteri	P42896 ricinus co	Q91ej0 hevea brasi	Q43321 alnus glut	Q9kpc5 vibrio chol			Q59269 caulobacter	Q10350 schizosacch	
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## ALIGNMENTS

DANAL STANDARD; PRT; 211 AA.  101-NOV-1997 (Rel. 35, Created) 101-NOV-1997 (Rel. 35, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) 16-CCT-
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BAK, HUMAN
BAK, HUMAN
AC Q1661
DT 01-NO
DT 01-NO
DT 16-OC
GN BAK, HOMO
OC BUNGET
RN GTIDN
RR GTIDN
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Apoptosis;
DOMAIN
DOMAIN
                              MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.
MEDLINE-5609131: PubMed-8521816;
Chittenden T., Flemington C., Houghton A.B.,
Elangovan B., Chinnadural G., Lutz R.J.;
"A conserved domain in Bak, distinct from BH1
death and protein binding functions.";
EMBO J. 14:5589-5596(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-95231653; PubMed-7715730;

Chittenden T., Harrington E.A., O'Connor R., Flemington Evan G.I., Guild B.C.;

"Induction of apoptosis by the Bc1-2 homologue Bak.";

Nature 374:733-736(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Farrow S.N., White J.H.M., Martinou I., Raven T., Pun K.-T., Grinham C.J., Martinou J.C., Brown R., "Cloning of a bel-2 homologue by interaction with adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAK, HUMAN STANDARD; PRT; 211 AA. 016611; 092533; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) Bcl-2 homologous antagonist/killer (Apoptosis BAK1 OR BAK.
                                                                                                                                                                           Eguchi H., Hayashi S.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                     Klafer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
Tomel L.D., Barr P.J.
Modulation of apoptosis by the widely distributed Bcl-2 home
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Williams S.,
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  STRUCTURE
                                                                                                                                                                                                              SEQUENCE OF 96-206 FROM N.A.
                                                                                                                                                                                                                                                 Submitted
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16; Conserv
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  ВΥ
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NMR OF 72-87
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184 E
205 F
23411 MW;
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                703875EC4DCCC1D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O'Connor R., Flemington
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7.7e-06;
0;
                                                                                                                                                                                                                                                                                                                                                       distributed Bcl-2 homologue
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                                                                                                      Ebb R.G.,
                                                                     and BH2,
                                                                                                                                                                              databases
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InterPro; IPR002712; BCL2.
Pfam; PF00452; Bcl-2; 1.
SMART; SM00337; BCL; 1.
SMOSITE; PS01258; BH2; 1.
PR0SITE; PS01258; BH2; 1.
PR0SITE; PS01259; BH3; 1.
PR0SITE; PS01259; BH3; 1.
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EMBL, U23765; AAA93066.1; --
EMBL, U18811; AAA74466.1; --
EMBL, 293017; CAB65626.1; --
EMBL, D88397; BAA13606.1; --
EMBL, D88396; BAA13606.1; JOIN
BAK_MOUSE STANDARD; PRT; 208 AA. 008734; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-NAR-2002 (Rel. 41, Last annotation update) Bcl-2 homologous antagonist/killer (Apoptosis
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E., Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J., Thompson C.B., Fesik S.W.;

"Structure of Bcl-xL-Bak peptide complex: recognition between regulators of apoptosis.";

Science 275:983-986 (1997).

-1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A REPRESSOR BCL-2 OR ITS AGENOVIROS HOMOLOG E1B 19K PROTEIN. AND BCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROM entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WIT
HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.
DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
BAX FOR THEIR PRO-PAPPOTIC ACTIVITY AND FOR THEIR INTERACTION
WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
APOPTOTIC MEMBERS OF THE BCL-2 HOMOLOGY DOMAIN 1 (BH1).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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211 AA;
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136
184
205
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   regulator
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InterPro; IPRO00712; BCL_2.
Pfam; PPO0452; BCL_2; 1.
SMART; SM00337; BCL; 1.
PROSITE; PS01080; BHI; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01258; BH3; 1.
PROSITE; PS0259; BH3; 1.
PROSITE; PS02062; BCL2_FAMILY; 1.
ATCU_ECOLI STAN
Q59385; P78245;
Q1-NOV-1997 (Rel. 3
Q1-NOV-1997 (Rel. 3
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"Gene Structure, cDNA sequence, and
proapoptotic Bcl-2 family member.";
Genomics 44:195-200(1997).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheri
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ulrich E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97446138; PubMed-9299236;
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                                                                                    ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1097161; Bak1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y13231; CAA73684.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                            2 GQVGRQLAIIGDDINR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Membrane-associated (Potential).
TISSUE SPECIFICITY: WIDELY EXPRESSED.
DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK,
DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK,
DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIT HEIR INTE
BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTE
WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).
APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ween the Swiss Institute of Bioinformatics and the EMBL outs:
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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SUBURIT: FORMS HETERODIMERS WITH
X(L) (BY SIMILARITY).
SUBCELLULAR LOCATION: Membrane-as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACC
PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE
REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG EIB 19K PROTEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                 GQVGRQLALIGDDINR 84
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15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                      ; Transmembrane.
71 85
114 133
166 181
185 202
208 AA; 23300
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                                                                                                                                                                                                                                                     Conservative
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                                                                STANDARD;
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    Last sequence update)
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                                                                                                                                                                                                                                                  Score 78; DB 1;
Pred. No. 1.6e-05;
1; Mismatches (
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                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                           DAFC11B160C523C9 CRC64;
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                                                                                                                                                                                                                                                                                               Length 208;
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STITTE STREET REPRESENTATION OF STREET STREE

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Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.
Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.
Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
'- FUNCTION: INVOLVED IN COPPER TRANSPORT.
'- CATALYTIC ACTIVITY: ATP + H(2)O - ADP + ORTHOPHOSPHATE.
'- SUBCELLULAR LOCATION. Integral membrane protein (Potential).
'- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(El-T2 ATPASES), SUBFAMILY IB.
'- SIMILARITY: CONTAINS 2 HMA DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.in-incommer.or.send an email to licensearch.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland
Blattner F.R., Plunkett G. III, Rode C.K., Mayhew G.F.
Riley M., Collado-Vdeds J., Glasner J.D., Rode C.K., Mayhew G.F.
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
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Das S., Chu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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InterPro; IPR001934;
InterPro; IPR001454;
                TRANSMEM
TRANSMEM
DOMAIN
                                                                                           TRANSMEM TRANSMEM
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PROSITE; PS50846; HMA_2; 2.
Prosphorylation; ATP-binding; Copper;
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DOMAIN
                                                                           TRANSMEM
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TRANSMEM 18
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                                                                                                                                                                                                                                                                                                                                                                        PF00403; HMA; 2.
PF00702; Hydrolase;
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P04129; 1AFJ.
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163
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ATPase; 1.
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yhew G.F.,
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Best Local
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       HSSP; P11215; 1A8X.

WormPep; F54F2.1; CE00194.

InterPro: IPR000413; Integrin
Pfam; PF01839; FG-GAP; 5.

Pfam: PF00357; Integrin_A; 1.
                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                EMBL; L23645; AAK26134.1;
PIR; S44824; S44824.
PRINTS;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                             Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                              Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhabditidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
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01-MAR-2002
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earns ":
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nes 8; Conser
                                                                                                                                                                          FUNCTION: POSSIBLE ROLE IN CELL-CELL INTERACTION SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBURANCE WITH BETA PAT-3. SUBCELLULAR LOCATION: Type I membrane protein (B SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
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                                                                                          a requires a license agreement (See http://www.an email to license@isb-sib.ch).
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(Rel. 28, Last sequence update)
(Rel. 41, Last annotation updat
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COPPER (POTENTIAL).
PHOSEHORYLATION (PROBABLE).
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KRILMILIAASASKKRPSLA (IN REF.
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Q -> R (IN REF. 1).
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ALPHA PAT-2
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                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                           Massidda O., Anderluzzi D., Friedli L., Feger
"Unconventional organization of the division a
cluster of Streptococcus pneumoniae.";
Microbiology 144:3069-3078(1998).
-i- SIMILARITY: BELONGS TO THE UPF0124 FAMILY.
 Hypothetical
SEQUENCE 2
                   Pfam; PF02578; DUF152; 1.
                             EMBL; AF068904; AAC95459.1; InterPro; IPR003730; DUF152.
                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restricted the suppose of the Entropean Bioinformatics Institute.
                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                          Massidda O., Anderluzzi D., Friedli "Unconventional organization of the
                                                                                                                                                                                               STRAIN=ATCC 14154;
MEDLINE=99061199; PubMed=9846742;
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Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis
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SEQUENCE
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ACT_SITE
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NATURE 397:176-180(1999).
-i- CATALYTIC ACTIVITY: 2-phospho-D-glycerate - phosphoenolpyruvate
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
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PR0114; ENCLASE:

PRO15TE; PS00164; ENCLASE;

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P48285;
01-FEB-1996
01-NOV-1997
16-OCT-2001
Enolase (EC
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STRAIN-26635 / AFCC 700392;
MEDLINE-97394467; PubMed-9252185;
MEDLINE-97394467; PubMed-9252185;
MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Melson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.B., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.
Hayes M.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H(2)O.
-!-COPACTOR: MAGNESIUM IS REQUIRED
-!-COPACTOR: MAGNESIUM IS REQUIRED
-!-PACHWAY: GLYCOLYSIS.
-!- PACHWAY: GLYCOLYSIS.
-!- SUBUNIT: HOMODIMER (BY SIMILARI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-178 FROM N.A.
STRAIN-ATCC 53726 / 84-183;
MEDLING-95280562; PubMed-7768597;
MEDLING-95280562; PubMed-7768597;
Thompson S.A., Blaser M.J.;
Thompson S.A., Blaser M.J.;
Tsolation of the Helicobacter pylori recA gene and involvement the recA region in resistance to low pH.";
Infect. Immun. 63:2185-2193(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori (Campylobacter pylori). Bacteria; Proteobacteria; epsilon subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycerate hydro-lyase).
ENO OR HP0154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000536; AAD07219.1; -. EMBL; U13756; AAC43380.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence
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SUBDELLULAR LOCATION: Cytoplasmic (By Similarity).
SIMILARITY: BELONGS TO THE ENGLASE FAMILY.
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7 (Rel. 35,
1 (Rel. 40,
2 4.2.1.11)
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Last annotation update)
(2-phosphoglycerate dehydratase) (2-phospho-D-
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                      IM; Complete proteome.
BY SIMILARITY:
AMORESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
V-> I (IN REF: 2).
I -> T (IN REF: 2).
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ATCU_BACSU
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Best Local Similarity

Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                  EMBL: Z99121: CAB15355.1; ...
HSSP; P04129; 1AFJ.
Subtilist: B014106; Y99X.
InterPro; IPR001366: Cad_ATPase.
InterPro; IPR001369: Cat_PATPaseA.
InterPro; IPR001879: Cat_PATPaseA.
InterPro; IPR001877: Cu_ATPase_I.
InterPro; IPR001877: Cu_ATPase_I.
InterPro; IPR001877: E1=Z_ATPase.
InterPro; IPR001802: HG_scavenger.
InterPro; IPR001802: HG_scavenger.
InterPro; IPR001802: HHA.
InterPro; IPR001434; Hydrolase.
PEMM; PF00012; E1=Z_ATPase; 1.
Pfmm; PF000103: HAA; 2.
PRINTS: PR00140: CATATPASEA.
PRINTS: PR001419: CATATPASEA.
                                                                                                                             PRINTS; PR00941; CDATPASE.
PRINTS; PR00943; CUATPASE.
PRINTS; PR00946; CUATPASE.
PRINTS; PR00946; HGSCAVENCER.
PROSITE; PS00154; ATPASE_EL_E2; 1
PR0SITE; PS01047; HMA_1; 2
PR0SITE; PS0846; HMA_2; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
   Metal-binding; Co
TRANSMEM 163
TRANSMEM 197
TRANSMEM 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-MAR-2002 (Rel. 41, Last annotation update)
Potential copper-transporting ATPase (EC 3.6.3.4).
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O32220;
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NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                      PRINTS;
                                                                                                       Hydrolase;
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SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(B1-F2 ATPASES). SUBFAMILY IB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 2 HMA DOMAINS.
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                                                                                                    Transmembrane;
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   ; Copper;
63 183
97 217
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                                                  ne; Phosphorylation; Magnesium; ATP-binding; Repeat; Complete proteome.
POTENTIAL.
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Pred. No. 6.6;
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Query Match Best Local Matches

Similarity 9; Conserv

51.2%;

Score 43.5; pred. No. 1

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Length 532;

Indels

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RESULT 10
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P21134;
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                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    Aphanocapsa sp.
Bacteria: Chroococcales: Aphanocapsa
Bacteria: Chroococcales: Aphanocapsa
NCBI_TaxID-1120:
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NP_BIND
SEQUENCE
                                                                                                                                               "Cloning and nucleotide sequence of the crtI gene encoding phytoene dehydrogenase from the cyanobacterium Aphanocapsa PCC6714."; Gene 91:113-117(1990).
                                                                                                                                                                                                                                                           STRAIN-PCC 6714;
MEDLINE-90382685; PubMed-2119326.
                                                                                                                                                                                                                                                                                                                                                  Phytoene dehydrogenase
 Carotenoid biosynthesis; Oxidoreductase; PAD; Flavoprotein; NAD
NP_BUS 22 49 FAD (ADP PART) (POTEWTIAL).
SEQUENCE 532 AA; 56754 MW; 0629CC65A914B19F CRC64;
                                                                                                                                                                                                                                                   Schmidt A.,
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                                PIR; JN0084; JN0084
                                          EMBL; M55647; AAA62573.1; -.
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hes 8; Conserv
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(Rel. 18, Last sequence update)
(Rel. 41, Last annotation update)
hydrogenase (EC 1.14.99-.-) (Phytoene desaturase).
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COPPER (POTENTIAL).

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RESULT 12
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Best Local
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PRINTS; PR00148; ENCLASE:
ProDom; PD00902; ENCLASE; 1.
PROSITE: PS00164; ENCLASE; 1.
Lyase; Glycolysis; Magnesium.
ACT_SITE

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PF00113; Magnesium.
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P26300;
01-MAY-1992
01-MAY-1992
15-JUL-1999
Enolase (EC
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METAL
SEQUENCE
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WEDLIKE-3934-4507; PubMed=1841726;
van der Straeten D., Rodrigues-Pousada R.A., Goodman H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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PGH1.
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COPACTOR: MAGNESIUM IS REQUIRED FOR THE DIMER (BY SIMILARITY)

PATHRAY: GLYCOLYSIS.

SUBUNIT: HOMODIMER (BY SIMILARITY)
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SIMILARITY: BELONGS TO THE ENGLASE FAMILY.
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(Rel. 22, Last sequence update)
(Rel. 38, Last annotation update)
4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
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RESULT 13
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AC Q4297
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DT 15-JU
DT 15-BE
DE Enola
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PROSITE: PSUULV...

LYNASE; Glycolysis; M
ACT_SITE 164 7

METAL 251

METAL 302

METAL 302
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 39, Last annotation update
30-MAY-2000 (Rel. 39, Last annotation update
Enclase 2 (EC 4.2.1.11) (2-phosphoglycerate
D-glycerate hydro-1yase 2).
ENO_ORYSA STANDARD: PRT: 446 AA Q42971;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Enolase (EC 4.2.1.11) (2-phosphoglycerate dglycerate hydro-lyase) (OSE1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Differential regulation of enolase during anaerobiosis in maize."; plant physiol. 118:1285-1293(1998).
-!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate - phosphoenolovruvate
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ProDom; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
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Mendel; 16623;
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-!- COFACTOR: MAGNESIUM IS REQUIRED THE DIMER (BY SIMILARITY).
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MEDLINE=99063764; PubMed=9847102;
Lal S.K., Lee C., Sachs M.M.;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
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InterPro; IPR000941; Enolase.
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SUBCELULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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Pred. No. 14;
5; Mismatches
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DC27708CF92F6850 CRC64;
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SEQUENCE FROM N.A.
STRAIN-CY. TAINUNG 67: TISSUE-Seed:
STRAIN-CY. TAINUNG 67: TISSUE-Seed:
STRAIN-CY. TSAO C.-W., Haleh J.-S.,
                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: U09450; AAC49173.1; .. HSSP; P56252; 1PDZ. InterPro; IPR000941; Enclase.
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae: Oryza,
                     Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                     NCBI_TaxID-6239;
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DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY EMBRYOGENESIS
SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
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47986 MW;
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     Hydrolase; Transmembrane; PMC11-binding; Copper; Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Report Re
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Finan T.M., Weldner S., Wong K., Buhrmester J., Chain P.,
Finan T.M., Weldner S., Wong K., Buhrmester J., Cowie A., Gouzy J.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
Golding B., Puehler A.;
The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-
fixing endosymbiont Sinorhizoblum meliloti.
From Natl. Acad. Sci. U.S.A. 98:9899-9894 (2001).
FOR NATL. Acad. Sci. U.S.A. 98:989-9894 (2001).
FUNCTION: INVOLVED IN COPPER TRANSPORT (BY SIMILARITY).
FUNCTION: INVOLVED IN COPPER TRANSPORT POTCHEN (BY SIMILARITY).
SUBCELLIJAR LOCATION: Integral membrane protein (By Similarity).
SUBCELIJAR LOCATION: THEGGRAPH POTCHEN (BY SIMILARITY).
EL-EZ ATPASES, SUBFAMILY IB.
EL-EZ ATPASES, SUBFAMILY IB.
SIMILARITY: CONTAINS 2 HMA DOMAINS.
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SEQUENCE 77
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                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
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01-MAR-2002 (Rei. 41, Last sequence update)
01-MAR-2002 (Rei. 41, Last sequence update)
01-MAR-2002 (Rei. 41, Last annotation update)
Copper-transporting ATPASE 2 (EC 3.6.3.4).
ACTP2 OR ATCUZ OR RB1018 OR SMB21758.
Rhizoblum meliloti (Sinorhizoblum meliloti).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision; Rhizoblaceae; Sinorhizoblum.
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PROSITE; PS50846; HMA_2; 2
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"Expression of apoptosis-associated genes in hibernating and
myocardium of pig";

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

R EMBL; AJ001204; CAA04598.1; -.

R HSSP; Q16611; 1BXL.
R HSSP; Q16611; 1BXL.
R InterPro; IPR0012475; BCL2_family.
R InterPro; IPR001272; BCL2_family.
R InterPro; IPR001273; BCL2_FAMILY; 1.

R PROSITE; BS50062; BCL2_FAMILY; 1.
R PROSITE; BS50062; BCL2_FAMILY; 1.
R PROSITE; PS01259; BH3; 1.
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"Bak in the sheep ovary.";
"Submitted (JUL-1999) to the EMBL/GenBank/DDBJ dal
EMBL, Ar[164518, AAF99533.1: -.

EMBL, Ar[164518, BAL2, BL12, Family.
InterPro: IPR002475, BC12_family.
InterPro: IPR000712; BC1_2.
InterPro: IPR000712; BC1_2.
InterPro: IPR00375; BC1_2.

Pfam: PF00459; BC1-2: 1.

SMARR: SM00337; BCL: 1.

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MEDLINE-2123800; Pubmed=11278671;
Sun Y.F., Yu L.Y., Saarma M., Timmusk T., Arumae U.;
*Neuron-specific Bc1-2 homology 3 domain-only splice variant of Bak is anti-apoptotic in neurons. but pro-apoptotic in non-neuronal cells.";
J. Biol. Chem. 276:16240-16247(2001).
EMBL; AF402617; AL01876 1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentla;
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Givaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
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Q1-OCT-2000 (TrEMBLrel. 15,
Q1-OCT-2000 (TrEMBLrel. 15,
Q1-DEC-2001 (TrEMBLrel. 19,
BAK PROTEIN (FRAGMENT).
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163 AA;
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18039 MW;
                                                 91.8%;
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19,
    Score 78; DB Pred. No. 3.6e

1; Mismatches
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Last annotation update)
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Pred. No. 2.6e-05;
1; Mismatches 0;
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Best Local S
Matches 15
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Q95253;
Q95253;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN PROSENHAYASE 2C-LIKE PROTEIN (AT#G31860/F11C18_60).
PROTEIN HOSSHMAYASE 2C-LIKE PROTEIN (AT#G31860/F11C18_60).
PROTEIN HOSSHMAYASE VILIDATION (MOUSE-ear cress).
ENERTYPOLE; VILIDATION (MOUSE-ear cress).
ENERTYPOLE; VILIDATION (MOUSE-ear cress).
ENERTYPOLE; VILIDATION (MOUSE-ear cress).
ENERTYPOLE; VILIDATION (MOUSE-ear cress).
ENERTYPOLE; Magnoliophyta; endicotyledons; core endicots; Rosidae;
enrosids II; Brassicales; Brassicaceae; Arabidopsis.
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Q9JK59;
Q1-OCT-2000
Q1-OCT-2000
Q1-DEC-2001
                                                                                                                                                                                                    SEQUENCE FROM N.A. Ardiles W., Buysshaert C., Das Bevan M., Terryn N., Ardiles W., Buysshaert C., Das De Clerck R., De Keyser A., Neyt P., Rouze P., Van Villaroel R., Glelen J., Van Montagu M., Hoheisel J Wayer K.F.X., Schueller C., Submitted (APR-1999) to the EMBL/GenBank/DDBJ datab
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PROSITE;
PROSITE;
              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
EU Arabidopsis sequencing project;
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InterPro; IPR000712; BCL_2.
Pfam; PF00452; BCL 2; 1.
SMART; SM00337; BCL; 1.
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL, AFZ59504; AAF71760.1; -.
HSSP; 016611; 1BXL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
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mes 15; Conserv
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2; PS01080; BH1; 1.

2; PS01258; BH2; 1.

2; PS01259; BH3; 1.

2; PS01259; BH3; 1.

209 AA; 23153 MW; 249
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(TrEMBLrel. 19,
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the EMBL/GenBank/DDBJ databases
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EMBL, AL049607; CAB40756.1; -
EMBL; AL161579; CAB40756.1; -
EMBL; AN057611; AAL14406.1; -
EMBL; AN057611, AAL14406.1; -
HSSP; P35811; 1A60.
InterPro; IPP000122; Pp2C.
InterPro; IPP001932; Pp2C_domain.
InterPro; IPP001932; Pp2C_domain.
INTERPORT | SP001032; Pp2C; 1.
SMART; SM00312; PP2C; 1.
SMART; SM0031; PP2C_SIG; 1.
PROSITE; SM0031; PP2C_SIG; 1.
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SEQUENCE FROM N.A.
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STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDILINE-20406833; PubMed-10952301;
Heidelberg J.F., Bisen J.A., Nelson W.G., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelln H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Pleischmann R.D., Nierman W.C., White O.,
McDonald L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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Q9KPZ7;
Q1-OCT-2000
D1-OCT-2000
O1-DEC-2001
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De Keyser A., Neyt P.,
Gielen J., Van Montagu
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                                                                                                                                                                     "DNA sequence of both cholerae.";
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                                                                                                              Nature 406:477-483(2000).
EMBL; AE004293; AAF95359.1;
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IPR000579; Cat_P_ATPaseA.
IPR001757; E1-E2_ATPase.
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Ney't P., Rouze P., Van Den Daele H., Villaroel R.
Montagu M., Newes H.W., Lencke K., Mayer K.F.X.;
-2000) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR001934; HMA.

R InterPro; IPR001454; Hydrolas
R InterPro; IPR000150; Hyporhet,
R Pfam; PF00122; E1-E2_ATBase; i
Pfam; PF00403; HMA; 3.
PF1MTS; PR00119; CATATPASE.
PRINTS; PR00119; CATATPASE.
PRINTS; PR00940; CATATPASE.
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Q99US8;
Q1-UN-2001 (Tremble1, 17, G
Q1-UN-2001 (Tremble1, 17, L
Q1-DEC-2001 (Tremble1, 19, L
HYPOTHETICAL PROTEIN SA1030 (
                                                                                                                                                                                                                  Lancet 357:1225-1240(2001).
EMBL, AP00313; BAB42282.1; -.
EMBL, AP003361, BAB57349.1; -.
InterPro; IPR003730; DUF152.
Pfam; PF02578; DUF155; DWP155; BF02578; DUF155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; DWP155; 
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SEQUENCE
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MEDILINE-21311992; PubMed-11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanebisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus."; 1007 114000011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain Mu50). Bacteria, Frimicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBI_TaxID-158879, 158878;
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PRINTS; PR00946; HGSCAVENGER.
PROSITE; PS00154; ATPASE_E1_E2; UNIPOROSITE; PS01229; COF_2; UNKNOWN_1
PROSITE; PS01047; HMA; 1.
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Last annotation update)
(HYPOTHETICAL PROTEIN SAV1187).
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                                                                                             Score 45; DB Pred. No. 19; 0; Mismatches
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Pred. No. 52;
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7AB013BD94EB07F9
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RESULT 081716

PRELIMINARY;

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RESULT
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InterPro; IPR000222; pp2C.
InterPro; IPR001932; pp2C_domain.
Pfam; pF00481; pp2C; 2.
SMART; SM00331; pp2Cc; 1.
SMART; SM00331; pp2Cc; 1.
SMART; SM00331; pp2Cc; 1.
Q9UXV1;
Q9UXV1;
Q1-MAY-2000
Q1-MAY-2000
Q1-DEC-2001
SY V-ATPASE;
                                                                                                                                                                                                                                                                                                                                                                                                              Vennada K. Liu S.X. Pham P.K. Banh J. Dale J.M., Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Vuach H.L., Tang C., Toriumi M., Yamanura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Chauk R., Hayashizaki Y., Ishida J., Jones T., Kamla A., Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M. Narusaka M., Nauyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Full Length cDNA of gene F27C12.1/At2g25070 (GI:4559345).", Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AC006585, AAD23006.1; ...
EMBL, AC00673, AAN28010.1; ...
EMBL, AY050873, AAN28010.1; ...
EMBL, AY050873, AAN28010.1; ...
EMBL, AY050873, AAN28010.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. COLUMBIA:
MEDLINE-20083487; PubMed-10617197;
Lin X. Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T. M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
hallana.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AT2025070.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
Spermatophyta: Magnollophyta; eudicotyledons; core eudicots; Rosidae:
Spermatophyta: Magnollophyta; eurosids II; Brassicales: Brassicaceae; Arabidopsis.
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01-NOV-1998 (TrEMBLIGEL 08, La
01-DEC-2001 (TrEMBLIGEL 19, La
MYPOTERTICAL 39.4 KDA PROTEIN.
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SEQUENCE 3
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9; Conserv
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355 AA; 3
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(TrEMBLrel.
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Last annotation update)
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Pred. No. 32;
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Matches 7
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Best Local
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Kawarabayasi Y., Sawada M., Horikawa H., Hosoyama A., Naga
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Naga
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku
Funahashi T., Tanaka T., Koshi Y., Yamazaki J., Kushida N., Oguc
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hype
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res 5-55-76(198).
EMBL; AP000007; BAA31097.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        057733 PRELIMINARY; PRT; 261 AA. 057733; 01-AUG-1998 (TrEMBLrel. 07, Created) 01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-DEC-2001 (TrEMBLREL 19, Last anottation update) 261AA LONG HYPOTHETICAL CHEMORECEPTOR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    structure and evolution. Summitted (UUL-1999) to the EMBL/GenBank/DDBJ databases EMBL, AA248288; CAB50662.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyrococcus horikoshii.
Archaea; Euryarchaeota;
MCBI_TaxID=53953;
                                                                                                                                                                                                                        SEQUENCE 261 AA;
                                                                                                                                                                                                                                                                   InterPro; IPR004089; Chemotaxis_transducer
Pfam; PF00015; MCPsignal; 1.
SMART; SM00283; MA; 1.
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InterPro: IPR004090; Me_chemotaxis.
Pfam; PF00015; MCPsignal; 1.
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125
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GEAGRGFAVVADEIRR 140
                                             GOVGROLATIGDDINK
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SM00283; MA;
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7; Conserv
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Pred. No. 27;
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horikoshii OT3.";
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Ra Delseny M., Boutry M., Givell L.A., Mache R., Puigdomenech P.,
Ra Wincker P., Chisne N., Artiguenave F., Robert C., Brottier P.,
Ra Wincker P., Chisne N., Artiguenave F., Robert C., Brottier P.,
Ra Wincker P., Chisne N., Artiguenave F., Robert C., Brottier P.,
Ra Wincker M., Weller-Auer S., Gabel C., Fuchs M., Benes V.,
Ra Winchann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Ra Winchann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
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Ra Winchann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
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Ra Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climont J.,
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Ra Reichelt J., Scharfe M., Schoen D., Bargues M., Terol J., Climont D.,
Ra Reichelt J., Scharfe M., Schoen D., Wurnelle B., Masuy D.,
Ra Rooney T., Rizzo M., Walturo C., Purnelle B., Masuy D.,
Ra Mannhaupt G., Haase D., Schooff H., Rudd S., Zaccaria P., Mewes H.-W.,
Ra Rooney T., Rizzo M., Walts A., Utterback T., Fujdin C.Y., Shea T.P.,
Ra Rooney T., Rizzo M., Walts R., Wu D., Peterson J., Van Aken S.,
Ra Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
Ra Raser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamixu E.,
Ra Masayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
Ra Masayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
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Q9LHLG;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last seq)
Q1-CCT-104-2001 (TrEMBLE-1. 17, Last and
GB|AAF30301.1 (HYPOTHETICAL 63.0 KDA
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Eukaryota; Viridiplantae; Streptophyta; Embryospermatophyta; Magnoliophyta; eudicotyledons;
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                                                                                                                                                                                                                                                                                                Hypothetical protein SEQUENCE 556 AA;
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11:1 :|1 :|1
262 GRRLVFVGDSLNR 274
                                                                                                                                                                 Local
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7; Conserv
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                                                                                                                                                                                                                                                                                                    63004 MW;
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                                                                                                                                                                 Last sequence update)
Last annotation updat
63.0 KDA PROTEIN).
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Pred. No.
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Best Local Similarity
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InterPro; IPR001140; ABC_transpor
InterPro; IPR003439; ABC_transpor
InterPro; IPR003687; ATP_GTP_A.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein coding regions."
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Tabata S.;
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-:- SIMILARITY: BELONGS TO THE
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01-JUN-2001 (TrEMBLrel.
EMB|CAB82953.1.
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01-MAR-2001
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ATP-binding; Complete proteome; Transport.
SEQUENCE 593 AA; 65761 MW; DA48CE3DEDAC6C9 CRC64;
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                  "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; Submitted (MAY-2000) to the EMEL/GenBank/DDBJ databases. EMBL, AP002032; BABD9804.1; Therefor, IPR000531; TonB_boxC.
                                                                                                                      Kaneko T., Katoh T.,
Tabata S.;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                          STRAIN=COLUMBIA;
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Cyanobacteria; Chroococcales;
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(TrEMBLrel. 16,
(TrEMBLrel. 17,
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TONB_DEPENDENT_REC_1; UNKNOWN_1
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Batones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.P., Costa M.C.R., Costa Neto C.M.,
Ra Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Facincani J.S., Franco M.C., Frohme M., Furlan L.R.,
RA Farenga J.S., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L.,
RA Krieger J.E., Kurame E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Krieger J.E., Kurame E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Krieger J.E., Kurame E.E., Laigret R.F., Machado J.A.,
RA Manchado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Manchado M.A., Marchas E.A., L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro "Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nasclmento A.I.T., Notetro M.E.,
RA Moon D.H., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Peixoto B.R., Foreira G.A.G., Santelli R.Y., Savasaki H.E.,
RA Ga Silveira M.C. de Sa R.G., Santelli R.Y., Savasaki H.E.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Arbat/55 1. -

EMBL, REGOLOS S.
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Matches 7
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Best Local :
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                                                                                                                         SEQUENCE 693 AA;
                                                                                                                                                                                         InterPro; IPR004089; Chemotaxis_transducer InterPro; IPR004090; Me_chemotaxis. Pfam; PF00015; MCPsignal; 1.
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NCBI_TaxID-2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xylella fastidiosa
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                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                   HSSP; P02942; 1QU7
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  2 GQVGRQLAIIGDDINR
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                                                                                                                                                           ; PR00260; CH
SM00283; MA;
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7; Conserv
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                                    Score 44; DB 16;
Pred. No. 82;
4; Mismatches 5
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Pred. No.
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                                                                                                                         EAD48C73BF573D80 CRC64;
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Search completed: September 20, 2002, 11:03:48 Job time: 1665 sec

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Best Local S
Matches
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InterPro; prb00132; FAD_byr_redox.
InterPro; prb00132; FAD_byr_redox.
InterPro; prb00133; Flavo_monoxygenase.
InterPro; prb002938; Moxy_FAD_binding.
InterPro; prb002055; MAD_binding.
InterPro; prb00103; Pyridine_redox_2.
InterPro; prb00100; pyr_redox.
InterPro; prb00100; pyr_redox.
InterPro; prb003042; Rng_mnoxygenase.
Pfbm; prb01494; FAD_binding_3; 1.
Pfbm; prb01494; FAD_binding_3; 1.
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098KM2;
01-0CT-2001
01-0CT-2001
01-0CT-2001
                                                                                                                                                                                                                                                                                   PRINTS; PRO0419; ADXRDTASE.
PRINTS; PRO0358; FADDNR.
PRINTS; PRO0458; FADDNR.
PRINTS; PRO04459; PRDRDTASEI.
PRINTS; PRO0469; PRDRDTASEI.
PRINTS; PRO0420; RNGMNOXGNASE.
MONDOXYYGENSE; COMPLETE PTOTEOSME.
SEQUENCE 421 AA; 45340 MM; 2B1EF11C87476F1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
DNA Res. 7.331-38(2000).
EMBL: AP002997, BAB46792.1;
TEMBL: AP002997, BAB46792.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
PROBABLE FAD-DEPENDENT MONOOXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21082930; PubMed-11214968;
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STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group: Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium loti (Mesorhizobium loti)
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294
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GEAGRGFAIVADEVQR
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8; Conser
                                                                                                                                 Conservative
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                                                                                                                             Score 43; DB Pred. No. 68; 2; Mismatches
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
 Database
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Gapop 10.0 , Gapext 0.5
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AAB74121	AAY69202	AAY70827	AAW87809	AAW87804	AAY05435	AAY34150	AAR71406	AAY34149	AAY70818	AAB37006		ID			SUMMARIES
Human bcl-2 associ	Amino acid sequenc	Human BAX alpha pr	A human Bcl-2 asso	A human Bcl-2 asso	Human BAX protein		Human Bax protein	Human truncated Ba	Human neuroprotect	Bcl2 polypeptide B		Description			. •

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AAW06296	AAB37033	AAY05426	AAB37032	AAY05418	AAY70823	AAY70821	AAY70822	AAY70820	AAY70817	AAY70816	AAY70824	AAB70373	AAY96323	AAY05411	AAY05430	AAW06298	AAB35128	AAB74125	AAB74122	AAY70828	AAW87808	AAW87805	AAY05434	AAR71407	AAY70819	AAB37007	AAY39263	AAW10688	AAY78512	AAB50539	AAB35129	AAB48286	AAB74126	
GD domain region f	Bcl2 polypeptide B		Bcl2 polypeptide B							neuroprotec	Mouse neuroprotect	onse	lian Bax	вах внз		ain region	Bax.	bc1-2	ര	BAX alp	Bc1-2	Murine Bcl-2 assoc	Mouse BAX protein	Murine Bax protein	Monae pouroprotect	Bcl2 polypentide B	Coding region of c	Bax omega protein	ated	Bax protein	Bax. Homo	Bax protein	Human bcl-2 associ	

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AAB37006 standard; peptide; 27 AΑ

AAB37006;

28-FEB-2001 (first entry)

Bcl2 polypeptide BH3 domain peptide #6.

Cytostatic: neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction

Homo sapiens.

W0200059526-A1

12-OCT-2000

06-APR-2000; 2000WO-US09352

07-APR-1999; 99US-0128202.

(UYJE-) UNIV JEFFERSON THOMAS

WPI; 2000-679325/66.

Huang Z,

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Shan S,

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New peptide conjugates for modulating apoptosis or for inhibiting B

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Best Local Similarity
Matches 27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; truncated BAX protein; tBAX78; BAX alpha; BCL-2 family; neuron; anti-apoptoic; cerebroprotective; meuroprotective; neuroactive; epoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human neuroprotective truncated BAX protein, tBAX78
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    22-OCT-1998;
                                                                             22-OCT-1999;
                                                                                                                                                      27-APR-2000
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                                                                                                                                                                                                                                                                                                                                             Domain
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treating neurodegenerative disorders, stroke, or cancer -
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                                                                             99WO-US24747
                                                                                                                                                                                                                                                                                                                                        /note= "N-terminal region of BAX alpha" 59..73
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                    /label- BH3_domain
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1-10; x =
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Matches 27
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                                                  New adenovirus vectors, cells and for treating
                                                                                                                             WPI; 1999-551404/46
N-PSDB; AAZ19763.
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                                                                                                                                                                                                                                                                                                                                          11-MAR-1998;
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                                                                           used for killing or inhibiting the growth
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Pred. No. 3.1e-12;
; Mismatches 0;
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Claim 26; Page 148-149; 151pp; English

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Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; bc1-2; alpha; beta; proto-oncogene; hematopoietic cell line; apoptosis; membrane-associated cytoplasmic protein; B cell; T cell; proliferation; cell cycle progression; Bax; apoptotic cell death; apoptosis; cytokine; death repressor; BHI; BH2; cancer therapy; hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contains a single base deletion relative to the wild type (AAZ19764), causing a frameshift which leads to translation of a premature stop codon, resulting in a truncated protein. However, the domain responsible
                                          WPI; 1995-106605/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR71406 standard; Protein; 192
    N-PSDB; AAQ97606
                                                                                                                                                                                                                                                                                 26-AUG-1993;
25-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Bax protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                 Korsmeyer SJ;
                                                                                                                                                                                                     (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ischaemic cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QDASTKKLSECLKRIGDELDSNMELQR 27
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ilarity 100.0%;
Conservative 0
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94US-0248819
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Pred. No. 5.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Sequence

192 AA;

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This sequence represents human Bax protein. Bax is a protein which is a socciated with the human bcl-2 alpha and beta proteins, the sequences of which are given in ARA7104-05 respectively. bcl-2 is encoded by a correct operation of the sequences of which are given in ARA7104-05 respectively. bcl-2 is encoded by a proto-oncogene and is capable of inhibiting appoptosis in many components of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of th
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RESULT
AAY34150
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Best Local
                                         11-MAR-1998;
                                                           11-MAR-1999;
                                                                                                                        Domain
                                                                                                                                                                  Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy
                                                                                                                                                                                                   30-NOV-1999 (first entry)
                                                                                                                                                                                                                      AAY34150;
                                                                                                                                                                                                                                       AAY34150 standard; Protein; 192
                                                                             16-SEP-1999
                                                                                             WO9946371-A2
                                                                                                                                                 Homo sapiens
                                                                                                                                                                                 Human wild-type Bax protein
                                                                                                                                                                                                                                                                                  52 qdastkklseclkrigdeldsnmelqr 78
                                                                                                                                                                                                                                                                                          1 QDASTKKLSECLKRIGDELDSNMELQR 27
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                                                                                                                                                                                                                                                                                                                   l Similarity
27; Conserv
                                                                                                                                                                                                                                                                                                                    Conservative
                                         98US-0077541
                                                           99WO-US05359
                                                                                                                       Location/Qualifiers 59..101
                                                                                                              /note= "Portion of BH3 domain
                                                                                                                                                                                                                                                                                                                   100.0%; Score 135; DB 16;
100.0%; Pred. No. 7.9e-12;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                        A
                                                                                                              essential for dimerisation"
                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                     192;
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McDonnell TJ, Ji L, Roth J

Roth JA;

Swisher SG,

Fang

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Bruckheimer EM,

Sarkiss MG;

(TEXA ) UNIV TEXAS SYSTEM

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AAYO5435
AAYO
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           induction of $53. Bax protein can function as a homodimer, or it can heterodimerise with other Bc1-2 gene family members such as the antiapoptotic protein Bc1-2. Heterodimerisation of Bc1-2 family members provides a means of controlling cell death via the "rheostat" model. This model suggests that the relative amounts of Bc1-2 and Bax determine the susceptibility of a cell to undergo apoptosis. If Bc1-2 is in excess, Bc1-2/Bax heterodimers predominate and cell death is inhibited. If Bax is in excess, however, Bax homodimers predominate and the cell becomes susceptible to apoptosis following exposure to an apoptotic stimulus. Additionally, Bax can function in its monomeric form to accelerate cell death. Use of novel adenoviral vectors containing the Bax gene may augment and complement wild-type p53 gene therapy, which induces a G1 cell cycle arrest and/or apoptosis in malignant cells carrying p53 mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bax functions as a primary response gene in the p53-regulated apoptotic pathway. The Bax gene promoter has 4 p53 binding sites and the expression of Bax is upregulated at the transcriptional level by p53, an Bax mRNA and protein expression have been shown to increase following induction of p53. Bax protein can function as a homodimar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH3 domain; cell death agonist; bcl homology domain; BCL-2 family, apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoprolliferative condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents human wild-type Bax protein. A naturally occurring mutant protein (AAV34149) was also isolated. Bax (Bcl-2 associated x protein) is a proapoptotic member of the Bcl-2 gene family.
                                                                                                                               07-OCT-1997;
26-SEP-1997;
                                                                                                                                                                                                                                                                                             08-APR-1999
                                                                                                                                                                                                                                                                                                                                                              W09916787-A1
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arthritis; autoimmune disease; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human BAX protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY05435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutations. In addition, Bax overexpression could provide the apoptotic effect of p53 without the need for p53 itself.
Korsmeyer SJ
                                                             (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                               22-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY05435 standard; peptide; 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New adenovirus vectors, used for killing or inhibiting the growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 27; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                               97US-0946039
97US-0060133
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Best Local
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26-AUG-1993;
25-MAY-1994;
           Example 1; Columns 71-74; 105pp; English
                                DNA composition encoding bcl-2 two-hybrid and reporter system - for identifying modulators of bcl-2 function
                                                                                                                                                                                                                            05-JAN-1999
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           A human Bcl-2 associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a bcl homology domain 3 (HB3 domain), derived from a proapoptotic member of the BCL-2 family. The BH3 polypeptide can be used in a method for promoting apoptosis in a target cell, especially where the cell is a cancer cell a virus infected cel or an autoantibody producing cell. The BH3 polypeptide can be used in therapeutic compositions for treating disease including cancer, other lymphoproliferative conditions, arthritis, inflammation, and autoimmune diseases, which may result from the down regulation of cell death
                                                                     WPI; 1999-105119/09.
N-PSDB; AAV84005.
                                                                                                       Korsmeyer
                                                                                                                              (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                   US5856171-A.
                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                  Human; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                     94US-0337646.
93US-0112208.
94US-0248819.
                                                                                                                                                                                                                                                                                                                                                                      function; apoptosis.
                                                                                                                                                                                                     94US-0337646
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                                                                                                                                                                                                                                                                                                 /note= "BH1 domain"
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Pred. No. 7.9e-12;
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Matches 27; Conserv
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26-AUG-1993;
25-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW87809;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Bcl-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW87809 standard; Protein; 192
                                                                                                          The present sequence represents a human Bcl-2 associated protein designated Bax. The Bax protein is used in a composition which designated Bax are bolled family member polypeptide. a naturally occurring Bax polypeptide and an antibody that binds to the Bax polypeptide. The composition is used to identify modulators of Bcl-2-related function, e.g. substances that inhibit binding of Bax to bcl-2, which would be potentially useful as drugs for modulating
                                                                                                                                                                                                                                                                                                                              Korsmeyer
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                                                                                                                                                                                                                            Example 7; Fig 7; 105pp; English.
                                                                                                                                                                                                                                                      {\tt DNA} composition encoding bcl-2 two-hybrid and reporter system identifying modulators of bcl-2 function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated protein; Bax; bcl-2; antibody; modulator;
d function; apoptosis.
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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93US-0112208.
94US-0248819.
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               100.0%;
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                 Score 135; DB 20;
Pred. No. 7.9e-12;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; truncated BAX protein; tBAX; BAX alpha; BCL-2 family; head trauma; neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroprotective; neuroprotective; neuroprotective; neuroprotest; treatment, neurodegenerative disease; peripheral nerve injury; spinal cord injury; stroke; pro-apoptotic; PCD; programmed cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY70827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY70827 standard; Protein; 192
                                                   The present sequence is a human BAX alpha protein, a pro-apoptotic protein which is a member of BCL-2 family of proteins that are involved in regulation of neuronal programmed cell death. The patent discloses specific truncated proteins derived from BAX alpha which inhibit neuronal apoptosis induced by trophic factor deprivation. The anti-apoptotic truncated BAX (tBAX) proteins include tBAX70, tBAX78 and their mutants. These proteins contain the N-terminal region and at least a portion of the BH3 domain of BAX alpha and lack the BH1, BH2 and C-terminal transmembrane domain has been shown to have anti-apoptotic activity. The tBAX proteins are used to treat diseases associated with neuronal management of the second of the terminal contains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
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                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                      Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                Johnson
                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-1998;
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 Sequence
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                                                                                                                                                                                                                                                                                                                                MH,
                              e.g. neurodegenerative diseases, peripheral nerve injury,
d injury, head trauma and stroke.
   192
                                                                                                                                                                                                                             Page 35-36; 43pp; English.
                            injury, head trauma
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/note= "BCL-2 Homo!
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Query Match Best Local Similarity

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Score 135; DB 21; Pred. No. 7.9e-12;

Length 192;

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Query Match
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                                                          Matches
                                                                                                                                                                                                                                                                  The present sequence represents the Bax protein A pro-apoptotic peptide can be derived from the BH3 domain. The peptide is an inducer of formation of a channel for transport of cytochrome C out of intochondria. The peptide induces apoptosis in a cell. The peptide changes the ion selectivity of an anti-apoptotic BCL-2 family member from potassium selective to chloride selective. The specification also describes inhibitors of apoptosis in cells The inhibitors and inducers can be used to treat patients, preferably humans with a condition mediated by excessive down-regulation of apoptosis, especially conditions chosen from neoplasias, diseases caused by posterin Barr virus, African swine fever virus and adenovirus, lymphoproliferative conditions, cancer, arthritis, Crohn's disease, lymphoproliferative conditions, cancer, arthritis, Crohn's disease.
                                                                                                                                                                                                          excessive apoptosis, especially immunodeficiency diseases, senescence, neurodegenerative disease, ischemic and reperfusion cell death, infertility and wounds. The methods can also be used to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytochrome C transport; mitochandria; apoptosis; ion selectivity; anti-apoptotic BCL-2 family member; neoplasia; Epstein Barr virus; African swine fever virus; adenovirus; lymphoproliferative condution; cancer; arthritis; Crohn's disease; inflammation; autoimmune disease; immunodeficiency; senescence; neurodegenerative disease; reperfusion cell death; infertility; wound.
                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 34; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modulating apoptosis in cells by modulating channel ion transport of cytochrome C -
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                                                                                                                                                                                              apoptosis-modulating
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                                                        Score 135; DB 21;
Pred. No. 7.9e-12;
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Best Local
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                                                                                                                                                                                                                                                                                       The present invention relates to a method of modulating apoptosis of a cell. The method comprises administrating to the cell an agent, comprising a BH1 domain or BH2 domain, capable of modulating formation of at least one complex selected from bcl-2:bcl-2 complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl-2:associated X protein (Bax):Bax complexes, bcl
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26-AUG-1993;
25-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apoptosis modulator; bol-2 associated X protein; cancer therapy; AIDS autoimmunity; immunodeficiency; reperitation injury; stroke; aging; myocardial infarction; traumetic brain injury; ischaemia; meurodegenerative diseases; hepatitis; transplant rejection; toxemia; lymphoproliferative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modulating apoptosis of a cell, useful in maintaining homeostasis in adult tissues, or treating proliferative or autoimmune diseases, comprises administering a bcl-2 polypeptide that interacts with a 21
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Fig 3; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bcl-2 associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Korsmeyer SJ;
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DB; AAF77704.
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                                                                                                                                                                                                                                                         192
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                                                                                                                                                                                                                                                         AΑ;
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94US-0248819.
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                                                                                                                                                                           Score 135;
Pred. No. 7.
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                                                                                                                                                        DB 22;
7.9e-12;
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26-AUG-1993;
25-MAY-1994;
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                                                                                                                                                                                                                                                                                                 complexes, bcl.2 associated y protein (Bax): Hax complexes, bcl.2: Bax complexes or bcl.7x; Bax complexes. Modulating apoptosis is especially useful in canner therapy, and treating autoimunity, immunodeficiency diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke, traumatic brain injury, neurodegenerative diseases, aging, ischaemia, toxemia, infection, hepartitis, transplant rejection, and lymphoproliferative diseases. The present sequence is human Bax, which was used in a sequence alignment in the present invention, with murine was used in a sequence alignment in the present invention, with murine was used in a sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence alignment in the present sequence is not alignment in the present sequence is not alignment in the present sequence is not alignment in the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method of modulating apoptosis of a cell. The method comprises administrating to the cell an agent, comprising a BHI domain or BHI domain, capable of modulating formation of at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL-bcl-XL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating apoptosis of a cell, useful in maintaining homeostasis adult tissues, or treating proliferative or autoimmune diseases, comprises administering a bcl-2 polypeptide that interacts with a bcl-2 associated X protein
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02-APR-2001
                             AAB48286;
                                                           AAB48286 standard;
                                                                                        13
                                                                                                                                    52
                                                                                                                                   . Similarity
27; Conserv
                                                                                                                                                                                                                                                                             192 AA;
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(first entry)
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93US-0112208.
94US-0248819.
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                                                           protein; 192
                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                 0;
                                                                                                                                                                                                                Score 135; DB 22;
Pred. No. 7.9e-12;
                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 100-101; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 - DEC - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                        Human
       14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                            52
                                                                                                                                                                                          Bax.
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S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; 2F; CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
                                                                                                                                                                                                                                                                                                                                                                                        Bad; Bc1-2; tumour; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Bax protein
N-PSDB; AAC84598
                                                                                                                                                           04-JUN-1999;
                                                                                                                                                                                                       05-JUN-2000; 2000WO-US15449.
                                                                                                                                                                                                                                                                                                  WO200075184-A1.
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                      WPI; 2001-061703/07
                                                                                                            (UYYA ) UNIV YALE.
                                                                  Tsvetkov LM,
                                                                                                                                                             99US-0137494
                                                                     Kondo
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The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the cullin/ CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or BC1-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for treating tumours.

192 AA;

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Query Match
Best Local Similarity
Matches 27; Conser
               1 QDASTKKLSECLKRIGDELDSNMELQR 27
qdastkklseclkrigdeldsnmelqr 78
                                               100.0%; ilarity 100.0%; Conservative
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                                                 Pred. No. 7.1
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                                                            Score 135; DB 2
Pred. No. 7.9e-1
                                                    0
                                                                     Length 192;
                                                    Indels
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03-APR-2001 AAB35129 standard; 31-JUL-1998; US6165732-A Homo sapiens Human; Bax; apoptosis modulator; BCL-2 26-DEC-2000 (first 9705-0061823 98US-0127048 protein; 192 A

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Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for identifying modulators of apoptosis which involves contacting a compound of interest with a lipid bilayer comprising a K+ or cl- selective channel. This channel is a member of the BCL-2 family. Apoptosis modulators are also provided, including bel-2deltaTM and BaxdeltaTM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying apoptosis-modulating compounds by contacting the compound with lipid bilayer containing an ion channel formed by anti-apoptotic polypeptide of Bcl-2 family and determining ion selectivity of the
The present invention describes a method for screening for an apoptosis inhibitor or an apoptosis promoter in which VDAC-ilprosome, an index substance which can pass VDAC and a sample are incubated and the change in the concentration of the index substance during the incubation is detected to judge the presence of apoptosis inhibition or apoptosis promotion. The apoptosis inhibitor or the apoptosis promoter can be used as a drug and a diagnostic agent for various diseases caused by
                                                                                                                                                                                                                                                                                                                                                                             JP2000287689-A
                                                                                                                                                  Screening of an apoptosis inhibitor or promoter which can be used as drug and a diagnostic agent for various diseases caused by apoptosis inhibition or apoptosis promotion -
                                                                                                                                                                                                                                                                                      08-APR-1999;
                                                                                                                                                                                                                                                                                                                   08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                17-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Bax protein sequence
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                                                                                                                     Claim 13; Page 17; 22pp; Japanese.
                                                                                                                                                                                                              WPI; 2001-065575/08.
N-PSDB; AAC90811.
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB50539 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                       (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bc1-2; Bc1-xL; Bax; VDAC; apoptosis inhibitor; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis
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                                      apoptosis inhibition or apoptosis promotion. The present sequence represents the human Bax protein, which is an apoptosis inhibitor used in the exemplification of the present invention.
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Sequence 192 AA;

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qdastkklseclkrigdeldsnmelqr
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larity 100.0%;
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Pred. No. 7.9e-12;
Mismatches 0;
78
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Search completed: Job time: 425 sec September 20, 2002, 10:35:57

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Listing first 45 summaries
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score greater than
and is derived by a
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Matches 27; Conserv
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REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
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APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING YSYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,597A
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH TITLE OF INVENTION: MODULATE APOPTOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1455 Penr
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1EH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            APPLICANT: CHTTENDEN, Thomas D.; and LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH MODULATE APOPTOSIS
                                                                                                                                                                                     NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
GY: linear
                                                                                                                   ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
                                                                                                         STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Hale and Dorr
1455 Pennsylvania Avenue, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 135; DB 2; ilarity 100.0%; Pred. No. 1.5e-13; Conservative 0; Mismatches 0;
                                                                                   20004
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; MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: 13: US-09-236-385A-13
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PCT-US96-06122-13
PCT-US96-06122-13
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Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                TELEPHONE: 202-942-8484
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 12-MAY-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                       TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: HEREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1455 Penr
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Hale and Dorr STREET: 1455 Pennsylvania Avenue, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QDASTKKLSECLKRIGDELDSNMELQR 27
                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 QDASTKKLSECLKRIGDELDSNMELQR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-6484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/236,385A FILING DATE: 25-Jan-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application PC/TUS9606122
                                                                              34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMUNOGEN, INC.
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                                                                                                                                                                  202-942-8400
                                                                                                                                                                                                                                                                                                                                                                                                HEREWITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY DOCKET NO. 104322.147CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Applic
Patent No. 5691179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                      Sequence 9, Application US/08112208C Patent No. 5691179
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NDMA:
APPLICATION NUMBER: US/08/112 2000
FILING DATE: 26-AND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
                                                           NUMBER OF SEQUENCES: 3: CORRESPONDENCE ADDRESS:
                                                                                          APPLICANT: KORSMEYER, Stanley J. TITLE OF INVENTION: CELL DEATH REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATE: 26-AUG-1993
CLASSIFICATION: 536
VOCASSIFICATION: 536
NAME: AUG-1993
                                                                                                                                                                                                                                   Local Similarity
nes 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                              ADDRESSEE:
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             r: 379 Lytton Avenue
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/081122080
California
                                                                                                                                                                                                                                                                                               100.0%;
ilarity 100.0%;
Conservative 0
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                                              Townsend and Townsend Khourie and Crew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 135; DB 5; 100.0%; Pred. No. 1.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2:
                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15726A-000610
                                                                                                                                                                                                                                                                                                              Score 135; DB 1
Pred. No. 1e-12;
                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                              DB 1;
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                                                                                                                                                                                                                                                                                                                              Length 192;
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                                                                                                                                                                                                                                                                                               Gaps.
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US-08-248-819A-2
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Patent No. 5700638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 135; DB 1
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches
                                   CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/112,208

FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:
NAME: SMITH, WILLIAM
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15726A-000610

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IIBM PC COMPOSTATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION UNDERE: US/08/248,819)
FILING DATE: 25-NAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/ACENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC:DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: CE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KORSMEYER, Stanley J.
VENTION: CELL DEATH REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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SEQUENCE CHARACTERISTICS:

192 amino acids

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RESULT 9
US-08-607-269-25
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                   Sequence 25, Application US/08607269 Patent No. 5702897
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                      Best
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION UNMER: US/08/248,819A
ETLING DATE: 25-NAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/112,208
PILING DATE: 26-AUG-1993
ATTORNEY/ACENT INFORMATION:
NAME: Smith, William M 23
REFERENCE/DOCKET NUMBER: 15726A-000
TELECHMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08248819A Patent No. 5700538 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 27; Conservative
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER RENABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CELL DEATH REGULATORS NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                        52 QDASTKKLSECLKRIGDELDSNMELQR 78
                                                                                                                                                                                                 Local Similarity
nes 27; Conserv
                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 QDASTKKLSECLKRIGDELDSNMELQR 78
                                                                                                                                                            1 QDASTKKLSECLKRIGDELDSNMELQR 27
                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QDASTKKLSECLKRIGDELDSNMELQR 27
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                                                                                                                                                                                                                                                                                                                                                                           192 amino acids
                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                             100.0%; Score 135; DB 1 100.0%; Pred. No. 1e-12; Pative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 135; DB 1 100.0%; Pred. No. 1e-12;
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 Mismatches

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RESULT 10
US-08-471-058-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08471058 Patent No. 5770443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/226,876

FILING DATE: 13-APR-1994

ATTORNEY FACENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 9882

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 25;
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
                                                                                                COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kiefer, Michael C. APPLICANT: Barr, Philip J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,269
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Interaction of Proteins Involved in TITLE OF INVENTION: Cell beath Pathway NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                     STREET: 755 PAGE CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 QDASTKKLSECLKRIGDELDSNMELQR 78
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STATE: Californi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ODASTKKLSECLKRIGDELDSNMELQR 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takaaki
                                                                                                                                                                                                                                                                                                     hilip J.
NOVEL APOPTOSIS MODULATING
PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 135; DB 1 100.0%; Pred. No. 1e-12;
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RESULT 11
US-08-337-646A-2
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Best Local Similarity
Watches 27; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5856171
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08337646A Patent No. 5856171
                                                                                                                 PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/248,819

FILING DATE: 25-MAX-1994

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/112,208

FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Smith, WIlliam W.

REGISTRATION NUMBER: 30,233

REGISTRATION NUMBER: 30,233
                                   TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 706141
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                   REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/337,646A FILING DATE: 10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsen-
empRET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lehnhardt, Susan K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/3 FILING DATE: 07-0CT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     9430
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WENTION: CELL DEATH REGULATORS
192 amino acids
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linear
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                                                                                                           15726A-000620
                                                                                                                                                                                                                                                                                                                                                           Version #1.25
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-337-646A-2
                                                                                                                                                     ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-337-646A-9
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В
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US-08-337-646A-9
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Patent No. 5856171
                                                                   Matches
                                                                                 Best
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/248,819
APPLICATION NUMBER: US 08/248,819
PIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 25-M0C-1993
FILING DATE: 25-M0C-1993
ATTORNEY/ACENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 15726A-000620
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
                                                                                                Query Match
                                                                                                                                                                                                                                                                          TELEFAX: (415) 326-24
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/337,646A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10-NOV CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 379 Lytton Avenue CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
52
                                                                 Local Similarity
les 27; Conserv
                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 QDASTKKLSECLKRIGDELDSNMELQR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                         LENGTH:
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                               1 QDASTKKLSECLKRIGDELDSNMELQR 27
  QDASTKKLSECLKRIGDELDSNMELQR 78
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                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                       192 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KORSHEYER, Stanley ...
KORSHEYER, Stanley ..
VENTION: CELL DEATH REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                 Conservative
                                                                                                                                                                                      linear
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ID NO: 9:
                                                            100.0%; 5c
100.0%; Pr
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100.0%; Pred. No. 1e-12;
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                                                                               Score 135; DB 2
Pred. No. 1e-12;
                                                                 Mismatches
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                                                                                                DB 2;
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                                                                                                Length 192;
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RESULT 13 US-08-856-531-2

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: LOCATION: 1..192
: OTHER INFORMATION: /note- "Human Bax polypeptide"
US-08-856-531-2
                                                                                                                                                                                                                                                                                                                                    US-08-856-531-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, Donald R.
REGISTRATION NUMBER: 9761:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHNOME: 314-727-638
TELEFAX: 314-727-692
TELEFAX: 317-7518
                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08856531 Patent No. 5942490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: KORSWEYER, Stanley J.
APPLICANT: HVENTION: CELL DEATH REGULATORS
TITLE OF INVENTION:
AUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Foreyth Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 192 anino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/856,531
APPLICATION NUMBER: US/08/856,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 773 Forsyth Blvd., Suite 1400
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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                                                                                                                      COUNTRY:
                                                                                                                                           STATE:
                                                                                                                                                      CITY: St. Louis
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    Application US/08856531
    5942490

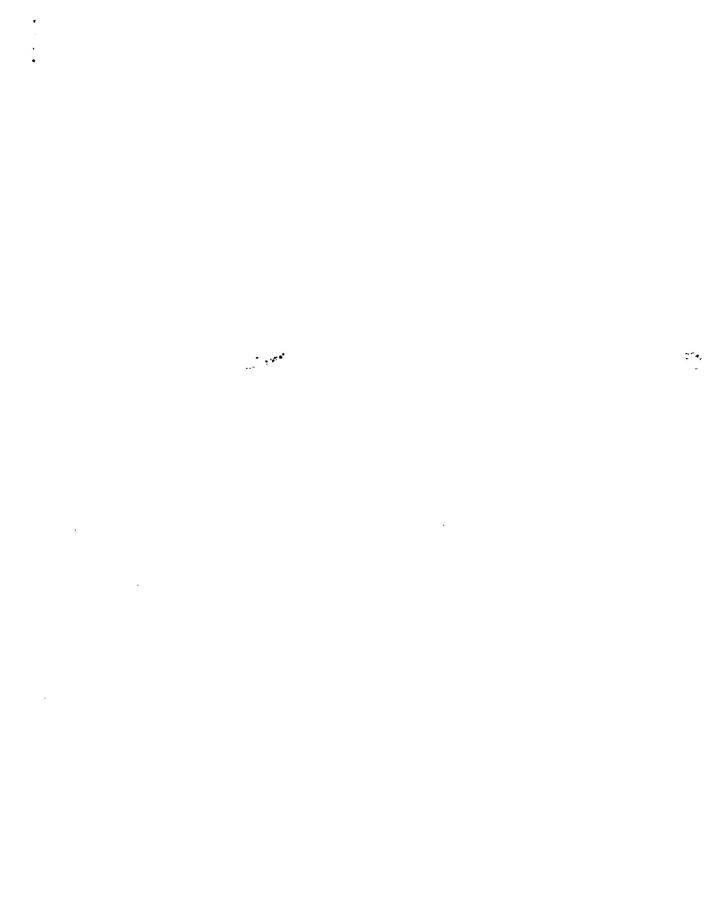
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Pred. No. 1e-12;
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; LOCATION: 1..192
; OTHER INFORMATION:
US-08-856-531-9
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                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/B56,034
FILMS DATE:
CLASSIPICATION: 435
ATTORNEY/AGENT IMPORMATION:
NAME: HOLLAND, DODALD R.
REGISTRATION NUMBER: 35.197
REFERENCE/DOVERT NUMBER: 976175
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 5955595
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Best Local S
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INFORMATION FOR SEQ ID NO: 2:
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TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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LENGTH: 192 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: HOLLAND, Donald R.
                                                                                                                       SEQUENCE CHARACTERISTICS:
                                MOLECULE TYPE:
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CITY: St.
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                                                 TOPOLOGY:
                                                                   STRANDEDNESS:
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nes 27; Conserv
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REFERENCE/DOCKET NUMBER: 97
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
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FENTION: CELL DEATH REGULATORS
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100.0%; Pred. No. 1e-12;
tive 0; Mismatches
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	Search completed: September 20, 2002, 10:37:19 Job time: 407 sec	OTHER INFORMATION: /note* "Human BAX polypeptide" US-08-856-034-2  OVERY MATCH BEST LOCAL Similarity 100.0%; Score 135; DB 2; Length 192; BEST LOCAL Similarity 100.0%; Pred. No. 1e-12; MATCHES 27; Conservative 0; Mismatches 0; Indels 0; MATCHES 27; CONSERVATIVE 0; MISMATCHES 0; OY 1 ODASTKKLSECLKRIGDELDSINELOR 79  Db 52 ODASTKKLSECLKRIGDELDSINELOR 78	
		Gaps 0;	



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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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## ALIGNMENTS

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R;Schmitt, E.; Paquet, C.; Beauchemin, M.; Dever-Bertrand, J.; Bertrand, R. Biochem. Biophys. Res. Commun. 270, 868-879, 2000
A;Title: Characterization of Bax-delta, a cell death-inducing isoform of Bax A;Reference number: JC7255
A;Recession: JC7255
A;Accession: JC7255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bax-delta protein - human G:Species: Homo sapiens (man) C:Species: Homo sapiens (man) C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 17-Nov-2000 C:Date: 07-255
A;Gene: GDB:BAX
A;Cross-references: GDB:228082; OMIM:600040
A;Map postition: 19q13.3-19q13.4
C;Superfamily: bcl transforming protein
C:Keywords: alternative splicing; blocked amino end; heterodimer; bomodimer; transmem
                                                                                                                                       A; Note: the C; Genetics:
                                                                                                                                                                                                                                                            C;Accession: A47538
R;Oltvai, 2.N.; Milliman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
Cell 74, 609-619, 1993
A;Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerate A;Reference number: A47538; MUID:93364978
A;Accession: A47538; MUID:93364978
A;Accession: A47538
                                                                                                                                                                                                                                                                                                                                                                                                                                                 bcl-2-associated protein x, alpha splice form - human
N;Alternate names: BAX; programmed cell death membrane protein x alpha
C;Species: Homo sapiens (man)
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C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-179 <SCH>
A;Cross references: GB:ARP247393
A;Experimental source: cancer promyelocytic cells
C;Comment: This protein, a member of the Bcl-2 family, has a proapoptotic effect.
                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-192 <OLT>
                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                          A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                       GB:L22473; NID: 9388165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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Pred. No. 2e-11;
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                                                                                                                                                                 PIDN:AAA03619.1; PID:g388166 is blocked
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probable

ABC

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bci-2-associated protein x - mouse

%Alternate names: BAX; programmed cell death membrane protein x
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: D47538
R:Oltvai. Z. N.; Millhan, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that & Reference number: A47538; MUID:93364978
A:Accession: D47538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:228082; OMIM:600040
A;Map position: 19q13.3-19q13.4
C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; blocked amino end; cytosol; heterodimer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-218 <OLTY
A;Cross-references: GB:L22474; NID:g388167; PIDN:AAA03620.1; PID:g388168
A;Note: the amino end of the mature protein is blocked
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell 74, 609-619, 1993
A;Title: Bcl-2 heterodimerizes in vivo with a conserved A;Reference number: A47538; MUID:93364978
A;Accession: B47538
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N;Alternate names: BAX; programmed cell death membrane protein x beta
C;Spscles: Homo sapiens (man)
C;Spscles: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1994 #sequence_revision 03-May-1
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A;Molecule type: mRNA
A;Residues: 1-192 <OLT>
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                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB:L22472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: GDB:BAX
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Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 26; Conserv
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Best Local
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                                          52 QDASTKKLSECLRRIGDELDSNMELQR 78
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                                                                                                           1 QDASTKKLSECLKRIGDELDSNMELQR 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDASTKKLSECLKRIGDELDSNMELQR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 100.0%; 1 Similarity 100.0%; 27; Conservative (
                                                                                                                                                                             Conservative
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                                                                                                                                                                                                        97.8%;
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                                                                                                                                                                     Score 132; DB 2;
Pred. No. 5.7e-11;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 135; DB 2;
Pred. No. 2.5e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 135; DB 2;
Pred. No. 2.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                               Length 192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218;
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C;Superfamily: bcl transforming protein
                                                                                                           hypothetical protein F20D21.19 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-car cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: D96585
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                                                                             R;Theologis,
                                                                                                                                                                                                                                              D96585
                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
Matches 10; Conserv
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Best Local
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25; Conserv
                                              Chung, M.K.; Conn, L.; Conway, A.B.;
                                                                                A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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bcl-2-associated protein x - rat (fragment)
NALternate names: BAX; programmed cell death membrane protein x
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 03-Nov-2000
C;Accession: IS3295
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in the immature rat onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A;Reference number: IS3295; MUID:95129487
A;Reference number: IS3295; MUID:95129487
                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: I53295
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;McJecule type; mRNA
A;Residues: 1-133 <RES>
                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U32098; NID:g975869; PIDN:AAA75200.1; PID:g975870
                                                            1 QDASTKKLSECLKRIGDELDSNMELQR 27
QDASTKKLSECLRRIGDELDNNMELQR 42
                                                                                                                    Mismatches
                                                                                                                                                      Score 129; DB 2
Pred. No. 1e-10;
                                                                                                                                                                                     S.
                                                                                                                                                                                 Length 133;
                                                                                                                    Indels
                                                                                                                            Gaps
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hypothetical protein HI1064 - Haemophilus Influenzae (strain Rd KW20)
C;Species: Haemophilus Influenzae
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 08-Oct-1999
C;Accession: F64165
C;Accession: F64165
C;Accession: F64165
C;Accession: F64165
C;Accession: F64165
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C;Accession: F64165
C;Accession: F64165
C;Accession: F64165 A;Cross·references: GB:U32786; GB:L42023; NID:g1574605; PIDN:AAC22718.1; PID:g1574615 A;Note: best homolog was a hypothetical protein from Escherichia coli A.Status: nucleic acid sequence not shown: translation A;Molecule type: DNA A;Residues: 1-465 CTIGR> Score 52; Pred. No. Mismatches рв 19; 2 6 Length 485 not shown 0 Gaps 0

Conway, A.R.; Creasy, T.H.;

S.; White, O.

nuclear antigen

pred

Gaps

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A;Molecule type: DNA
A;Residues: 1-471 <RIE>
A;Residues: 1-471 <RIE>
A;Residues: 1-471 <RIE>
A;Cross-references: EMBL:272804; NID:g1322986; PIDN:CAA97002.1; PID:g1322987; MIPS:YGR01
A;Cxperimental source: strain S288C
R;Andre, B.; Jauniaux, J.C.
Nucleic Acids Res. 18, 3049, 1990
A;Title: Nucleotide sequence of the yeast UGA1 gene encoding GABA transaminase.
A;Reference number: S26708; MUID:90272415
A;Recession: S26708
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Nature 408, 815-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4-aminobutyrate transaminase (EC 2.6.1.19) - yeast (Saccharomyces cerevisiae) N;Alternate names: 4-aminobutyrate aminotransferase; gamma-aminobutyrate transaminase; C:Species: Saccharomyces cerevisiae C:Date: 17-May-1996 *sequence_revision 17-May-1996 *text_change 20-Jun-2000 C;Accession: $64310; $26708 R:Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M. Submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 7R
C;Superfamily: 4-aminobutyrate transaminase
C;Keywords: aminotransferase; pyridoxal phosphate
                                                     RESULT
A37244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-33, 'R', 241-471 <ANDl> A; Cross references: EMBL.X52600; NID:94745; PIDN:CAA36833.1; A; Experimental source: strain sigma 1278b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S64071
A; Accession: S64310
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A; Map position: 1
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A; Residues: 1-575 <STO>
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nuclear autoantigen Sp-100 - human
C; Species: Homo sapiens (man)
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A;Cross-references: SGD:S0003251; MIPS:YGR019w
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                367
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                                                                                                                                                                                          QDASTKKLSECLKRIGDELDSNME-LQR 27
                                                                                                                                                                QEISDKKLTEQCSRVGDYLFKKLEGLQK 394
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                                                                                                                                                                                                                                                                                           38.1%;
46.4%;
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Pred. No. 2
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Pred. No. 23;
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R;Szostecki, C; Guldber, H.H.; Netter, H.J.; Will, H.
J. Immunol: 145, 4338-4347, 1990
A;Title: Isolation and characterization of cDNA encoding a human nuclear ant A;Reference number: A37244; MUID:91079525
A;Accession: A37244
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-480 <S20>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RiPraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Grson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; M they, I.; Weidman, J.; Smith, H.O.; Venter, J.C.;
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770
A;Accession: H71317
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-845 <COL>
A;Cross-references: GB;AED01225; GB;AED00520; NID:g3322775; PIDN:AAC65475.1; PID:g332
A;Genetics:
C;Genetics:
                                                                            A:Cross references: EMBL:L10112; NID:9159851; PID:9159852
A:Note: the authors did not translate the codon for residue
C:Superfamily: intermediate filament protein AV71
                                                                                                                                                                                                                                         C;Accession: $43427
R:Tomarev, S. I.: Zinovieva, R.D.; Piatigorsky, J.
Biochim. Blophys. Acta 1216, 245-254, 1993
A;Title: Primary structure and lens-specific expression of A;Reference number: $43425; MUID:94060097
A;Accession: $43427
                                                                                                                                                                                                                                                                                                                                                                                  intermediate filament protein - Sloane's squid
C;Species: Ommastrephes sloanei (Sloane's squid)
C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 26-Aug-1999
C;Accession: $43427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable methyl-accepting chemotaxis protein (mcp2-1) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
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                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-614 <TOM>
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Best Local Similarity 52...
Thes 11; Conservative
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Best Local Similarity 33.3
Query Match
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52.4%;
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37.0%;
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Pred. No. 46;
   Score
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Length 614;
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hypothetical protein T29M8.1 - Arabidopsis thaliane
C;Species: Arabidopsis thaliana (mouso-ear cross)
C;Date: 02-Mar-2001 *text_change 31-Dec-2001
C;Date: 03-Mar-2001 *tesquence_revision 02-Mar-2001 *text_change 31-Dec-2001
C;Accession: G86324
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, C;Accession: R;Chung, M.K.; Con, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Malti, R.; Marziali,
R;Zato, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Stetus: prelininary
A;Stetus: prelininary
A;Stetus: prelininary
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Jong, I.; Jeffrles, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, I
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ser/thr protein kinase, probable [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Decies: 44-May-2001 #text_change 24-May-2001 #text_change 24-May-2001 C;Accession: A90506
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A90506
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A;Map position: 1
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G86324
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                                                                                                                                                                                             C;Genetics:
A;Gene: SSO3207
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A;Molecule type: DNA
A;Residues: 1-669 <KUR>
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A; Accession: A90506
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A; Residues: 1-311 <STO>
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Best Local Similarity 42.1
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                                                                                    hes 7; Conser
                                       8 LSECLKRIGDELDS 21
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VAQCMERIGDELEA 188
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                                                                                    Conservative
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                                                                                 Score 49; DB
Pred. No. 69;
7; Mismatches
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7; M1smatches
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Pred. No.
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32;
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A; NoLecule type: DNA
A; Rosidues: 1-732 <WIL>
A; Cross-references: EMBL: Z69787; PIDN:CAA93636.1; GSPDB:GN00028; CESP:C44C10.2
                                                                                                                                                                                                                                                                                                                                 R;Cottage, A.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19197
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T19923
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A;Experimental source: cultivar Columbia; BAC clone T21H19
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein c44ClO.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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A; Introns: 271/3;
A; Note: T21H19_100
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A; Residues: 1-718 <SAT>
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A; Accession: T51488
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                                                                                                                                           A; Introns: 54/3; 102/3; 119/3; 388/1; 427/3; 490/3;
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	Bos t	aurus	(Bovine)					
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	NCBI_	TaxID=	9913;					
	SEQUE	NCE FR	SEQUENCE FROM N.A. STRAIN=HOLSTEIN; TISSUE=Thymus;	SSUE-Th	ymus	**		
	Reyes	R.A.,	Cocker	PubMed=9	, 20102	÷.		
3 3	"Incr	eased	ratio of	bc1-2/	k and	"Increased ratio of bcl-2/bax expression is associated with bovine	d with k	ŏ
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8 8	7	IMILAR	ITY: COL	TAINS 1	BCL	-2 HOMOLOGY DOMAIN 2 (B	(BH2).	
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ದೆ	This	-SSIWS	PROT ent	ry is c	TAGO	right. It is produced th	rough a	collaboration
റ്	betwe	en th	e Swiss	Institu	te o	of Bioinformatics and t	he EMBL outstation	
	the E	uropea	n Bioin	formatic	tuti	use by non-profit institutions as long as its content in	restrictions	~ ;;
	modified	ied an	d this	statemen	יל ה מנה	not removed. Usage by and for commercia	y and i	0
	or se	nd an	email to	licens	eeis	send an email to license@isb-sib.ch).	i 6	- 1
á 'n	EMBI.	1192569.	9. 33648806	3806 1.	1 }	- 1		

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RESULT 2
BAXA_HUMAN
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAXA_HUMAN STANDARD; PRT; 192 AN OO7812; O1-FEB-1995 (Rel. 31, Created) O1-FEB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) O1-FEB-1995 (Rel. 40) Last annotation update)
                                                                                                                                                                                                                                                       VARIANT T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ARG-67.
MEDLINE-98200607; PubMed-9531611;
Meijerink J.P.P., Mensink E.J.B.M., Wang K., Sedlak T.W.,
Sloetjes A.W., de Witte T., Waksman G., Korsmeyer S.J.;
"Hematopoletic malignancies demonstrate loss-of-function mutations
                                                                                                                                                                                                                                                                                                                                                   MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.
MEDLINE-96091131; PubMed-8521816;
Chittenden T., Flenington C., Houghton A.B., Ebb R.G.,
Elangovan B., Chinnadurai G., Lutz R.J.;
*A conserved domain in Bak, distinct from BH1 and BH2,
death and protein binding functions.*;
EMBO J. 14:5589-5596(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93364978; PubMed-8358790;
Oltval Z.N., Milliman C.L., Korsmeyer S.J.;
"Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, accelerates programmed cell death.";
Cell 74:609-619(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00337; BCL; 1.
PROSITE; PS01080; BH1: 1.
PROSITE; PS01258; BH2: 1.
PROSITE; PS01259; BH3: 1.
PROSITE; PS01259; BH3: 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
-1- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REFRESSOR BCL-2 OR ITS ADEMOVIBUS HOMOLOG ELB 19K PROTEIN, INDUCES THE RELEASE OF CYTOCHROME C, ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
-1- SUBGURIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2, ELB 19K PROTEIN, BCL-X(L), MCL-1 AND AL.
-1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING:
-1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
-1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND BAX FOR THEIR ROPAPOPTOTIC ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                              Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis regulator BAX, membrane isoform alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91:2991-2997(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 135; DB 1;
Pred. No. 1.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6B4D5BABF1D5F87E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                    and BH2, mediates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Best Local
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Q07814;
Q1-FEB-1995
Q1-FEB-1995
16-CCT-2001
                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis;
DOMAIN
DOMAIN
                                                "BCL-2 heterodimerizes in vivo with a accelerates programmed cell death." Cell 74:609-619(1993).
                                                                                                                                                Elikaryota; Metazoa; Chordata; Craniata; Vertebrata; Biteleostomi;
Mammalla; Elitheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50062; BCL2_FAMILY; PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; BCL_2.
Pfam; PF00452; BCl_2; 1.
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                               SEQUENCE FROM N.A.
TISSUE-B-cell;
                                                                                                                                                                                                              Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  +
                                                                                                   MEDLINE-93364978; PubMed-8358790;
                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A47538; A47538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L22473; AAA03619.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                      52
                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
DISEASE: DEFECTS IN BAX ARE FOUND IN SOME PATIE
ACUTE LYMPHOBLASTIC LECKEMIA.
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3
FUNCTION: ACCELERATES PROGRAMED CELL ANTAGONIZING THE APOPTOSIS REPRESSOR HOMOLOG ELB 19K PROTEIN.
SUBUNIT: FORMS HOMODIMERS AND HETEROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Q07817; 1MAZ.
600040; -.
                                                                                                                                                                                                                                                                                                                                                  QDASTKKLSECLKRIGDELDSNMELQR 27
                                                                                                                                                                                                                                                                                                                                      QDASTKKLSECLKRIGDELDSNMELQR
                                                                                                                                                                                                                                                                                                                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Transmembrane; Alternative s
150 73 BH3.
98 128 BH1.
150 165 BH2.
172 192 POTENTIAL.
67 67 G -> R (IN
                                                                                                                                                                                                              regulator BAX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 192
                                                                                                                                                                                                                        (Rel. 31, Created)
(Rel. 31, Last sequence up)
(Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą,
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21184 MW;
                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                              cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
G -> R (IN T-CELL
LEUKEMIA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR_007809.
6C0CDB0A7DEE4994
                                                                                                                                                                                                                                                                                                                                                                                               Score 135;
Pred. No. 1
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
    RETERODIMERS
                                                                                                                                                                                                              on update)
c isoform |
                                                                                                                                                                                                                                                                          218
                                                                         S.J.;
conserved
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                           BCL-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOME PATIENTS WITH
                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
1.8e-11;
                                                                                                                                                                                                               beta
                                                                                                                                                                                                                                                                                                                                                                                     0;
                           S BY
    TOGETHER WITH BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACUTE LYMPHOBLASTIC
                                                                           homolog,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Length
                           BINDING TO, AN ITS ADENOVIRUS
                                                                                                                                                                                                                                                                                                                                                                                     Indels
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(BH2).
(BH3).
                                                                                                                                                                                                                                                                                                                                                                                                              192;
                                                                           вах,
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                                                                                                                                                                                                                                                                                                                                                                                     0;
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Best Local S
Matches 27
                                                                                                                                                                     Q07813;
Q1-FEB-1995 (Rel. 31, Created)
Q1-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                   SEQUENCE FROM N.A.
STRAIN=C578L/6 X DBA/2;
STRAIN=C578L/6 X DBA/2;
MEDLINE=93364978; PubMed=8358790;
Oltvai Z.N., Milliman C.L., Korsmeyer
"BCl-2 heterodimerizes in vivo with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00337; BCL; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÷÷
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     +
           accelerates programmed cell death."; Cell 74:609-619(1993).
                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                   BAXA_MOUSE
                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apoptosis; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L22474; AAA03620.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                    52
                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.

DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
BAX FOR THEIR PRO APOPTOTIC MCTYVITY AND FOR THEIR INTERACTION
WITH ANTI-APOPTOTIC MCMBERS OF THE BCL-2 FAMILY.

APOPTOTIC MCMBERS OF THE BCL-2 FAMILY.

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: BELLONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIB 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.
FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B47538; B47538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                       Similarity
27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                  59
98
150
218
                                                                                                                                                                                                                                                                                                                                                                     100.
Milarity 100.
Conservative
ACCELERATES PROGRAMED CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                       ĀĀ,
                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                     165
24220 MW;
                                                                                                                                                                                                                                                                                                                                                                                    0.0%;
                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                  Score 135;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH2
                                                                                                                                                                                                                                                                                                                                                                                                                                       F69DCD70F960192F
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                   192
                                                 S.J.;
                                      conserved
                                                                                                                                                                                                                                                                                                                                                                                    2e-11;
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DEATH
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                                                                                                                                                                                                                                                                                                                                                                       0;
ВY
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                                      homolog,
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BINDING
                                      Bax,
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                                                                                                                                                                                  RESULT
BAXA_RAT
 RAN OCC OCC PRINTERS
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                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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InterPro: IPR002712; BCL_2.
Pram; PP00472; BCL_2; 1.
SMART; SM00337; BCL; 1.
PR0SITE; PS01080; BH1; 1.
PR0SITE; PS01258; BH2; 1.
PR0SITE; PS01258; BH3; 1.
PR0SITE; PS01258; BH3; 1.
PR0SITE; PS0162; BCLZ_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                BANA_RAT STANDARD; PRT; 1
63560; Q62995; Q6488;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-997 (Rel. 35, Last sequence up
16-CCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                                                                                                            Apoptosis; Transmembrane; Alternative splicing.
DOMAIN 59 73 BH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L22472; AAA036;
HSSP; Q07817; 1MAZ.
MGD; MGI:99702; Bax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
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SEQUENCE FROM N.A MEDLINE-96178771;
                                                                                                      Apoptosis
                                                                                                                                                                                                                                       52
                                                                                                                                                                                                                                                               1 QDASTKKLSECLKRIGDELDSNMELQR 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: INTACT BH3 DOMAIN IN A WIDE VARIETY OF TIS
DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAX
BAX FOR THEEIR PRO-ADOPTOTIC ACTIVITY AND FOR THEIR IN
WITH ANYI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2, E1B 19K PROTEIN, BCL-X(L), MCL-1 AND AL. SUBCELLJUAR LOCATION: Membrane-bound.
ALTERNATIVE PRODUCTS: A 21 KDA MEMBRANE PROTEIN ALPHA AND THE TWO CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
                                                                                                                                                                                                S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEADS TO LYMPHOID HYPERPLASIA AND MALE CESSATION OF SPERM PRODUCTION.
                                                                                                                                                                                                                                     Similarity
                                                                                                     regulator
                                                                                                                                                                                                                                                                                                                                                          192 AA;
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98
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172
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PubMed-8600029
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118
165
192
                                                 Chordata;
Rodentia;
                                                                                                      BAX,
                                                                                                                                                                                                                                                                                                                                                          21394 MW;
                                                                                                                                                                                                                                                                                                     97.8%;
                                                                                                        membrane
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BH2.
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Pred. No. 4.5e-11;
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p2E0B3566579FAFF
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isoform alpha.
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ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C. ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY STERILITY, BECAUSE QF. THE

ID, BAK, BAD AND

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CRC64;

Length 192; 0; Gaps 0;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat Rattus

SQ

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RA TILLY J.L., TELLY K.I., Kenton M.L., Johnson A.L.;

RT "Expression of members of the bcl-2 gene family in the immature rat repression of members of the bcl-2 gene family in the immature rat rowary: equine chorionic gonadotropin-mediated inhibition of granulosa representations and bcl-xiong messenger ribonucleic acid levels.";

RT coll apoptosis is associated with decreased box and constitutive bcl-2 and bcl-xiong messenger ribonucleic acid levels.";

RE ndocrinology 136:332-241(1995).

CI - FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS CHANGED THE APOPTOSIS.

CI HOMOLOG EIL JOK ROPTIN. INDUCES THE RELEASE OF CYTOCHROME C., ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.

CI - SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.

CI - SUBCELLULAR LOCATION: Membrane-Dound.

- I- SUBCELLULAR LOCATION: Membrane-Dound.

- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO CYTOCHROME.

CI - SUBCELLURA COCATION: Membrane-Dound.

- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO CYTOCHROME.

CI - SUBLICING.

- SPLICING.
                                                                                                                                                                                           PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01062; BCL2 PANDPLOSIS; Transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-Y/14/27, ...
MEDLINE-Y/14/27, ...
MEDLINE-Y/14/27, Pfeiffer S.E.;
Cloning of the 3' end of rat bax-alpha and corresponding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U49729; AAC26327.1; -.
EMBL; U59184; AAC52998.1; -.
EMBL; U359189; AAA75200.1; -.
EMBL; S76511; AAC60700.2; -.
HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way nodified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
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InterPro; IPR000712; BCL_2.
Pfam; PF00452; BcL-2; 1.
SMART; SM00337; BCL; 1.
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                                                                                                                          DOMAIN
                                                                                                                                                       DOMAIN
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DOMAIN: INTRACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
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       59
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MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fleids C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Googhagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Wehler J.C.;
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influenzae Rd.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                   CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
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RESULT 8
SP10_HUMAN
ID SP10_HUMAN
                                                                                        Š
                                                                                                                                                                                    GATA_YEAST
                                                                                                                                 Query Match
Best Local
                                                                                                                    Matches
                                                                                                                                                  P17649;
01-AUG-1990 (Rel. 15, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
4-aminobutyrate aminotransferase (EC 2.6.1.19) (Gamma-amino-N-butyrate
4-aminobutyrate aminotransferase) (GABA aminotransferase) (GABA-AT).
                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                EMBL; X52600; CAA36833.1; EMBL; Z72804; CAA97002.1;
                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Institute. There are no the European Bioinformatics Institute. There are no the European Bioinformatics institute of as its con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae chromosome VII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.
                                                                                                                                                                                                                                                          PTR: $26708; $26708.
HSSP: B80147; ICTX.
SCD: $5003251; UGA1.
InterPTO: IPR000954; Aminotran_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rieger M., Brueckner M., Schaefer M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97435481; PubMed=9290212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence of the yeast UGA1 gene encoding GABA transaminase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andre B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90272415; PubMed=2190186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATA_YEAST
                                                                  367
                                                                                                                   Local Similarity 46. 
nes 13; Conservative
                                                                                          Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               St 13:1077-1090(1997).
CATALTYIC ACTIVITY: 4-aminobutanoate +
semialdehyde + L-glutamate.
COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMODIMER (POSSIBLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMINOTRANSFERASES
                                                                                          QDASTKKLSECLKRIGDELDSNME-LQR 27
                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                 QEISDKKLTEQCSRVGDYLFKKLEGLQK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jauniaux J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Res.
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18:3049-3049(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetaceae;
                                                                                                                               38.1%;
                                                                                                                              Score
Pred.
 PRT;
                                                                                                                   Mismatches
                                                                                                                               No. 9
 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mueller-Auer S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces
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                                                                                                                   9.
                                                                                                                                          Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
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                                                                                                                   Gaps
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ubiquitin-like modifiers.";

J. Biol. Chem. 274:12555-12566(1999).

-:- FUNCTION: MAY PLAY A ROLE IN THE CONTROL OF GENE EXPRESSION.

-:- SUBUNIT: HOMODIMER. SPLICE VARIANTS HETERODIMERIZE. INTERACTS WITH MEMBERS OF THE HPI FAMILY OF NONHISTONE CHROMOSOMAL PROTEIN, SUCH AS HETEROCHROMATIN PROTEIN 1-ALPHA (HPI-ALPHA) AND HETEROCHROMATIN
                                                                                                                                                                                                 CHARACTERIZATION, AND COVALENT BINDING TO SUMO-1.

MEDLINE-99330277; PubMed-10212234;

Sternsdorf T., Jensen K., Reich B., Will H.;

"The nuclear dot protein spl00, characterization of domains necessary

"The nuclear dot protein spl00, characterization, and modification by small

for dimerization, subcellular localization, and modification by small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILING-96411734; PubMed-8810287;
Groetzinger T., Jensen K., Will H.;
"The interferon (IFN)-stimulated gene Sp100 promoter contains an IFN-
gamma activation site and an imperfect IFN-stimulated response elemen
which mediate type I IFN inducibility.";
J. Biol. Chem. 271:25253-25260(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Szostecki C., Guldner H.H., Netter H.J., Will H.; "Isolation and characterization of cDNA encoding a antigen predominantly recognized by autoantibodies primary biliary cirrhosis."; J., Immunol. 145:4338-4347(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P23497; 013343; 075450; Q9UE32; 01-NOV-1991 (Rel. 20, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Nuclear autoantigen Sp-100 (Speckled 100 kDa)
                                                                                                                                                                                                                                                                                                                                 Guldner H.H., Szostocki C., Schroeder P., Matschl U., Jensen K., Lueders C., Will H., Sternsdorf T., "Splice variants of the nuclear dot-associated Spl00 protein contain homologies to HMG-1 and a human nuclear phosphoprotein-box motif.";
                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Cervical adenocarcinoma; MEDLINE-99141186; PubMed-9973607;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE SPLICING (ISOFORMS SP100-B; SPALT-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blood 88:1423-1426(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "LYSP100-associated nuclear domains class of subnuclear structures and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-96329578; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver, and Placenta; MEDLINE=91079525; PubMed=2258622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promyelocytic leukemia-associated nuclear bodies and the chromatin compartment. ^{\mathtt{m}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seeler J.-S., Marchio A., Sitterlin D., Transy C., Dejean "Interaction of SP100 with HP1 proteins: a link between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM TISSUE-Breast cancer; MEDLINE-98301571; PubMed-963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sp100 protein) (Lysp100b).
                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                      J. Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-10 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dent A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
PROTEIN 1-GAMMA (HP1-GAMMA).
SUBCELLULAR LOCATION: NUCLEAR. FOUND IN THE NUCLEAR BODY, ALSO
KNOWN AS NUCLEAR DOMAIN 10 (ND10), PML ONCOGENIC DOMAIN (POD),
NUCLEAR DOTS. (ND) AND KR BODY. THE NUCLEAR BODY IS A NUCLEOPLY
STRUCTURE OF PUNCTATE SHAPE, WHICH VARIES IN SIZE AND NUMBER.
                                                                                                                                                                                                                                                                                                                  Sci. 112:733-747(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yewdell J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acad. Sci. U.S.A. 95:7316-7321(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=8695863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed-9636146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISOFORM SP100-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Puvion-Dutilleul F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SP100-HMG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SP100-A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LANDs): description their relationship to
                      NUCLEAR BODY IS A NUCLEOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koken M.H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Nuclear dot-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                               AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human nuclear
from patients with
                                                                                                                                                                                                                                                                                                                                                                                                                                               SP100-HMG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                     protein contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of a new
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                                                         ALSO
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DOMAIN
DOMAIN
DOMAIN
BINDING
VARSPLIC
                                                                                                                                                                                                                                                                                            DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0886; HIGHMOBLTY12.
SMART; SM00398; HMG; 2.
SMART; SM00258; SAND; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF056322; AAC39790.1; -. EMBL; M60618; AAA33537.1; -. EMBL; U36501; AAC350743.1; -. EMBL; X95472; CAA64744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00505; HMC_box; 2. Pfam; PF01342; SAND; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000910; HMG_12_box.
InterPro; IPR000135; Highmobity_12.
InterPro; IPR000770; SAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
VARSPLIC
                                                                                                   VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             Colled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A37244; A37244
HSSP; P07155; 1HME
                                                                VARSPLIC
                                                                                  VARSPLIC
                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: THIS ANTIGEN IS RECOGNIZED BY AUTOANTIBOD PATIENTS WITH PRIMARY BILLARY CIRRHOSIS (PBC).
MISCELLANEOUS: THE MAJOR SPLICE VARIANT, SPLOO-A, MAY OF 54 KDA, BUT EXHEBITS ABERRANT ELECTROPHORETI WITH AN APPARENT MO OF 100 KDA.
SIMILARITY: CONTAINS 1 SAND DOMAIN.
SIMILARITY: CONTAINS 2 HMG BOXES.
SIMILARITY: TO NUCLEAR AUTOANTIGEN SP-140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDICTION: BY INTERFERON.

DOMAIN: THE HSR DOMAIN IS IMPORTANT FOR THE NUCLEAR BODY TARGETTING AS WELL AS FOR THE DIMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDUCTION BY INTERPERON AND MAY BE CELL CYCLE STAGES MODULATE THE SUBNUCLEAR LOCALIZATION OF THE ISOFORMS.

ALTERNATIVE PRODUCTS: 4 ISOFORMS; SP100-A/SP100, SP100-B/SPALT-212, SPALT-C AND SP100-HHG/SPALT-HHG (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. SP100-A IS THE MORE ABUNDANT ISOFORM.

SP100-HHG CONTAINS AN ALMOST COMPLETE AND HIGHLY CONSERVED COPY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: COVALENTLY CONJUGATED TO ONE SMALL UBIQUITIN-RELATED PROTEIN SUMO-1. SUMOYLATION DEBENDS ON A FUNCTIONAL NUCLEAR LOCALIZATION SIGNAL BUT IS NOT NECESSARY FOR NUCLEAR IMPORT OR NUCLEAR BODY TARGETTING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: PHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: WIDELY EXPRESSED. SP100-B IS EXPRESSED ONLY IN SPLEEN, TONSIL, THYMUS, MATURE B-CELL LINE AND SOME T-CELL LINE,
                                                                                                                                                                                                                                                                                                                                                                                                                                             coll;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOT IN BRAIN, LIVER, MUSCLE OR NONLYMPHOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-BINDING HMG1 BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear protein; DNA-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                     33 1496

53 553

558 592

714 794

715 794

717 794

718 719 719

719 719 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A37244
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3156
759
759
854
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297
478
481
685
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764
764
859
868
879
688
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553
592
734
676
837
837
                                                                                                                                                                                                                                                                                                                                                                                                                                             splicing;
                                                                                                                                                                  POLY-LYS.
POLY-GLU.
RFSSSDFSDLSNGEELQETCSSSL -> LKKKKKKKQCHPQ PQPQRGLLEQS (IN ISOFORM SP100-C). MISSING (IN ISOFORM SP100-C).
                                                         SUMO-1 (PROBABLE),
SQP -> KED (IN ISOFORM SP100-A).
MISSING (IN ISOFORM SP100-B).
RILE -> VTIK (IN ISOFORM SP100-B).
MISSING (IN ISOFORM SP100-B).
                                                                                                                                                                                                                                                                                                                                       NUCLEAR
SAND.
                                                                                                                                                                                                                                                                                                                                                        NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                   POLY-GLU.
                                                                                                                                                                                                                                                       POLY-GLY
                                                                                                                                                                                                                                                                           COILED COIL
                                                                                                                                                                                                                                                                                               XO8
                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IANT, SP100-A, HAS A CALCULATED ELECTROPHORETIC MOBILITIES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY AUTOANTIBODIES
                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOME T-CELL
CELL LINES.
                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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RESULT 10
RBSK_BACHD
ID RBSK_B
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RBSK_BACHD STANDARD;
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Q1-MAR-2002 (Rel. 41, Created)
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Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
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S -> P (IN HELA CELLS).
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Matches 8
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01-APR-1990
01-APR-1990
01-MAR-2002
SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.

STRAIN-V245 / DSM 2088;
MEDLINE-90236834; PubMed-2110059;
MEDLINE-90236834; PubMed-2110059;
MEDLINE-90236834; PubMed-2110059;
MEDLINE-90236834; PubMed-2110059;
Properties and primary structure of the L-malate dehydrogenase from the extremely thermophilic archaebacterium Methanothermus fervidus.";
Eur. J. Biochem. 188:623-632(1990).
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PROSITE; PS00584; PFKB_KINASES_2; 1.
Transferase; Kinase; Complete proteome.
SEQUENCE 294 AA; 31089 MW; 8C13E0FCF5E89FDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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"Complete genome sequence of the alkaliphilic halodurans and genomic sequence comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (Rel. 41, Last 01-MAR-2002 (Rel. 41, Last Ribokinase (EC 2.7.1.15).
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Ol-APR-1990 (Rel. 14, Last sequence update)
Ol-MAR-2002 (Rel. 41, Last snoctation update)
Malate/L-sulfolactate dehydrogenase (EC 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002173; PfkB.
InterPro; IPR002139; Ribokinase
Pfam; PF00294; pfkB; 1
PRINTS; PR00990; RIBOKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               halodurans and genomic sequence comparison with Bacillus subtilis.",
Nucleic Acids Res. 28:4317-431(2000).
-! CATALYTIC ACTIVITY: ATP - D-ribose - ADP + D-ribose 5-phosphate.
-! PATHWAY: FIRST STEP IN RIBOSE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20512582; PubMed=11058132;
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NCBI_TaxID=86665;
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01-MAR-2002
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Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
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                                                                                                                                                                                                                                                                                                             Methanothermus fervidus
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SIMILARITY: BELONGS TO THE PEKB FAMILY OF CARBOHYDRATE KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.8%;
53.3%;
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                                                                                                                                                                                                                                                                                 Methanobacteriales; Methanothermaceae;
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annotation updat
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Pred. No. 23;
4; Mismatches
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(EC 1.1.1
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., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                     .37)
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Best Local :
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007820; Q9NRQ3; Q9NRQ4;
01 FEB-1995 (Rel. 31, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Induced myeloid leukemia cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Graupner M., Xu H., White R.H.;

'Identification of an archaeal 2-hydroxy acid dehydrogenase catalyzing reactions involved in coenzyme biosynthesis in methanoarchaea.';

J. Bacteriol. 182:3688-3692(2000).

J. FUNCTION: Acts on oxaloaccetate, sulfopyruvate but not on pyruvate. Has a higher selectivity for the coenzyme NADH than for NADH.

-! CAPALYTIC ACTIVITY: (S)-malate + NAD(P)(+) - oxaloaccetate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR003767; ldh_2.

Pfam: pF02615; ldh_2; l.

Oxidoreductase; Tricarboxyl
SEQUENCE 339 AA; 36762 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FUNCTION.
"Exon skipping in Mcl-1 results in a product that promotes cell death."; J. Biol. Chem. 275:22136-22146(2000)
                                                                          SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
MEDLINE-20357335; PubMed-10766760;
Bingle C.D. (Traig R.W., Swales B.M.,
Whyte M.K.B.;
                                                                                                                                                                                                         Kozopas K.M., Yang T., Buchan H.L., Zhou P., Cra, "MCLI, a gene expressed in programmed myeloid celhas sequence similarity to BCL2.";
Proc. Natl. Acad. Sci. U.S.A. 90:3516-3520(1993)
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Myeloid leukemia cells;
MEDLINE-93234528; PubMed-7682708;
KOZOPAS K.M., Yang T., Buchan H.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: X51714; CAA36010.1;
EMBL: X51840; CAA36133.1;
PIR: S08689; S08689.
PIR: S08981; S08981.
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                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID~9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 KKLVEKLKEIADEL -- NIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homodimer
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13; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid cycle; NAD; NADP.
2319D822DB275835 CRC64;
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                                                       homology
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d cell
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differentiation
                                                                                                       Zhou
                                                          domain 3 only gene
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Best Local
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CONFLICT
SEQUENCE
                                                                                                           P3090;

01-OCT-1996 (Rel. 34, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

15-DEC-1998 (Rel. 37, Last annotation update)

Aromatic amino acid aminotransferase I (EC 2.6.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART: SM00337; BCL: 1.
PROSITE: PS50052; BCL2_PAMILY;
PROSITE: PS01258; BH2; 1.
PROSITE: PS01259; BH2; 1.
PROSITE: PS01259; BH3; 1.
 SEQUENCE FROM N.A. STRAIN-SIGMA 1278B:
                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID-4932;
                                                                                                                                                                                                           YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR002475; BCL2_family InterPro; IPR000712; BCL_2. Pfam; PF00452; BCL-2; 1. SMART; SM00337; BCL; 1.
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EMBL; AF198614; AAF64255.1; -.
EMBL; AF198614; AAF64256.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license(sib)-sib.ch).
                                                                                                                                                                                           ARO8_YEAST
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SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are produced by alternative splicing INDUCTION. EXPRESSION INCREASES EARLY DURING PHORBOL-ESTER INDUCED DIFFERENTIATION ALONG THE MONOCYTE/MACROPHAGE PATHWAY IN MYELOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Involved in programing of differentiation and concombitant maintenance of viability but not of proliferation. Isoform 1 inhibits apoptosis while isoform 2 promotes it. SUBCELLULAR LOCATION: Membrane-bound (Potential).
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/delta S/TM:
                                                                                                    OR YGL202W
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9; Conserv
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173
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37323
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POTENTIAL.
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ALL (IN ISOFORM 2)
MISSING (IN ISOFORM 2).
D -> E (IN REF. 1).
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Pred. No.
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(BH2).
(BH3).
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Best Local S
Matches 10
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01-NOV-1988
16-OCT-2001
                                                                                                Noegel A., Witke W., Schleicher M.;
"Calcium-sensitive non-muscle alpha-actinin
structures and highly conserved regions.";
FEBS Lett. 221:391-396(1987).
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P05095;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bjourson A.J., McReynolds A.D.K., Wright L.F.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
-1- SIMILARITY: TO YEAST ARO9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIAIRS-98151783; PubMed-9491083;
Iraqui I., Vissers S., Cartiaux M., Urrestarazu A.;
"Characterisation of Saccharomyces cerevisiae ARO8 and
encoding aromatic aminotransferases I and II reveals a
                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aminotransferase subfamily.";
Mol. Gen. Genet. 257:238-248(1998).
                                                                                                                                                                                         MEDLINE-86304574; PubMed-3745276;
                                                                                                                                                                                                                                                                                                        MEDLINE-87304850;
                                                                                                                                                                                                                                                                                                                          STRAIN-AX2
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=44689;
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              SUBUNIT: HOMODIMER, ANTIPARALLEL.
SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) I
SIMILARITY: CONTAINS 2 EF-HAND CALCIUN-BINDING
SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
                                                                                         PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPEKLTEGLKRLGDTL 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STKKLSECLKRIGDEL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 62.1
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   7 (Rel. 05,
3 (Rel. 09,
1 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               500 AA;
                                                                                                                                                                                                                      92-505 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aminotransferase.
00 AA; 56177 MW;
                                                                                                                                                                                                                                                                                                                                     N.A
                                                                                                                                                                                                                                                                                                                                                                                                                   el. 09, Last sequence update)
el. 40, Last annotation update)
non-muscular (f-actin cross linking protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                        PubMed-3622778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB
Pred. No. 40;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D0D111640D2C560D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            862 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 500
                                                                                                                                                                                                                                                                             contains EF-hand
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CRC64;

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EMBL; Y00689; CAA68685.1; -. EMBL; X04324; CAA27855.1; -. EMBL; S00103; FADOAA.

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Best Local
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Pfam; PF00035; efhand; 2.
Pfam; PF00435; spectrin; 4.
SMART; SM00033; CH; 2.
SMART; SM00034; EFh; 2.
SMART; SM00150; SPEC; 3.
SMART; SM00150; SPEC; 3.
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InterPro; IPR001589; Actinin_act_bind.
InterPro; IPR001715; Calponin_hom.
InterPro; IPR002017; Spectrin.
                             Badcock K., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.; • Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARY: TO YEAST YNL132W AND AN A.AMBISEXUALIS HYPOTHETICAL PROTEIN (AC P54008).
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        NCBI_TaxID-4896;
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hes 9; Conserv
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EF_HAND;
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SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
EF-HAND 1 (BY SIMILARITY).
EF-HAND 2 (BY SIMILARITY).
T-> P (IN REF. 2).
T-> T (IN REF. 2).
W; 15608ADB71213226 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIN-BINDING.
CH 1.
CH 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 1;
Pred. No. 68;
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SPERGOCOCOCO
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                                                                        Query Match
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Matches 11
                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                    EMBL; Z95334; CAB08603.1; -. Hypothetical protein; ATP-binding. NP_BIND 282 289 ATP (
                                                                                                                                                                    SEQUENCE
661 KAVKHSLKRIGDEEIENTALQ
                                                                        Local Similarity 52. hes 11; Conservative
                                    σ
                                    KKLSECLKRIGDELDSNMELQ 26
                                                                                                                                                                  282 289 ATP (POTENTIAL).
1033 AA; 116463 MW; 8432B313DB18E135 CRC64;
                                                                                       34.1%; 52.4%;
  681
                                                                        Score 46; DB 1; L
Pred. No. 1.1e+02;
1; Mismatches 9;
                                                                                                         Length 1033;
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Search completed: September 20, Job time: 1627 sec 2002, 11:04:30

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Title:
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                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
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Gapop 10.0 , Gapext 0.5
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135
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                  sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length DB	BB	₽	Description
р.	135	100.0	149	6	Q9GMG7	Q9gmg7 ovis aries
2	135	100.0	164	4	90006	Q9uqd6 homo sapien
ω	135	100.0	179	4	Q9NYG7	Q9nyg7 homo sapien
4	129	95.6	173	11	Q9JKL3	Q9jkl3 rattus norv
<sub>U</sub>	107	79.3	221	13	098013	Q98ul3 xenopus lae
ō	83	61.5	192	13	Q919N4	Q9i9n4 brachydanio
7	66	48.9	15	4	Q9UCZ7	Q9ucz7 homo sapien
ω	54	40.0	1124	12	Q9DVW1	Q9dvwl plutella xy
9	53	39.3	913	G	Q94893	Q94893 drosophila
10	53	39.3	1861	u	Q9VF02	Q9vf02 drosophila
11	52	38.5	575	10	Q9SLJ7	Q9slj7 arabidopsis
12	51	37.8	427	N	030773	030773 treponema p
13	51	37.8	480	4	Q96F70	Q96f70 homo sapien
14	51	37.8	845	16	083501	083501 treponema p
15	51	37.8	885	4	Q96T95	Q96t95 homo sapien
16	51	37.8	1252	Ŋ	Q9VTY9	Q9vty9 drosophila

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## ALIGNMENTS

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Query Match 100.0%; Score 135; DB 6; Length 149; Best Local Similarity 100.0%; Pred. No. 2.le-11; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ULT 1  OGGMC7 PRELIMINARY; PRT; 149 AA.  OGGMC7; PRELIMINARY; PRT; 149 AA.  OGGMC7; Ol-MAR-2001 (TrEMBLrel. 16, Care ted) Ol-MAR-2001 (TrEMBLrel. 19, Last annotation update) Ol-MAR-2001 (TrEMBLrel. 19, Last annotation update) BCL2-ASSOCIATED PROTEIN BAX (FRAGMENT). BAX.  Ovis aries (Sheep). Covis aries (Sheep). Covis Elharyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota, Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.  NCBL_TaxID-9940;  REL_TaxID-9940;  REL_TaxID-9940;  REL_TaxID-9940;  REL_TaxID-9940;  SEQUENCE FROM N.A.  TISSUE-OVARY; MUTTAY J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.; "Bax in the sheep ovary."; Submitted (JUN-199) to the EMBL/GenBank/DDBJ databases.  EMBL; AF163774; AAF98242.1;  HSSP; O07817, MAF98242.1; HSSP; O07817, MAF98242.1; HSSP; O07817, MAF98242.1;  HSSP; O07817, MAF98242.1;  SMART; SMO0337; BCL:2 family.  InterPro; IPRO02475; BCL:2_family.  PROSITE; PSS0062; BCL:2_FAMILY; 1.  PROSITE; PSS0062; BCL:2_FAMILY; 1.  PROSITE; PS01080; BH1; 1.  NON_TER 149 149  SEQUENCE 149 AA; 16917 MM; ABC10CBB5C64EA2D CRC64;	

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InterPro; IPR000712; Bcl_2.
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SMART; SM00337; BCL; 1.
PR0SITE; PS01080; BCL2_FAMILY; 1.
PR0SITE; PS01080; BH1; 1.
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EMBL; AF007826; AND2706.1; -.
InterPro; IPR00717; BCL2_family.
InterPro; IPR00717; BCL2_family.
Ffam: PF00455; Bcl-2; 1.
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01-JUN-2001 (
BAX EPSILON.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
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HSSP; Q07817; 1MAZ
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MEDLINE-20237095; PubMed-10772918;
Schmitt E., Paquet C., Beauchemin
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-MAY-2000
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                                        5802B0AC73B2E4CE CRC64;
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Best Local S
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Q98U13;
01-JUN-2001
01-JUN-2001
01-DEC-2001
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MEDLINE-21107661; PubMed-11158585;
Finkle1stein C.V., Levellyn A.L., Maller J.L.;
The midblastula transition in Xenopus embryos activates multiple pathways to prevent apoptosis in response to DNA damage.";
Proc. Natl. Acad. Sci. U.S.A. 98:1006-1011(2001).
EMBL: AF288809; ANK06406.1; -.
HSSP: P53563; 1AF3.
InterPro; IPR0007475; BCL2_family.
InterPro; IPR0007475; BCL2_family.
Pfam; PF00475; Bcl-2; 1.
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
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Jin K. He X., Greenberg D.A.,
Submitted (FEB-2000) to the EM
EMBL; AF235993; AAF36411.1; -.
HSSP: Q07817; IMAZ.
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01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BAX PROTEIN SPLICE YARIANT K.
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
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InterPro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl-2; 1.
SMART; SM00337; BCL; 1.
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(TrEMBLiel.
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; Pred. No. 2.6e-11;
0; Mismatches 0;
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Pred. No. 1
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la; Pipoidea; Pipidae;
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Q919N4;
Q1-OCT-2000
Q1-OCT-2000
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PROSITE;
SEQUENCE
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Ol-MAY-2000 (TIEMBLIEL 13,
Ol-MAY-2000 (TIEMBLIEL 13,
OL-JUN-2000 (TIEMBLIEL 14,
BCL2-INTERACTIVE CELL DEATH
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Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID~7955;
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EMBL: AF231015; AAF66960.1; -.
HSSP; P53563; 1AF3.
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MEDLINE-20373792; PubMed-10917738;
Inohara N., Nunez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001
SEQUENCE FROM N.A. MEDLINE=96071131; Meijerink J.P., Sm
                                                                                                                                                                         Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; |
                                                                                                                                                                                                                                                                                                                                       Q9UC27
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InterPro; IPR000712; BCl_2.
Pfam; PF00452; BCl_2; 1.
SMART; SM00337; BCL; 1.
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                                                                                                                                                      NCBI_TaxID=9606;
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E; PS50062; BCL2_FAMILY;
CE 221 AA; 24251 MW;
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with homology to mammalian apoptosis regulators
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| Similarity 76.9%;
| 20; Conservative
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192 AA; 21401 MW;
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                                                                        Smetsers
                                                                      PubMed=7475270;
metsers T.F., Sloetjes
                                                                                                                                                                         Chordata;
Primates;
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Pred. No. 0.00
6; Mismatches
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Pred. No. 2.7e
4; Mismatches
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SUSCEPTIBILITY REGULATOR
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Craniata; Vertebrata;
Teleostei; Euteleostei;
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Catarrhini; Hominidae
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36DBA2E2240793FA CRC64;
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?.7e-07;
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                                 hematological
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01-FEB-1997 (TrEMBLrel. 0:
01-NOV-1999 (TrEMBLrel. 1:
01-DEC-2001 (TrEMBLrel. 1:
89B HELICASE (FRAGMENT).
HEL89B OR CG4261.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-2045581: PubMed-10998336:
Hashimoto Y., Hayakawa T., Ueno Y., Fujita T.,
"Sequence analysis of the Plutella xylostella
Virology 275:358-372(2000).
EMBL. AP270937: AAC27370.1: -.
SEQUENCE 1124 AA: 132875 MW; 83EA3311E4596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plutella xylostella granulovirus.
Viruses; dsDNA viruses, no RNA st
NCBI_TaxID=98383;
                                                                                                                                                 SEQUENCE TRANS INC.
MEDLINE-96371055; PubMed-8774890;
GOldman-Levi R., Miller C., Bogoch J., Zak N.B.;
Goldman-Levi R., Miller C., Bogoch J., Zak n.B.;
"Expanding the Motl subfamily: 89B helicase encodes a new Drosophila
"Expanding the Motl subfamily: 89B helicase encodes a new Drosophila
"Expanding the Motl subfamily: 89B helicase encodes a new Drosophila
"Expanding the Motl subfamily: 89B helicase encodes a new Drosophila
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterryota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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            Goldman-Levi R., Miller C
Submitted (APR-1999) to t
EMBL; U45025; AAB95091.2;
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Nucleic Acids Res. 24:3121-3128(1996)
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15 AA; 1860 MW;
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InterPro;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pfam: PF00176; SNF2_N; 1.
SMARR; SM00487; DEXDC; 1.
SMARR; SM00490; HELICC; 1.
ATP-binding; Helicase,
SEQUENCE 1861 AA; 206155 MW;
                                               030773
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01-JAN-1998
01-JAN-1998
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01-MAY-2000 (TrEMBLrel. 1
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Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,

Rederspiel N.A., Kraujo R., Hulzar L., Rowley D., Buehler E., Dunn i

Gonzalez A., Kremenetskala I., Kim C., Lenz C., Li J., Liu S.,

Luros S., Schwartz J., Shinn P., Torlumi M., Vysotskala V.S.,

Walker M., Yu G., Ecker J., Theologis A., Davis R.H.;

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AG005287, AAD25617.1;

InterPro; IPR00676; NaH, Exchanger.

Ffam. PF00999, Na—H. Exchanger.

SEQUENCE 575 AA; 64043 MN; 49BZE078070EE3D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core et
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL: AE003711; AAF55260.1; ...
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InterPro; IPR001650; Helicase_C
InterPro; IPR000330; SNF2_N.
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Liu S.,
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TP0488,
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Bacteria; Spirocha
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01-NOV-1998
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096F70; O1-DEC-2001 (TEMBLTel. 19, Created)
01-DEC-2001 (TEMBLTel. 19, Last sequence update)
01-DEC-2001 (TEMBLTel. 19, Last annotation update)
SIMILAR TO UNCLEAR ANTIGEN SPI00.
Homo spiens (Human)
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Infect Immun 66:299:3002(1998).
EMBL; AF016689; AAC18612.1;
InterPro; IPR004089; Chemotaxis_transducer.
InterPro; IPR003409; Chemotaxis_transducer.
InterPro; IPR00350; HAMP
InterPro; IPR00350; HAMP
PIGEN; PF00672; HAMP; 1.
Pfam; PF00672; HAMP; 1.
Pfam; PF00612; MCPsignal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-KIDERY, DAR RENAL CELL ADENOCARCINOMA;
Strausberg R.;
SUBmitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; BC011562; AAH11562.1;
EMBL; BC011562; AAH11562.1;
SEQUENCE 480 AA; 53768 MW; 10351A33BF3A4C1
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SMART; SM00283; MA; 1.
SROSITE; PS003007; LECTIN_LEGUME_BETA; UNKNOWN_1.
SEQUENCE 427 AA; 45896 MH; BFDDABC94CBE0C6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treponema pallidum.
Bacteria; Spirochaetales;
NCBI_TaxID=160;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Greene S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular characterization of treponema pallidum mcp2, a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-NICHOLS STRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 33...
pallidum.
Spirochaetales;
                                                                                              B (TrEMBLIEL 08, 08, 08 (TrEMBLIEL 08, 11 (TrEMBLIEL 19, 12) 11 (TrEMBLIEL 19, 12) 12 (TrEMBLIEL 19, 13) 13 (TrEMBLIEL 19, 13) 14 (TrEMBLIEL 19, 14) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (TrEMBLIEL 19, 15) 15 (T
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Primates;
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Spirochaetaceae;
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                                                                                              Created)
Last sequence update)
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PROTEIN (MCP2-1).
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Pred. No. 39;
4; Mismatches
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Pred. No. 45;
10; Mismatches
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                                                                                                                                                                                                                                                                    PRT;
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    Treponema
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Best Local S
Matches 10
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Best Local 9
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01-DEC-2001
01-DEC-2001
01-DEC-2001
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Complete
SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98332770; PubMed-9665876;
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                                  DISTRRINECISPVANEMNHLPAHSHDLQR
                                                                                                                                                                                                Similarity
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845 AA; 91517 MW;
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(TremBLrel. 19, Last seq
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                                                                                                                                                                      Conservative
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Pred.
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밁 QV.

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SEDUENCE FROM N.A.

SEDUENCE FROM N.A.

MEDLINE-21214370; PubMed-11313457;

Seeler J.S. Marchio A., Losson R., Desterro J.

Seeler J.S. Marchio A., Losson R., Desterro J.

Chambon properties of nuclear protein SP100 an factor: role of SUMO modification.",

MOI. Cell. Biol. 21:3314-324(2001).

EMBL: APS5565; AAKS1202.1:

EMBL: APS5565; AAKS1202.1:

SEQUENCE 885 AA; 101544 MW; 3D33A46EA871CF
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Piam; PE0243; Cache; 1.
Piam; PE00672; HAMP; 1.
Piam; PE00015; MCPSignal; 1.
SMARP; SM00304; HAMP; 1.
SMARP; SM00283; MA; 1.
PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
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Science 281:375-388(1998).
EMBL: AB00125: AAC65475.1: ...
MEXOPS: 538.UPW: ...
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DASTKKLSECLKRIGDELD ---- SNMELOR 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR004010; Cache.
IPR004089; Chemotaxis_transducer.
IPR003660; HAMP.
                                               Score 51; DB
Pred. NO. 85;
10; Mismatches
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Last annotation update)
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